



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 10:58 pm BST

PDB ID : 5L6K
Title : Crystal Structure of Human Carbonic Anhydrase II in Complex with a Quino-
line Oligoamide Foldamer
Authors : Jewginski, M.; Langlois d'Estaintot, B.; Granier, T.; Huc, Y.
Deposited on : 2016-05-30
Resolution : 1.70 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

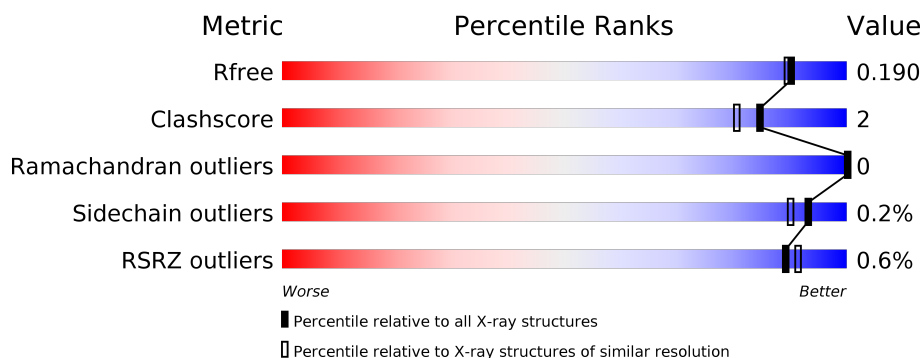
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

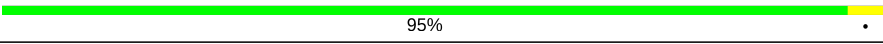
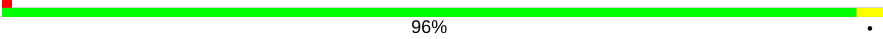
The reported resolution of this entry is 1.70 Å.

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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	260	 95%
1	B	260	 96%

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 4929 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.

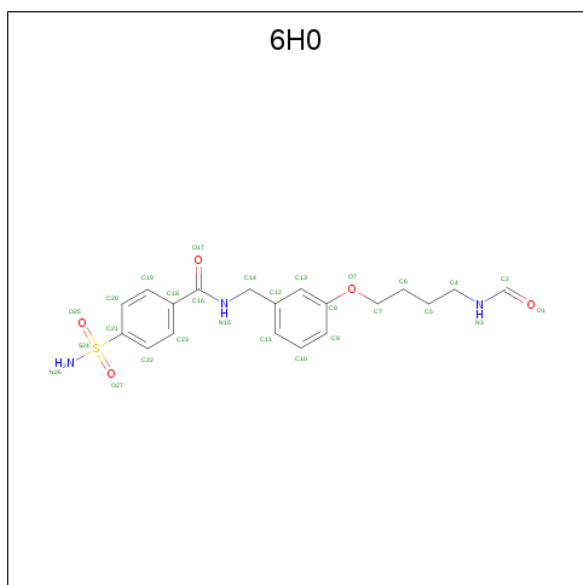
- Molecule 1 is a protein called Carbonic anhydrase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	8	0
			2094	1351	358	383	2			
1	B	259	Total	C	N	O	S	0	6	0
			2081	1342	355	382	2			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

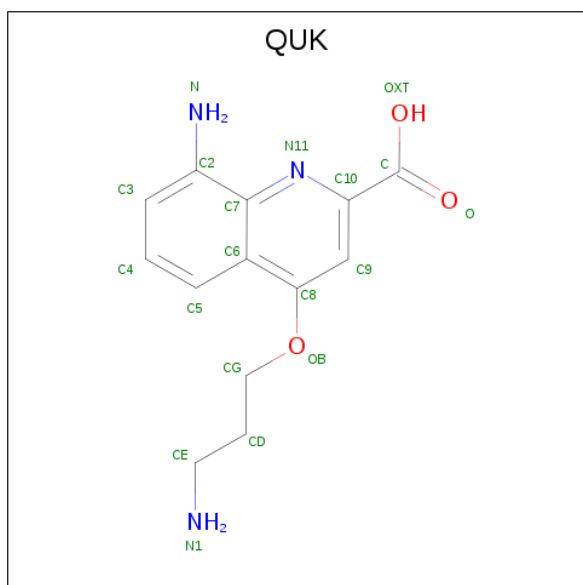
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is {N}-[[3-(4-formamidobutoxy)phenyl]methyl]-4-sulfamoyl-benzamide (three-letter code: 6H0) (formula: C₁₉H₂₃N₃O₅S).



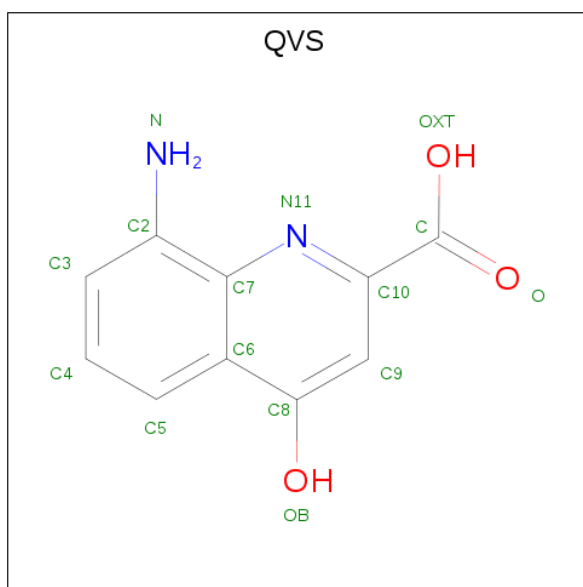
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			28	19	3	5	1		
3	B	1	Total	C	N	O	S	0	0
			28	19	3	5	1		

- Molecule 4 is 8-azanyl-4-(3-azanylpropoxy)quinoline-2-carboxylic acid (three-letter code: QUK) (formula: C₁₃H₁₅N₃O₃).



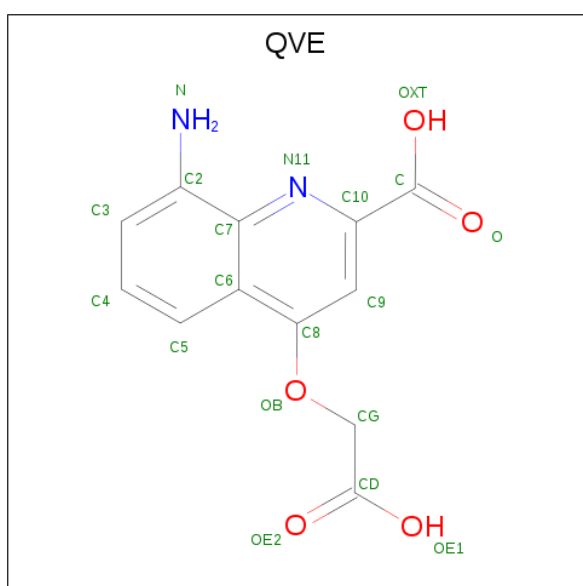
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O		0	0
			17	13	2	2			
4	A	1	Total	C	N	O		0	1
			14	10	2	2			
4	B	1	Total	C	N	O		0	0
			17	13	2	2			
4	B	1	Total	C	N	O		0	1
			14	10	2	2			

- Molecule 5 is 8-azanyl-4-oxidanyl-quinoline-2-carboxylic acid (three-letter code: QVS) (formula: C₁₀H₈N₂O₃).



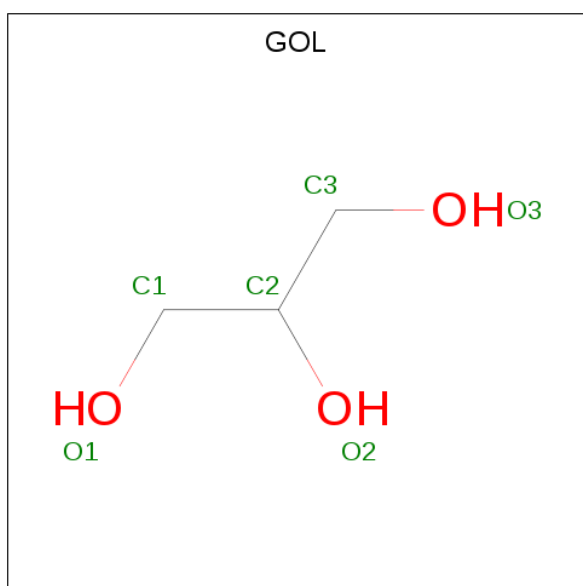
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	10	2	2		
5	A	1	Total	C	N	O	0	1
			14	10	2	2		
5	B	1	Total	C	N	O	0	1
			14	10	2	2		
5	B	1	Total	C	N	O	0	0
			14	10	2	2		

- Molecule 6 is 8-azanyl-4-(2-hydroxy-2-oxoethoxy)quinoline-2-carboxylic acid (three-letter code: QVE) (formula: C₁₂H₁₀N₂O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			19	12	2	5		
6	A	1	Total	C	N	O	0	1
			19	12	2	5		
6	B	1	Total	C	N	O	0	0
			19	12	2	5		
6	B	1	Total	C	N	O	0	1
			15	10	2	3		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



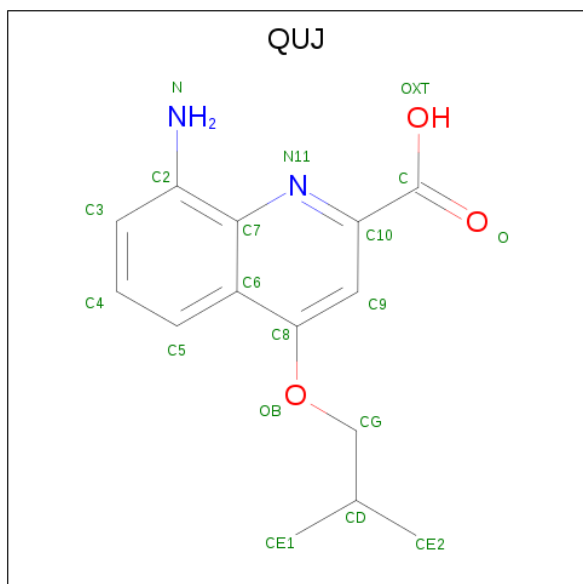
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	1
			3	2	1		
8	B	1	Total	C	O	0	1
			7	4	3		

- Molecule 9 is 8-azanyl-4-(2-methylpropoxy)quinoline-2-carboxylic acid (three-letter code: QUJ) (formula: $C_{14}H_{16}N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	1
			18	14	2	2		

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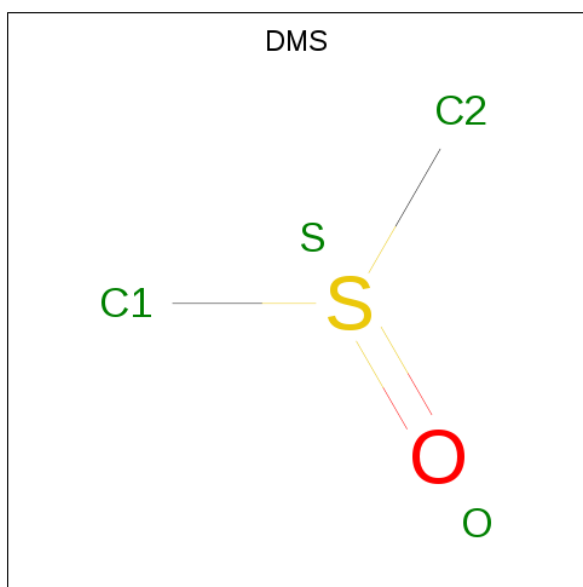
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			17	13	2	2		
9	B	1	Total	C	N	O	0	0
			17	13	2	2		
9	B	1	Total	C	N	O	0	1
			18	14	2	2		

- Molecule 10 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	Na	0	0
			1	1		

- Molecule 11 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	229	Total	O	0	0
			229	229		
12	B	168	Total	O	0	0
			168	168		

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: Carbonic anhydrase 2

Chain A:  95%



- Molecule 1: Carbonic anhydrase 2

Chain B:  96%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.07Å 84.87Å 77.22Å 90.00° 97.81° 90.00°	Depositor
Resolution (Å)	76.50 – 1.70 56.82 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (76.50-1.70) 99.7 (56.82-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.154 , 0.181 0.163 , 0.190	Depositor DCC
R_{free} test set	3137 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	19.7	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4929	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.03% 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: GOL, ZN, NA, 6H0, PG4, DMS, QVE, QUK, QUJ, QVS

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	0.89	2/2178 (0.1%)	0.96	3/2956 (0.1%)
1	B	0.82	1/2162 (0.0%)	0.91	0/2934
All	All	0.86	3/4340 (0.1%)	0.94	3/5890 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	196	SER	CA-CB	5.89	1.61	1.52
1	A	219	SER	CB-OG	-5.06	1.35	1.42
1	A	51	TYR	CG-CD1	5.00	1.45	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	ARG	NE-CZ-NH1	5.75	123.18	120.30
1	A	51	TYR	CB-CG-CD1	5.19	124.11	121.00
1	A	138	ASP	CB-CG-OD1	5.09	122.88	118.30

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	2094	0	2043	7	0
1	B	2081	0	2042	4	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	28	0	0	0	0
3	B	28	0	0	0	0
4	A	31	0	0	0	0
4	B	31	0	0	1	0
5	A	28	0	0	3	0
5	B	28	0	0	2	0
6	A	38	0	0	0	0
6	B	34	0	0	1	0
7	A	12	0	16	0	0
7	B	12	0	16	0	0
8	A	3	0	0	4	0
8	B	7	0	6	3	0
9	A	35	0	0	2	0
9	B	35	0	0	1	0
10	A	1	0	0	0	0
11	A	4	0	6	0	0
12	A	229	0	0	6	0
12	B	168	0	0	1	0
All	All	4929	0	4129	20	1

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 2.

The worst 5 of 20 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)
8:A:310[B]:PG4:C2	5:A:312[B]:QVS:C3	2.60	0.80
8:A:310[B]:PG4:C2	5:A:312[B]:QVS:C2	2.65	0.75
1:A:17[A]:HIS:HE1	12:A:408:HOH:O	1.74	0.71
1:A:45:LYS:NZ	12:A:403:HOH:O	2.29	0.66
1:A:135:GLN:NE2	12:A:404:HOH:O	2.32	0.62

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:ASP:OD2	1:B:74:GLN:NE2[1_655]	2.18	0.02

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 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	265/260 (102%)	260 (98%)	5 (2%)	0	100	100
1	B	263/260 (101%)	257 (98%)	6 (2%)	0	100	100
All	All	528/520 (102%)	517 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	225/225 (100%)	224 (100%)	1 (0%)	91	87
1	B	227/225 (101%)	227 (100%)	0	100	100
All	All	452/450 (100%)	451 (100%)	1 (0%)	93	90

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

Of 28 ligands modelled in this entry, 3 are monoatomic - leaving 25 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 > 2$
6	QVE	A	305	5	14,20,20	0.96	1 (7%)	18,28,28	2.52	4 (22%)
7	GOL	B	312	-	5,5,5	0.15	0	5,5,5	0.98	0
7	GOL	A	308	-	5,5,5	0.29	0	5,5,5	0.35	0
8	PG4	B	302[A]	9	6,6,12	1.50	1 (16%)	5,5,11	1.30	0
4	QUK	A	306[A]	9,5	15,15,20	2.14	2 (13%)	19,21,27	2.18	4 (21%)
3	6H0	B	306	9,2	29,29,29	1.45	5 (17%)	37,38,38	1.20	3 (8%)
9	QUJ	A	311[B]	8,4	19,19,20	2.30	1 (5%)	23,26,28	1.76	6 (26%)
7	GOL	A	309	-	5,5,5	0.57	0	5,5,5	0.86	0
5	QVS	A	304	4,6	15,15,16	2.27	2 (13%)	19,21,23	2.42	5 (26%)
9	QUJ	B	301	3,4	18,18,20	1.96	2 (11%)	21,24,28	2.35	4 (19%)
4	QUK	B	307	9,5	18,18,20	1.64	1 (5%)	21,24,27	2.61	6 (28%)
6	QVE	B	311[B]	5	13,16,20	1.07	0	17,23,28	1.68	3 (17%)
9	QUJ	A	315	3,4	18,18,20	2.00	2 (11%)	21,24,28	2.77	6 (28%)
3	6H0	A	302	9,2	29,29,29	1.56	4 (13%)	37,38,38	1.92	6 (16%)
5	QVS	A	312[B]	4,6	15,15,16	2.31	2 (13%)	19,21,23	1.87	4 (21%)
5	QVS	B	304[A]	4,6	15,15,16	2.20	1 (6%)	19,21,23	2.10	6 (31%)
9	QUJ	B	303[A]	8,4	19,19,20	2.15	2 (10%)	23,26,28	1.72	3 (13%)
8	PG4	A	310[B]	9	2,2,12	1.58	0	1,1,11	0.70	0
6	QVE	A	307[A]	5	14,20,20	1.12	1 (7%)	18,28,28	1.63	5 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	QUK	A	303	9,5	18,18,20	1.80	2 (11%)	21,24,27	2.39	5 (23%)
7	GOL	B	313	-	5,5,5	0.25	0	5,5,5	0.90	0
5	QVS	B	308	4,6	15,15,16	1.89	1 (6%)	19,21,23	2.33	6 (31%)
6	QVE	B	309	5	14,20,20	0.95	0	18,28,28	2.10	4 (22%)
4	QUK	B	310[B]	9,5	15,15,20	2.50	1 (6%)	19,21,27	1.97	3 (15%)
11	DMS	A	314	-	3,3,3	0.48	0	3,3,3	0.88	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	QVE	A	305	5	-	3/3/9/9	0/2/2/2
7	GOL	B	312	-	-	2/4/4/4	-
7	GOL	A	308	-	-	0/4/4/4	-
8	PG4	B	302[A]	9	-	3/4/4/10	-
4	QUK	A	306[A]	9,5	-	2/2/2/9	0/2/2/2
3	6H0	B	306	9,2	-	6/23/23/23	0/2/2/2
9	QUJ	A	311[B]	8,4	-	4/7/7/9	0/2/2/2
7	GOL	A	309	-	-	0/4/4/4	-
5	QVS	A	304	4,6	-	0/2/2/4	0/2/2/2
9	QUJ	B	301	3,4	-	1/6/6/9	0/2/2/2
4	QUK	B	307	9,5	-	2/6/6/9	0/2/2/2
6	QVE	B	311[B]	5	-	0/0/4/9	0/2/2/2
9	QUJ	A	315	3,4	-	0/6/6/9	0/2/2/2
3	6H0	A	302	9,2	-	5/23/23/23	0/2/2/2
5	QVS	A	312[B]	4,6	-	0/2/2/4	0/2/2/2
5	QVS	B	304[A]	4,6	-	0/2/2/4	0/2/2/2
9	QUJ	B	303[A]	8,4	-	4/7/7/9	0/2/2/2
6	QVE	A	307[A]	5	-	1/3/9/9	0/2/2/2
4	QUK	A	303	9,5	-	3/6/6/9	0/2/2/2
7	GOL	B	313	-	-	0/4/4/4	-
5	QVS	B	308	4,6	-	0/2/2/4	0/2/2/2
6	QVE	B	309	5	-	0/3/9/9	0/2/2/2
4	QUK	B	310[B]	9,5	-	0/2/2/9	0/2/2/2

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	311[B]	QUJ	C10-C	-8.96	1.39	1.48
4	B	310[B]	QUK	C10-C	-8.64	1.39	1.48
5	A	304	QVS	C10-C	-8.17	1.40	1.48
9	B	303[A]	QUJ	C10-C	-8.12	1.40	1.48
5	A	312[B]	QVS	C10-C	-7.72	1.40	1.48

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	315	QUJ	C10-N11-C7	9.21	125.10	118.11
4	B	307	QUK	C10-N11-C7	8.22	124.34	118.11
4	A	303	QUK	C10-N11-C7	7.14	123.52	118.11
6	A	305	QVE	C10-N11-C7	7.07	123.68	118.26
9	B	301	QUJ	C10-N11-C7	6.45	123.00	118.11

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	312	GOL	O1-C1-C2-O2
7	B	312	GOL	O1-C1-C2-C3
4	A	306[A]	QUK	O-C-C10-N11
4	A	306[A]	QUK	O-C-C10-C9
9	A	311[B]	QUJ	O-C-C10-C9

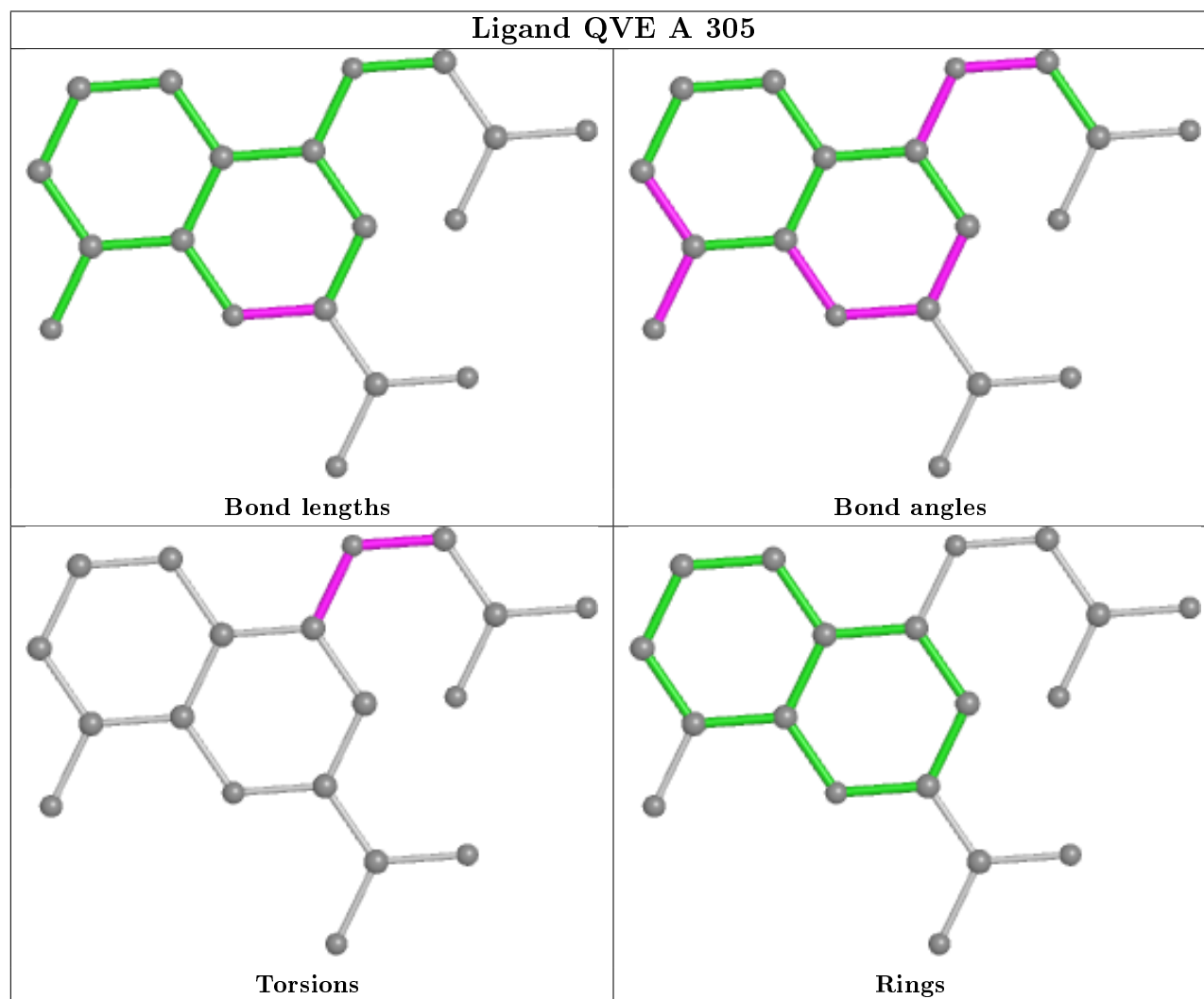
There are no ring outliers.

8 monomers are involved in 9 short contacts:

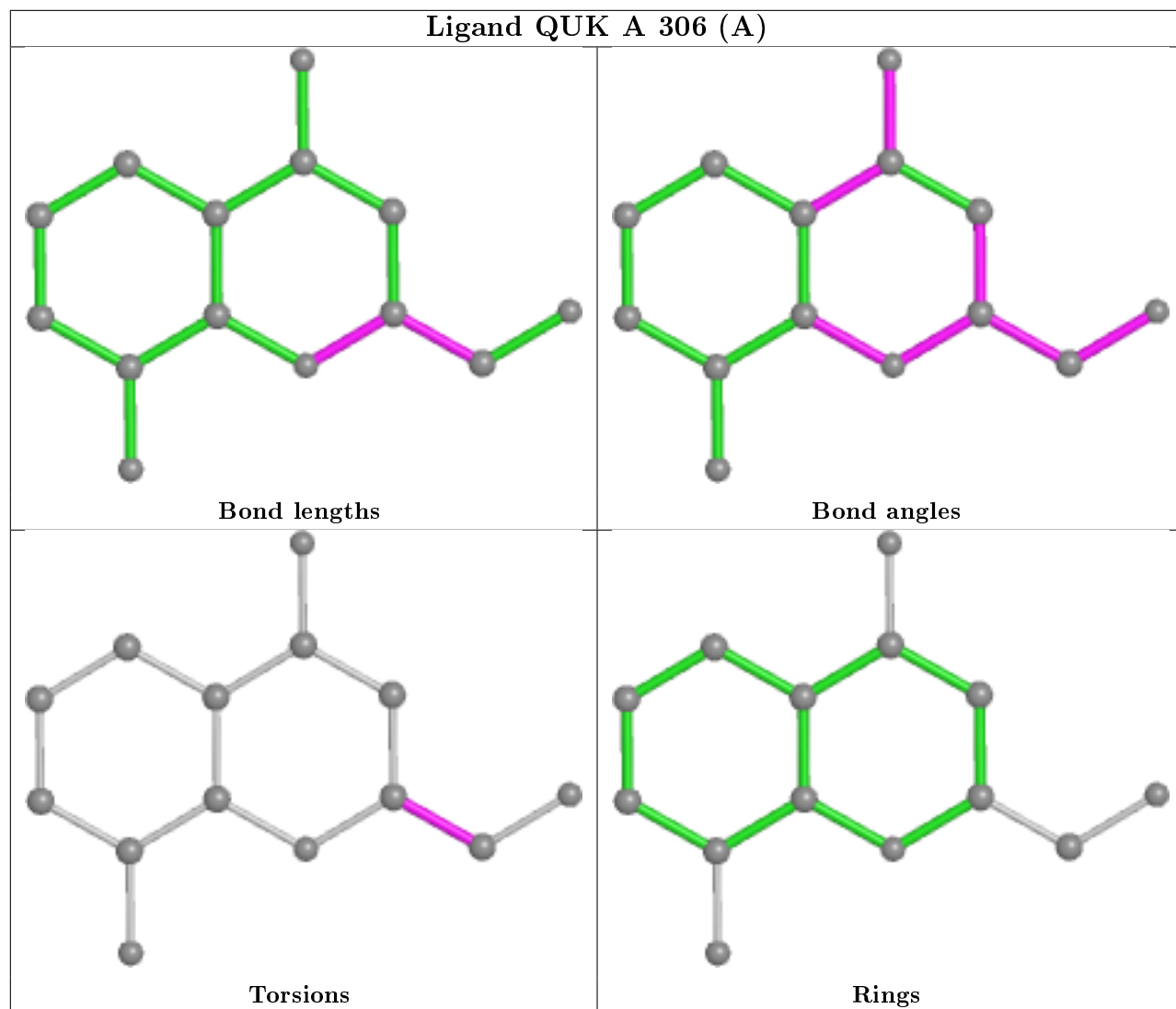
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	302[A]	PG4	3	0
9	A	311[B]	QUJ	2	0
6	B	311[B]	QVE	1	0
5	A	312[B]	QVS	3	0
5	B	304[A]	QVS	2	0
9	B	303[A]	QUJ	1	0
8	A	310[B]	PG4	4	0
4	B	310[B]	QUK	1	0

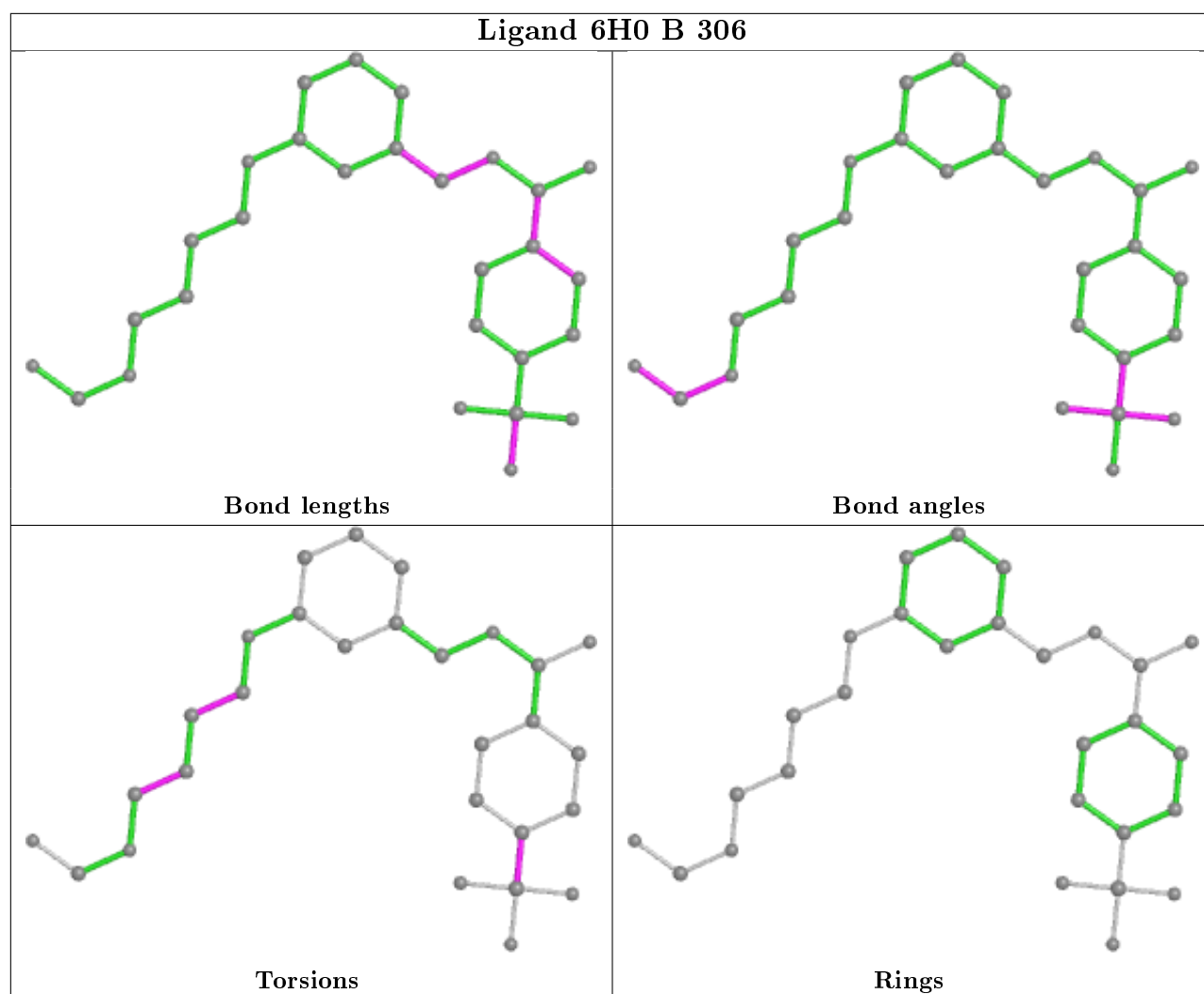
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

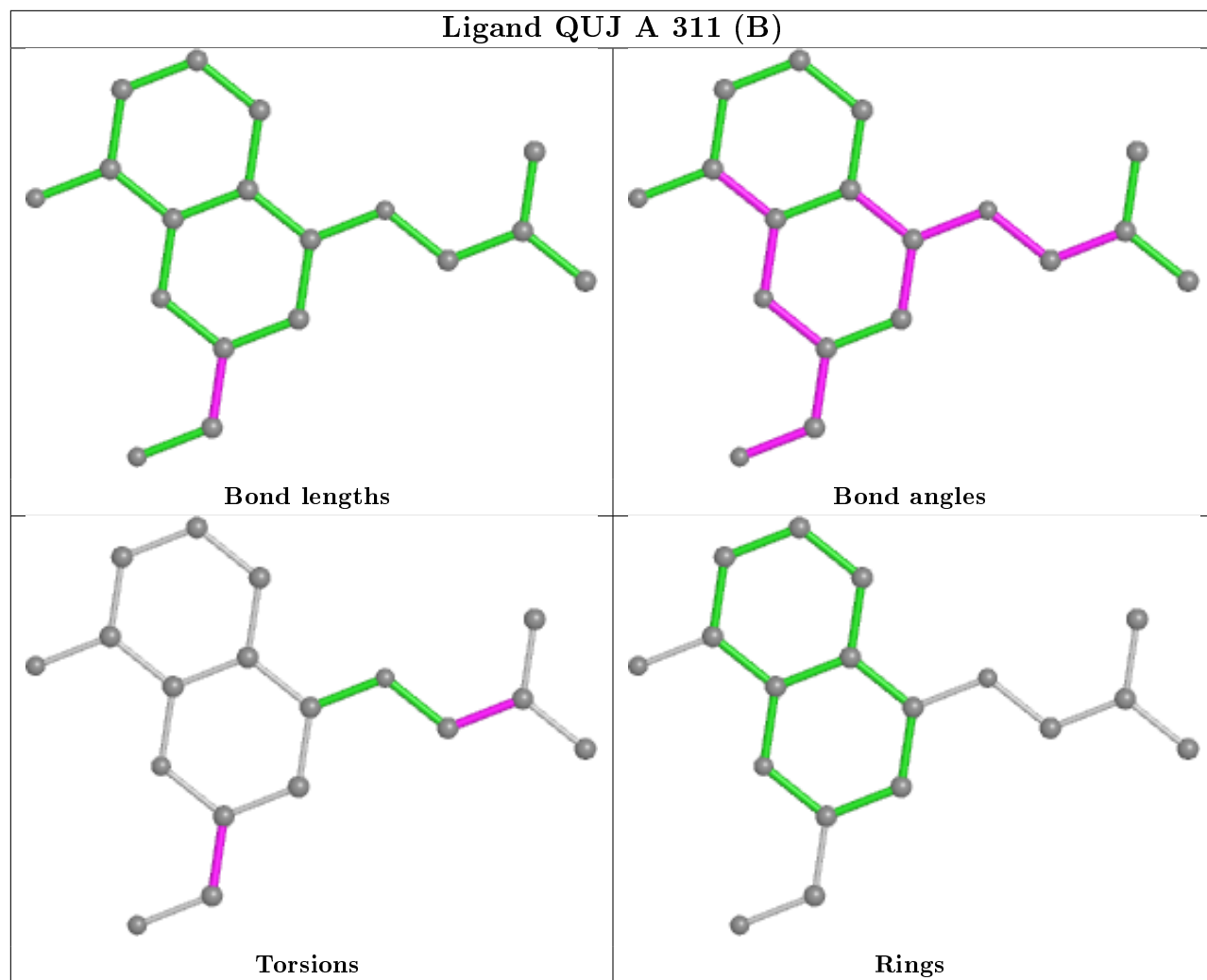


Ligand QUK A 306 (A)

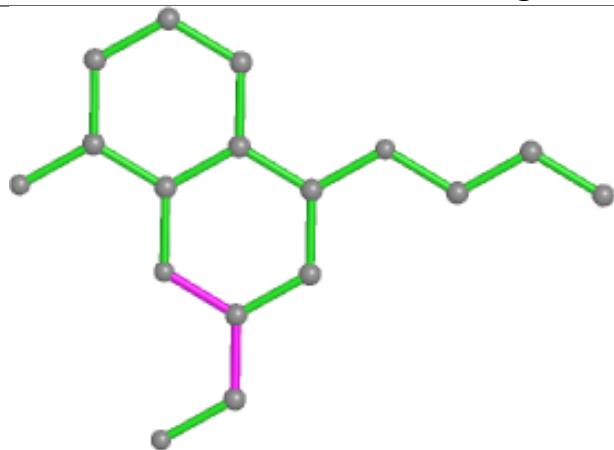




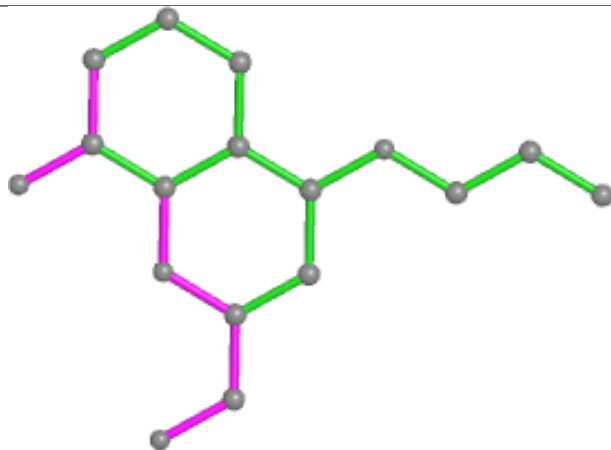
Ligand QUJ A 311 (B)



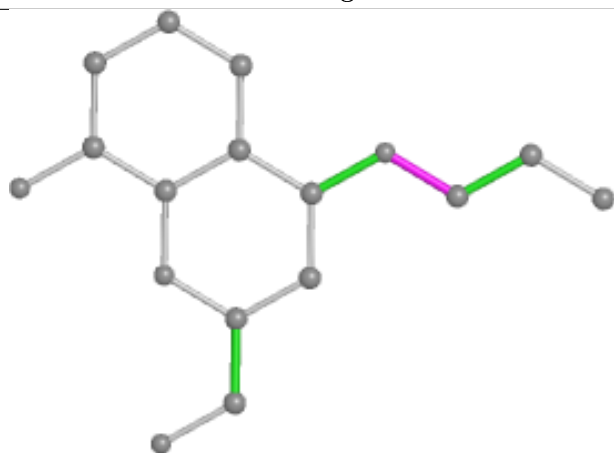
Ligand QUJ B 301



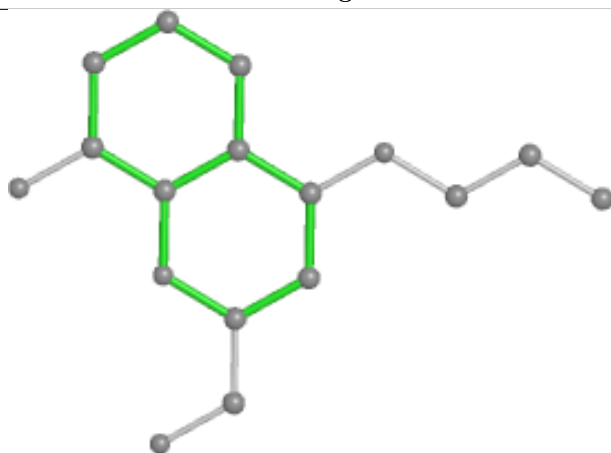
Bond lengths



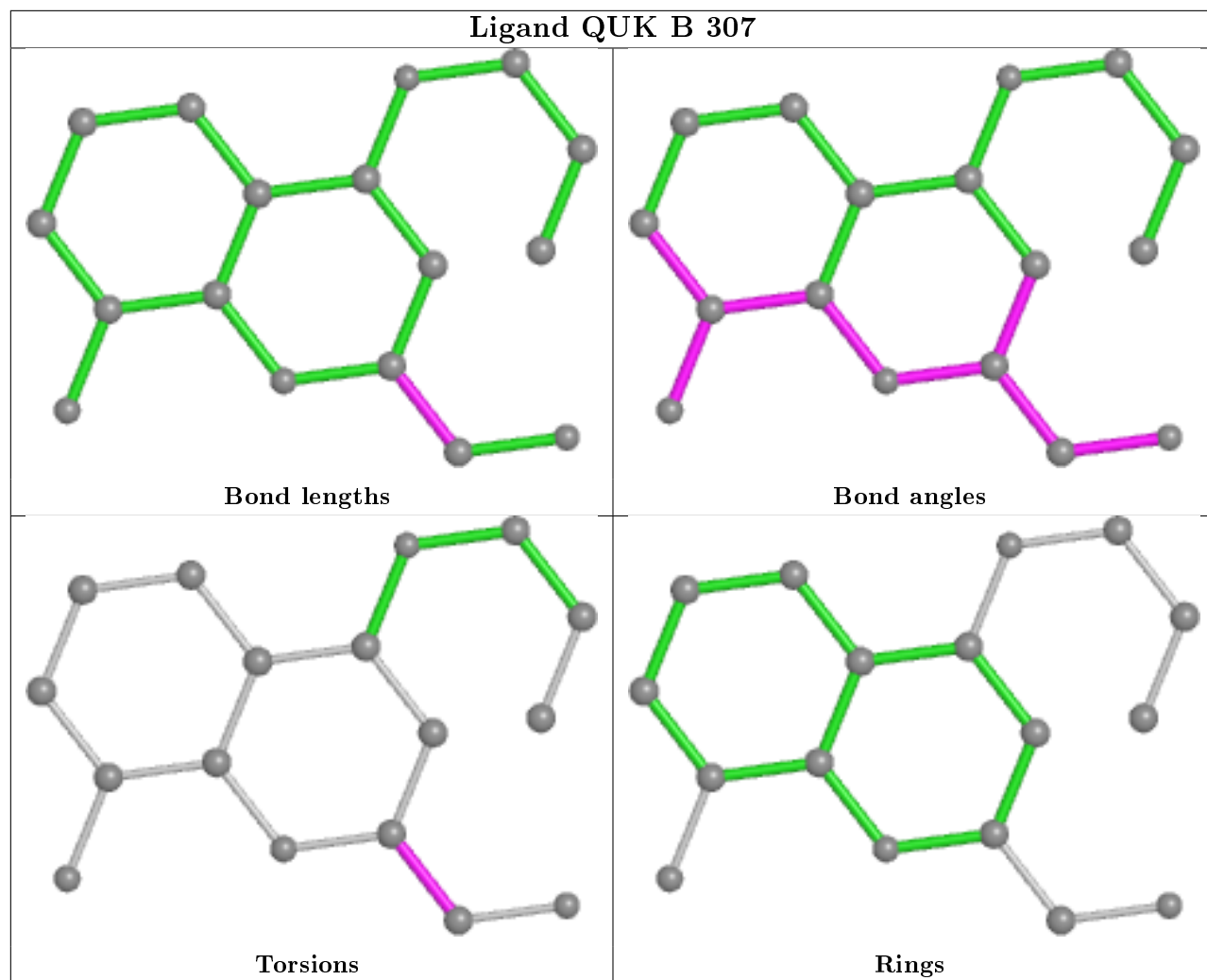
Bond angles



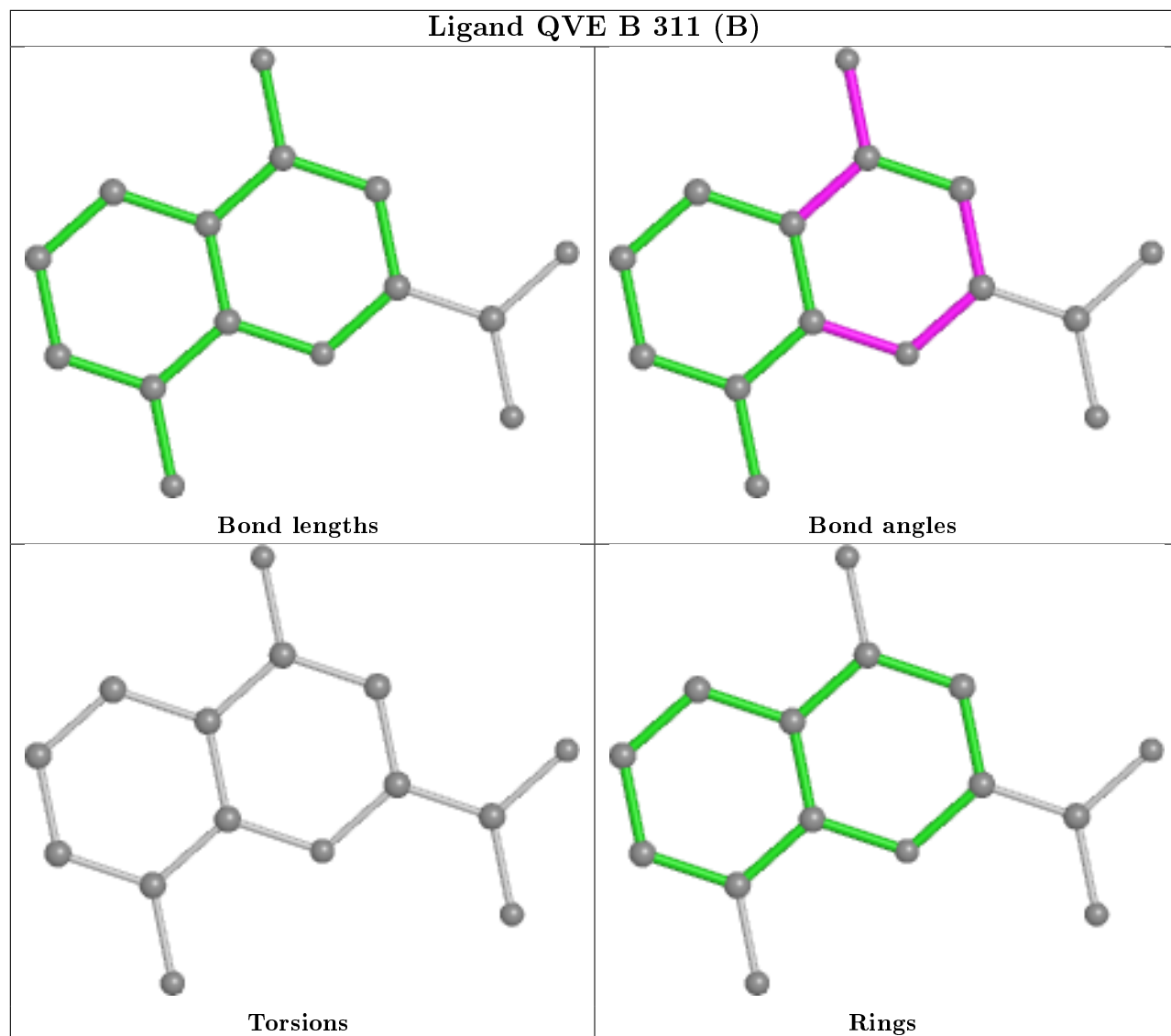
Torsions



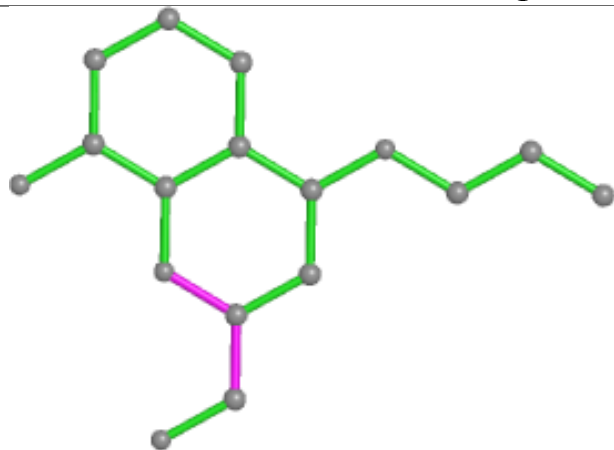
Rings



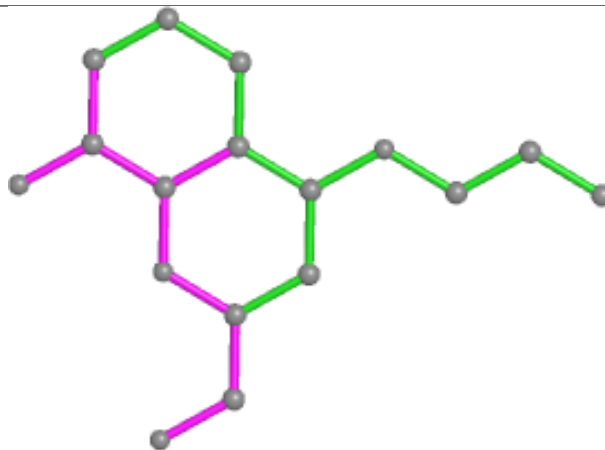
Ligand QVE B 311 (B)



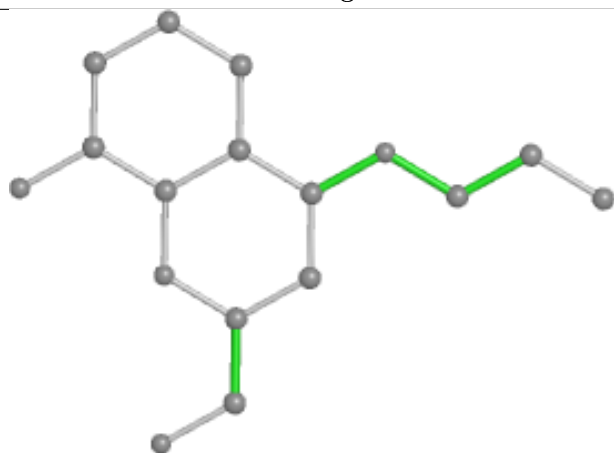
Ligand QUJ A 315



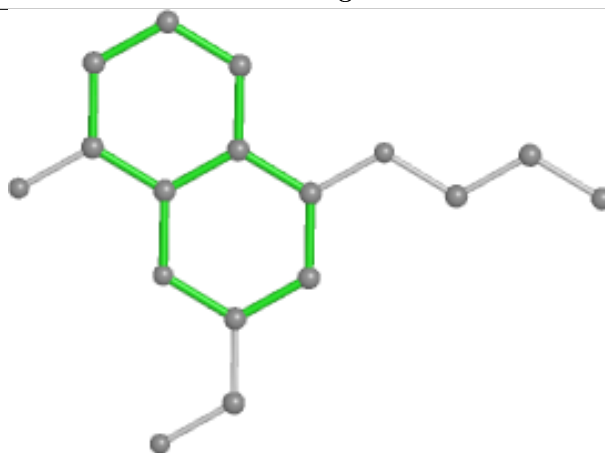
Bond lengths



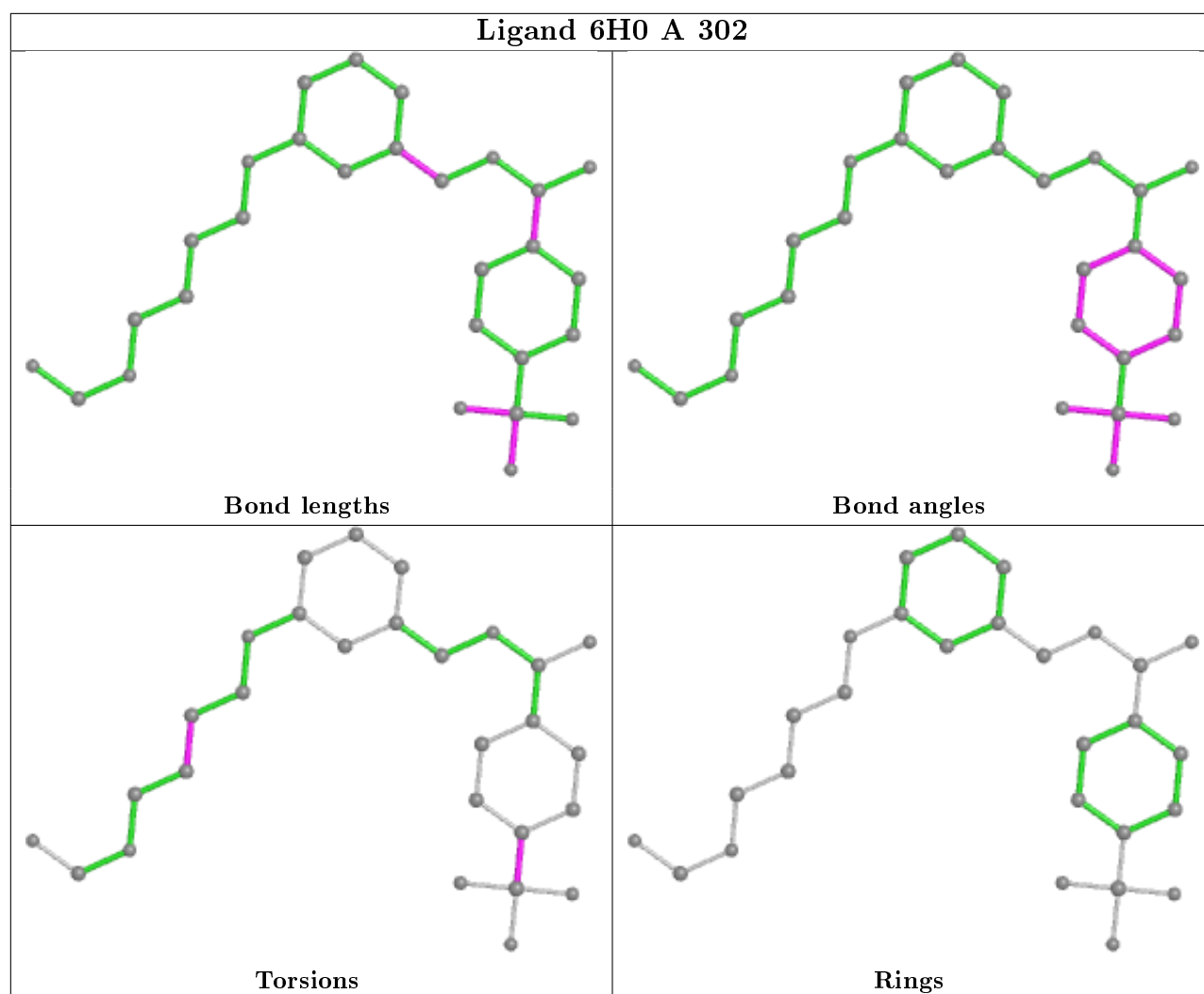
Bond angles



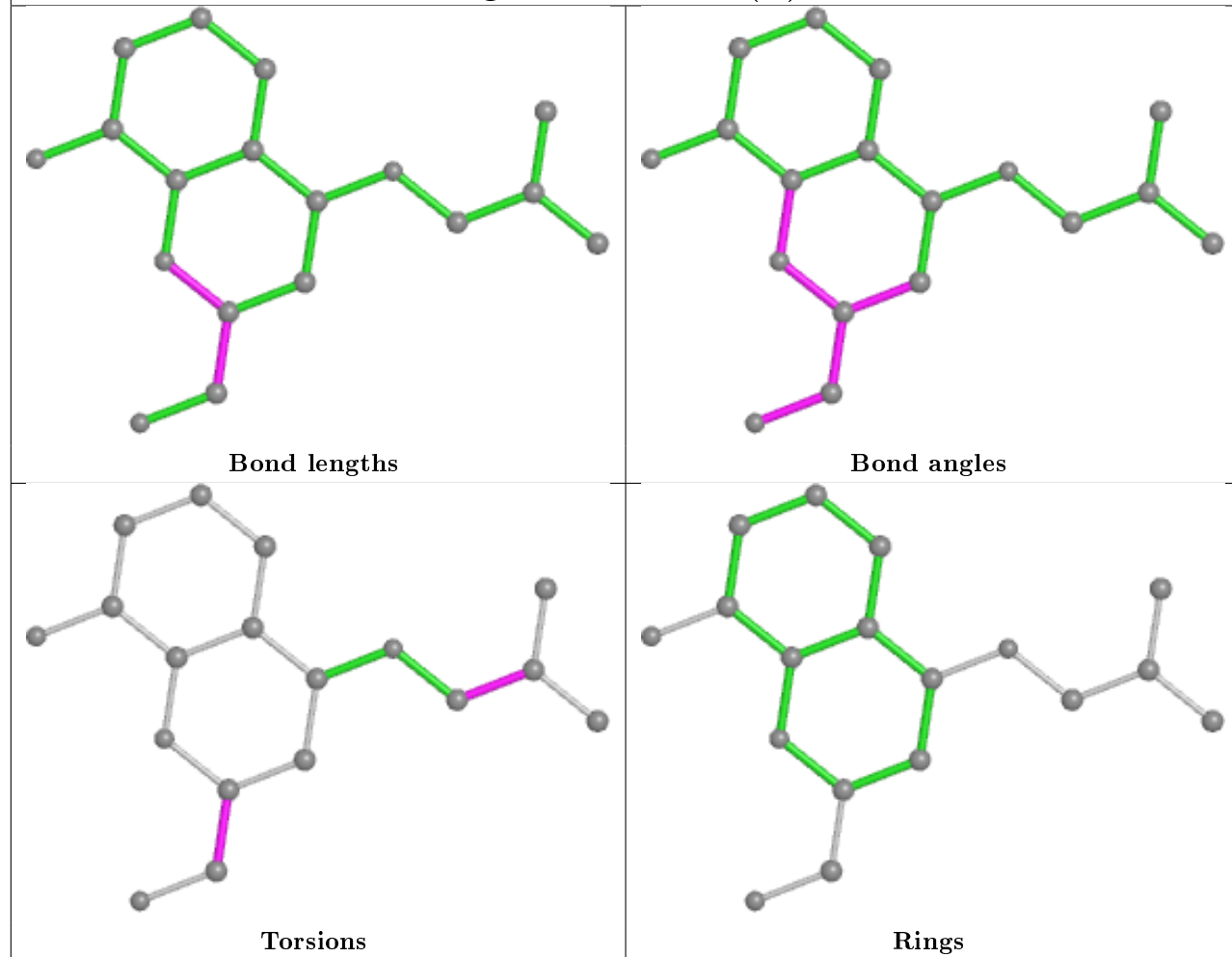
Torsions

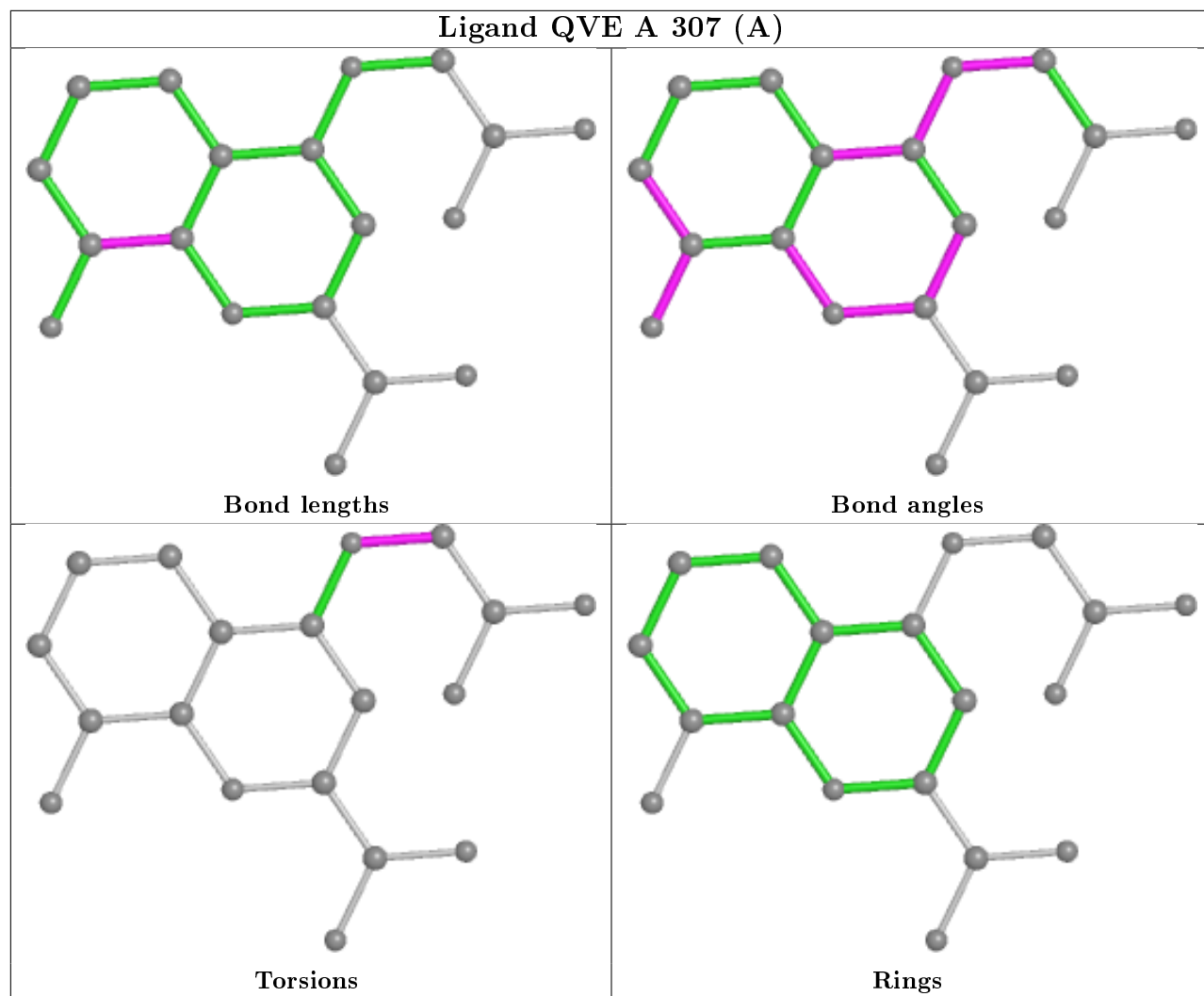


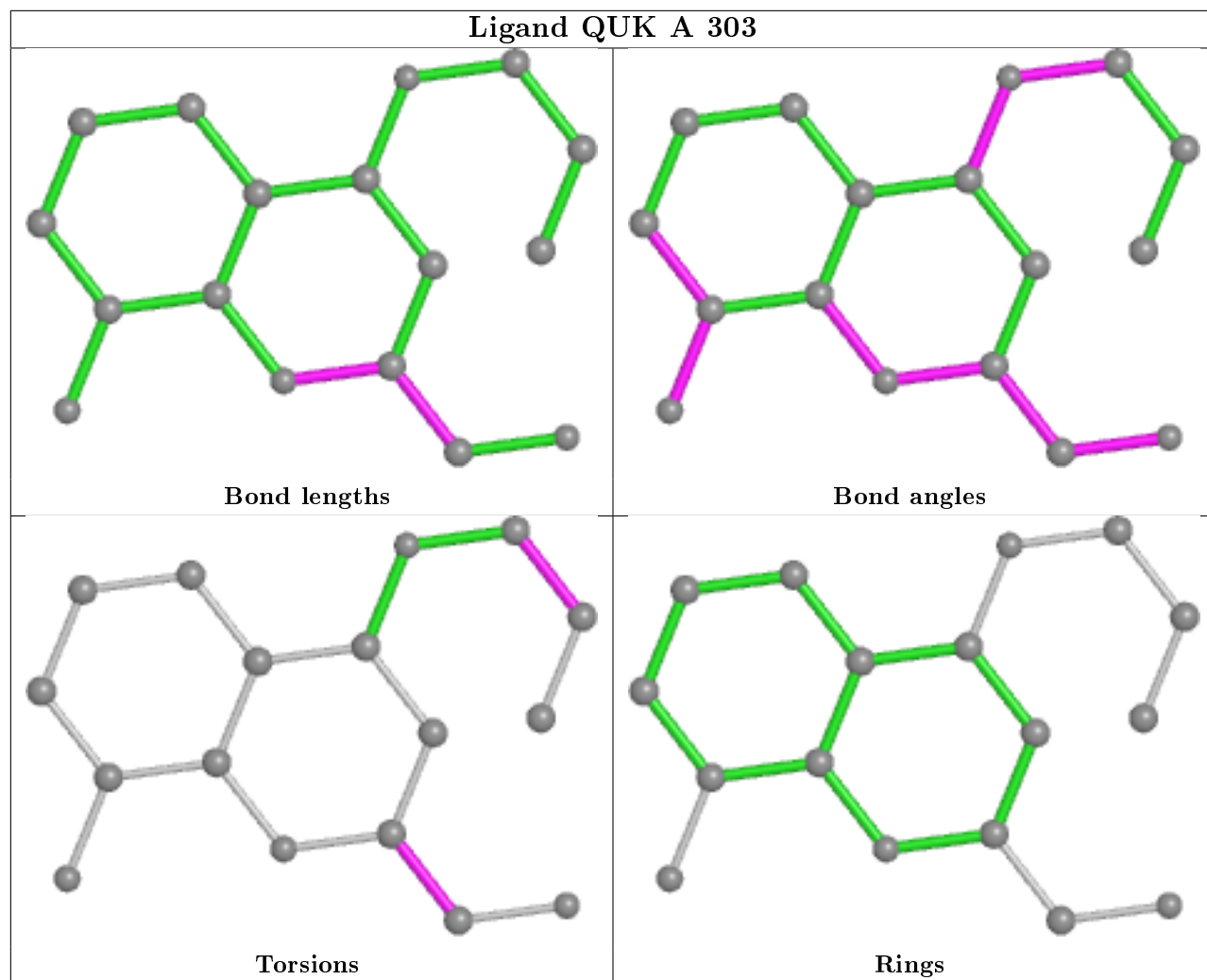
Rings

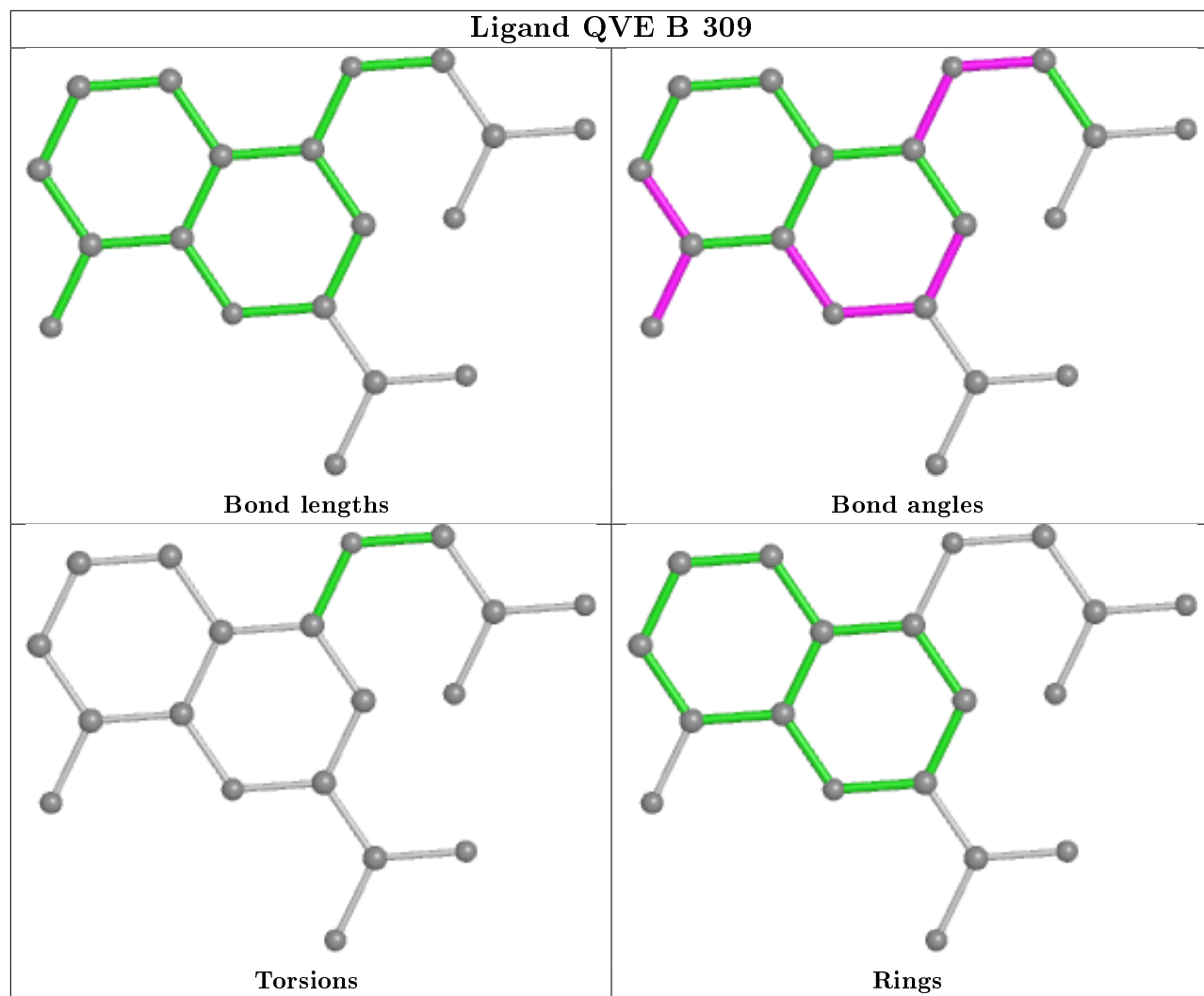


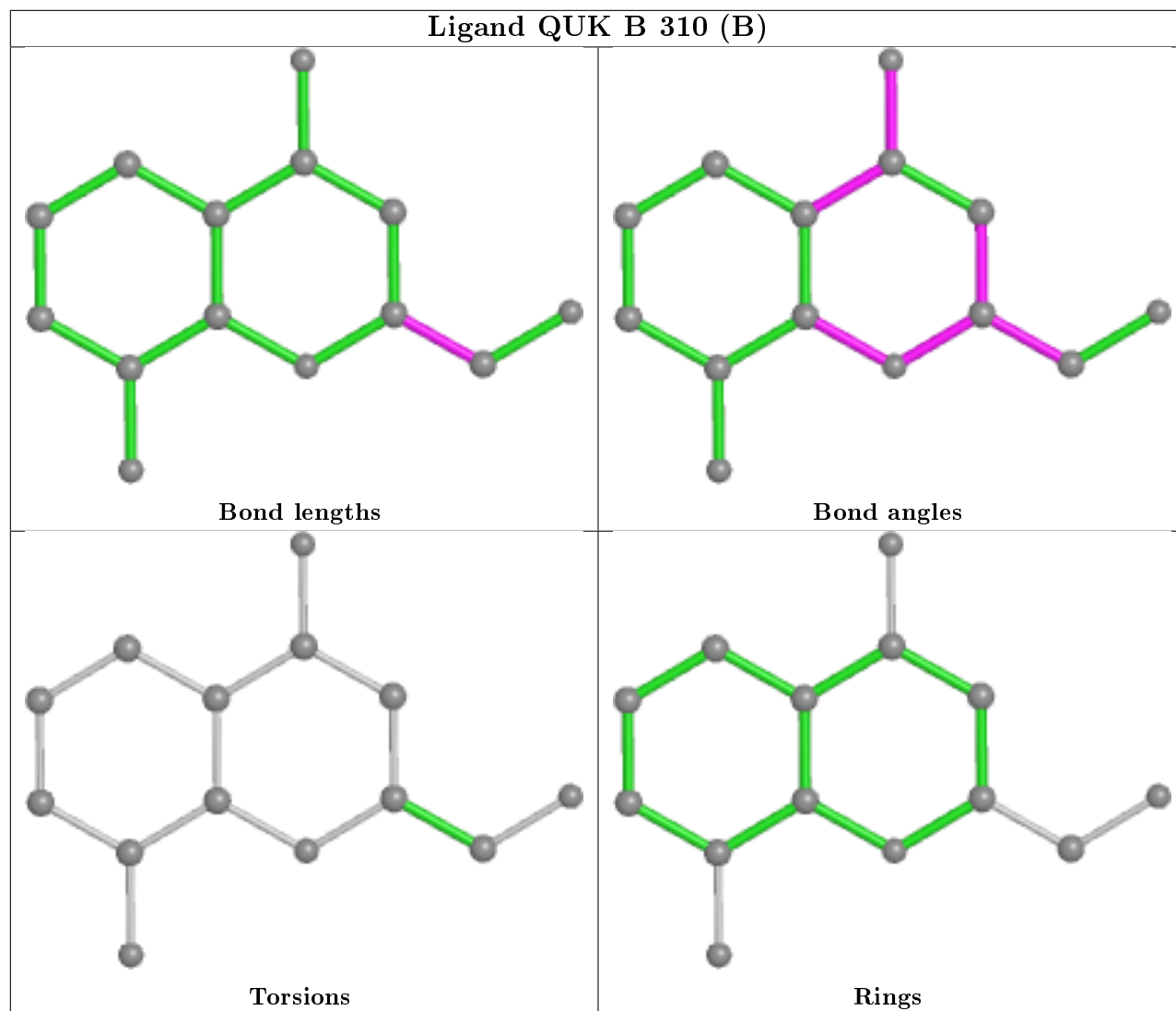
Ligand QUJ B 303 (A)











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	259/260 (99%)	-0.33	0 100 100	12, 20, 39, 64	0
1	B	259/260 (99%)	-0.25	3 (1%) 79 82	14, 24, 43, 76	0
All	All	518/520 (99%)	-0.29	3 (0%) 89 91	12, 22, 42, 76	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	10	HIS	3.4
1	B	234	GLY	3.0
1	B	236	PRO	2.1

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
11	DMS	A	314	4/4	0.85	0.14	30,33,54,92	0
7	GOL	B	313	6/6	0.87	0.15	30,37,54,54	0

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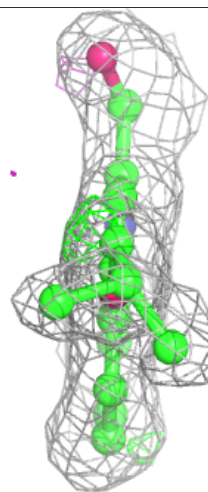
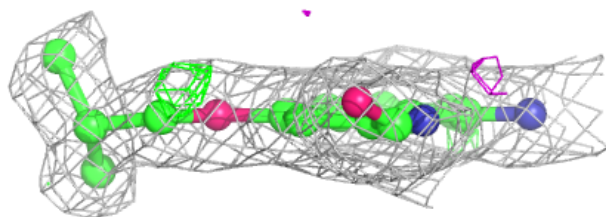
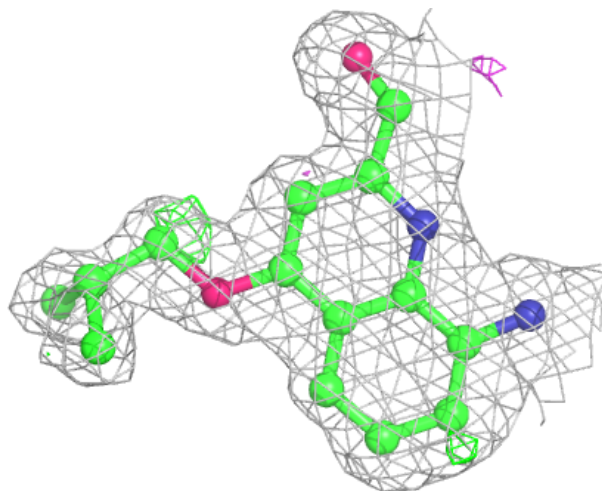
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	PG4	B	302[A]	7/13	0.89	0.17	24,30,45,49	7
7	GOL	A	309	6/6	0.90	0.12	24,30,37,50	0
9	QUJ	B	303[A]	18/19	0.91	0.12	13,16,23,23	18
4	QUK	A	306[A]	14/19	0.92	0.09	12,18,22,24	14
6	QVE	A	307[A]	19/19	0.92	0.10	10,17,30,31	19
7	GOL	B	312	6/6	0.93	0.12	25,30,31,42	0
9	QUJ	A	311[B]	18/19	0.93	0.12	17,29,38,45	18
6	QVE	A	305	19/19	0.93	0.09	22,28,62,79	0
9	QUJ	A	315	17/19	0.93	0.10	19,23,40,41	0
10	NA	A	313	1/1	0.94	0.10	44,44,44,44	0
6	QVE	B	309	19/19	0.94	0.10	18,23,39,44	0
8	PG4	A	310[B]	3/13	0.95	0.10	37,37,39,45	3
4	QUK	B	310[B]	14/19	0.95	0.10	22,34,43,51	14
4	QUK	A	303	17/19	0.95	0.08	20,25,42,45	0
5	QVS	A	304	14/15	0.96	0.07	17,19,25,25	0
5	QVS	A	312[B]	14/15	0.96	0.14	20,36,46,48	14
5	QVS	B	304[A]	14/15	0.96	0.07	12,18,23,26	14
9	QUJ	B	301	17/19	0.96	0.08	16,21,37,42	0
4	QUK	B	307	17/19	0.96	0.07	20,23,36,40	0
6	QVE	B	311[B]	15/19	0.96	0.10	22,30,40,46	15
7	GOL	A	308	6/6	0.97	0.09	16,17,19,21	0
3	6H0	A	302	28/28	0.97	0.09	10,17,24,28	0
3	6H0	B	306	28/28	0.97	0.09	15,20,33,40	0
5	QVS	B	308	14/15	0.97	0.07	11,16,22,23	0
2	ZN	B	305	1/1	0.99	0.09	16,16,16,16	0
2	ZN	A	301	1/1	0.99	0.11	12,12,12,12	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.

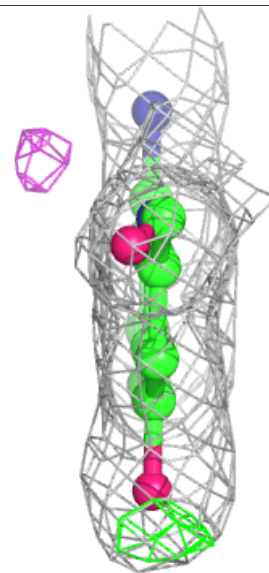
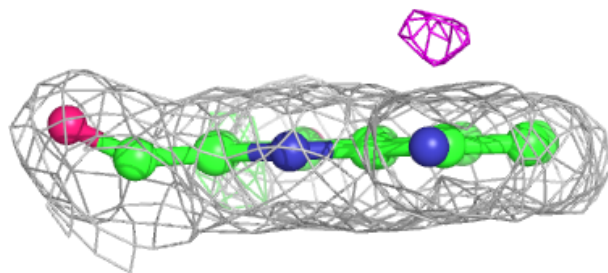
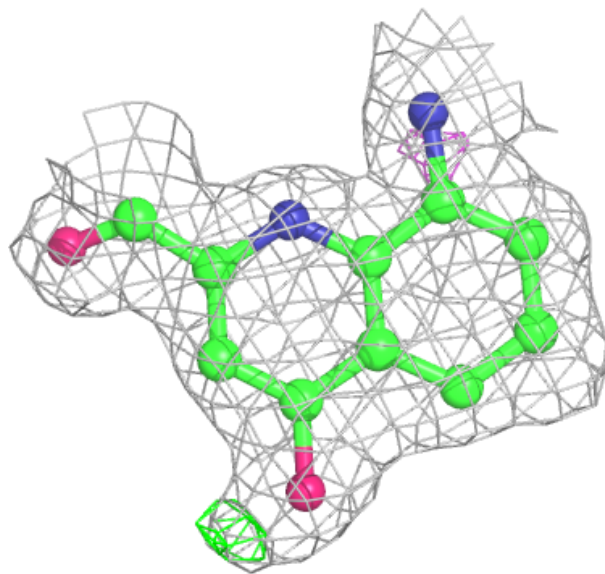
Electron density around QUJ B 303 (A):

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



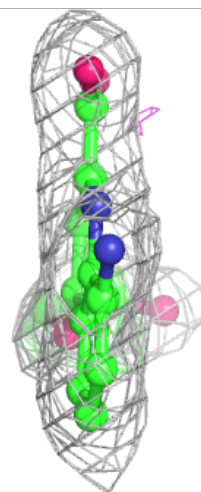
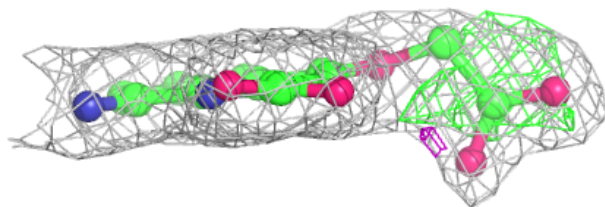
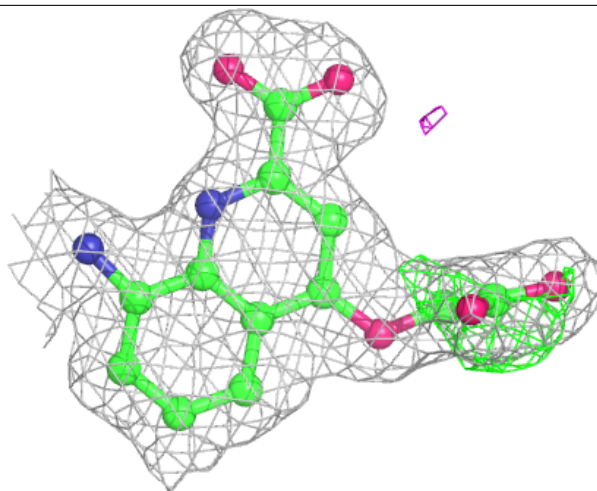
Electron density around QUK A 306 (A):

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



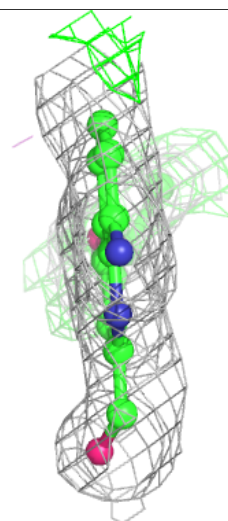
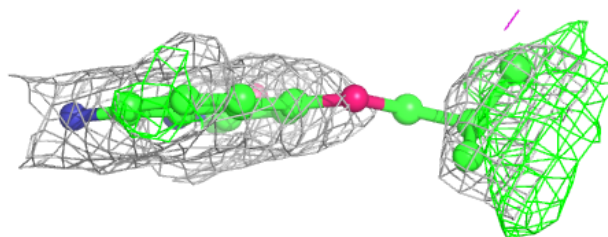
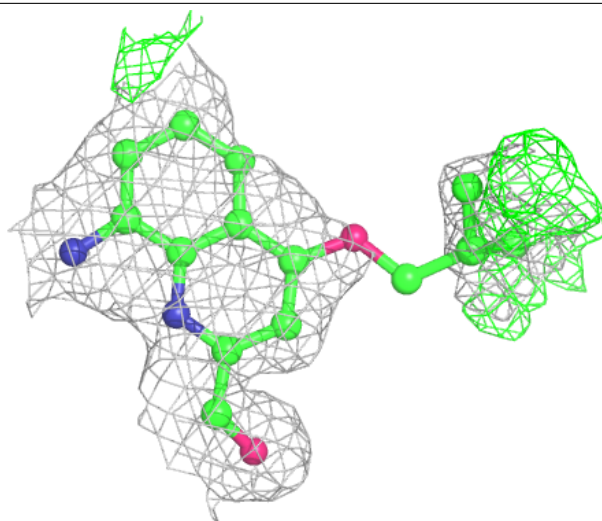
Electron density around QVE A 307 (A):

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



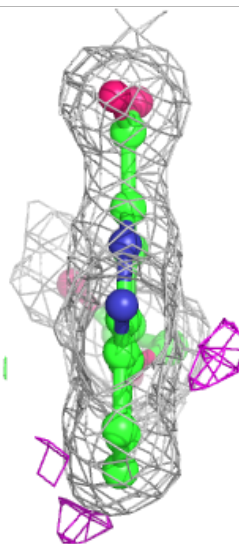
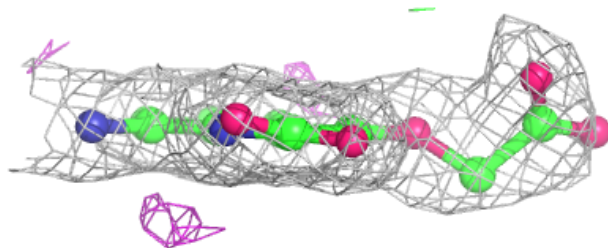
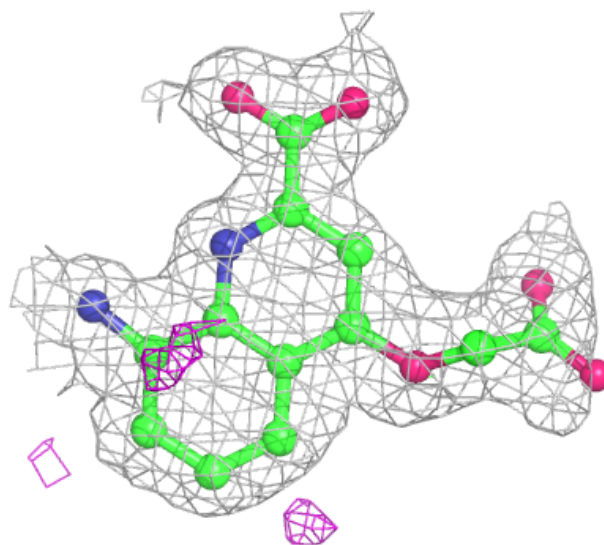
Electron density around QUJ A 311 (B):

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



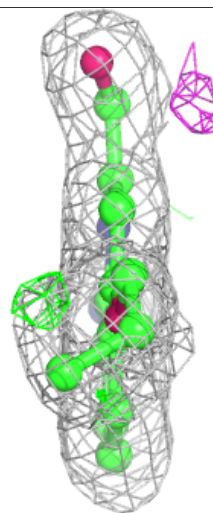
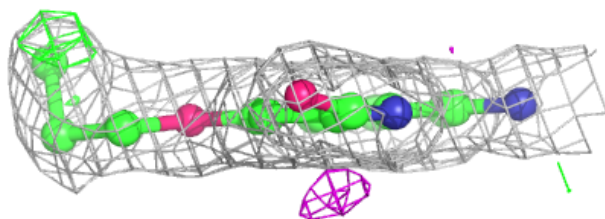
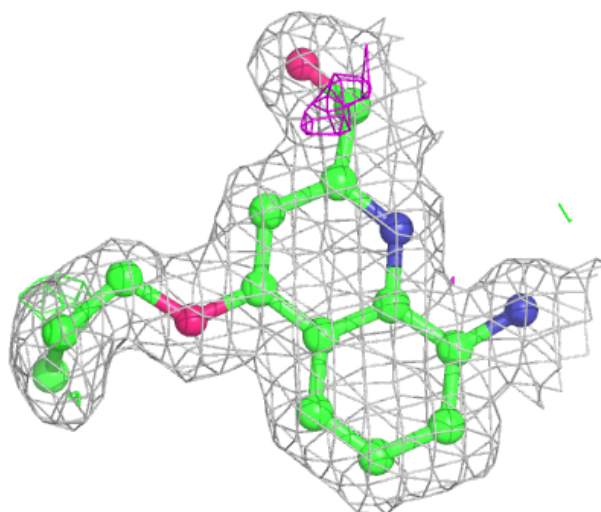
Electron density around QVE A 305:

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



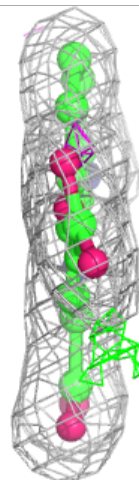
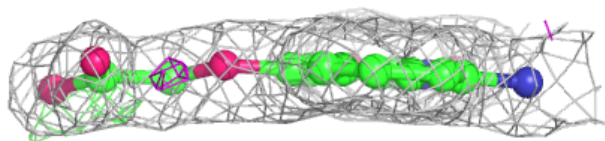
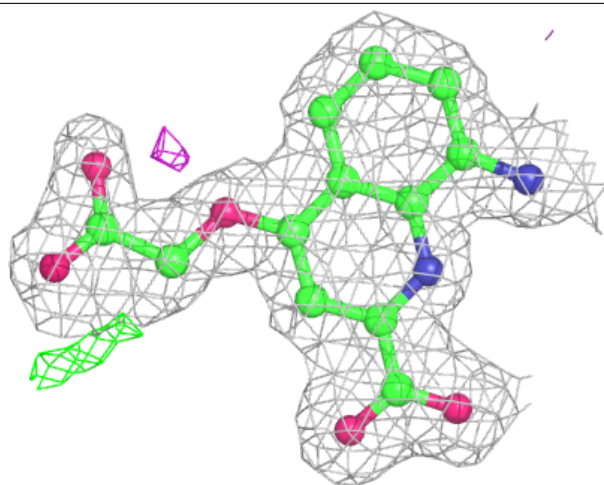
Electron density around QUJ A 315:

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and green (positive)



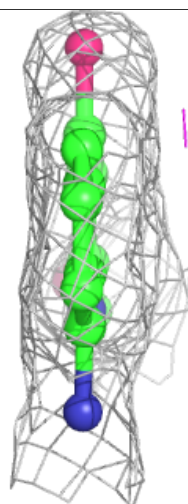
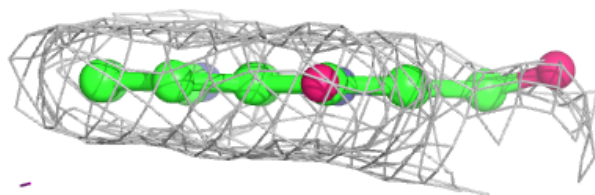
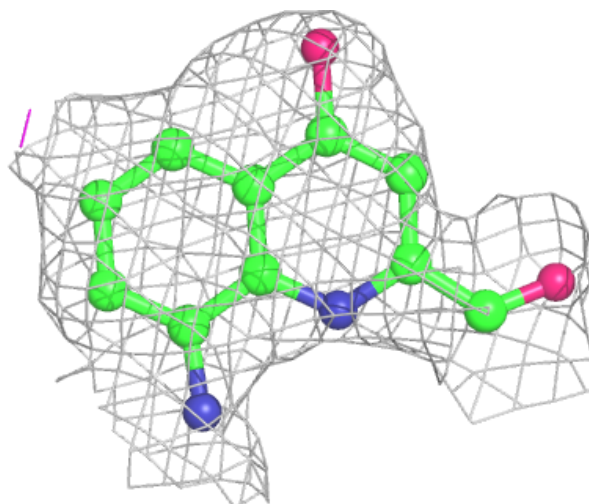
Electron density around QVE B 309:

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



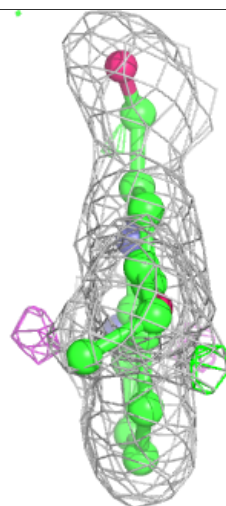
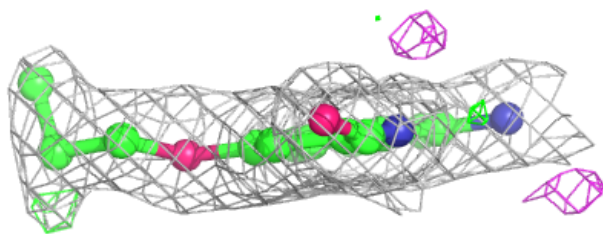
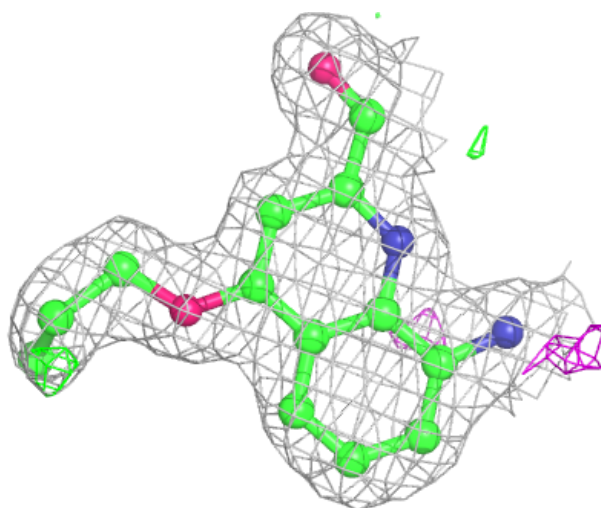
Electron density around QUK B 310 (B):

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



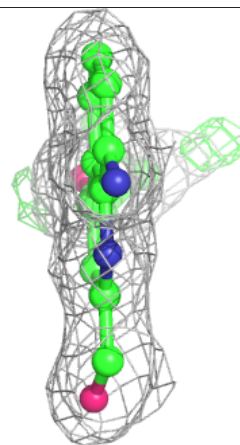
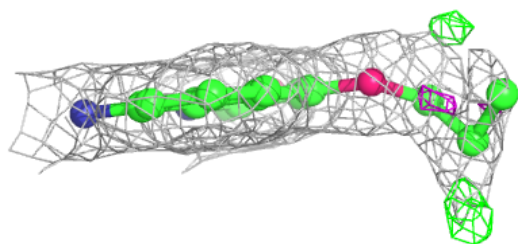
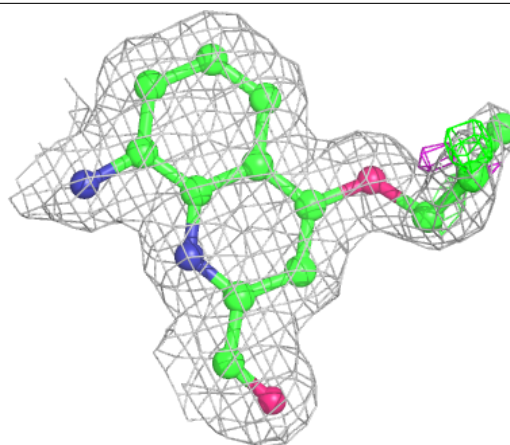
Electron density around QUK A 303:

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



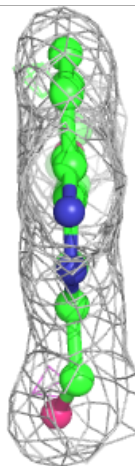
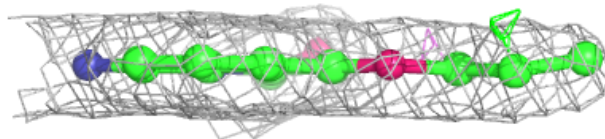
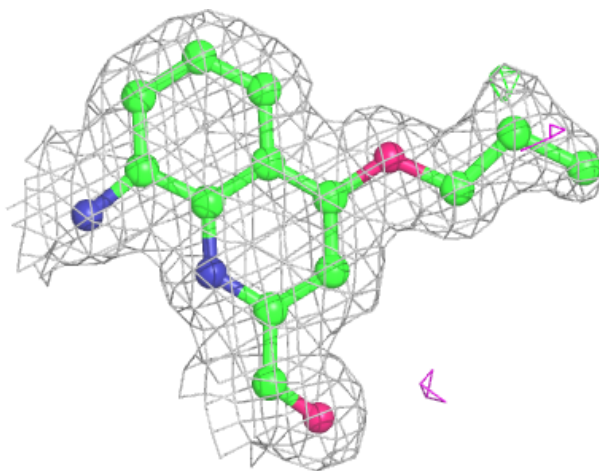
Electron density around QUJ B 301:

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



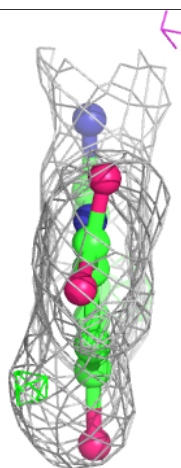
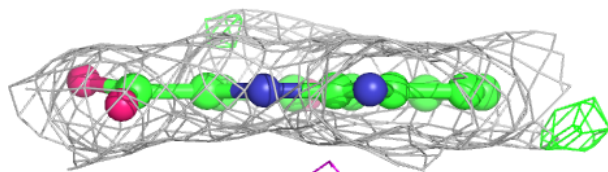
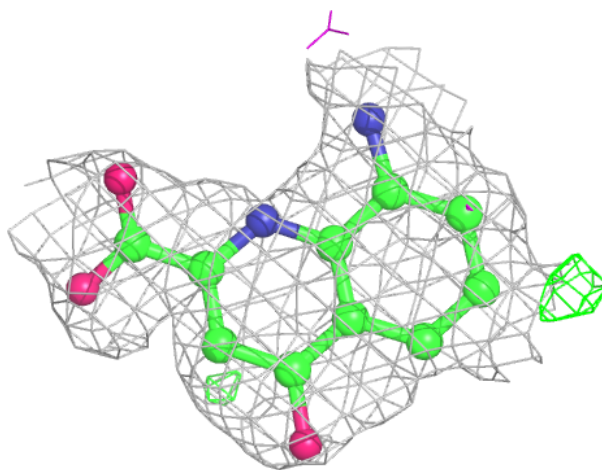
Electron density around QUK B 307:

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



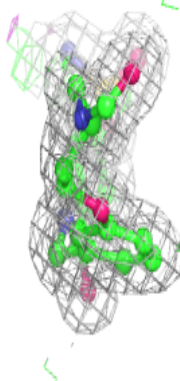
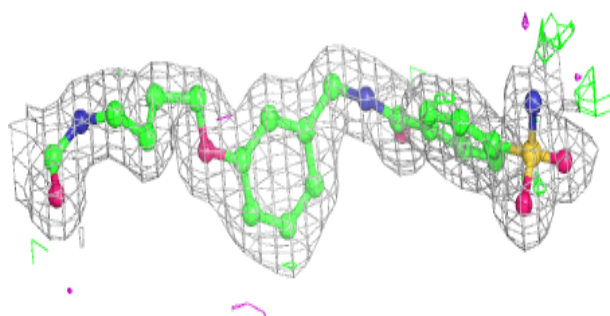
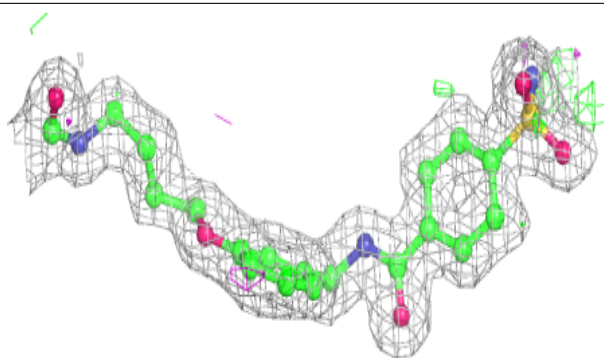
Electron density around QVE B 311 (B):

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

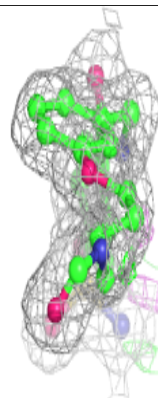
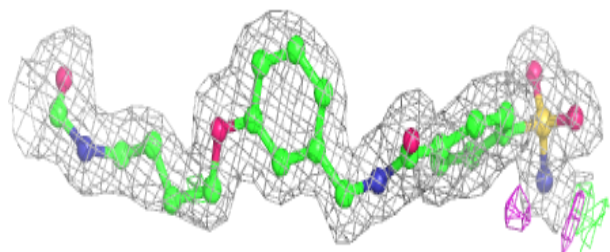
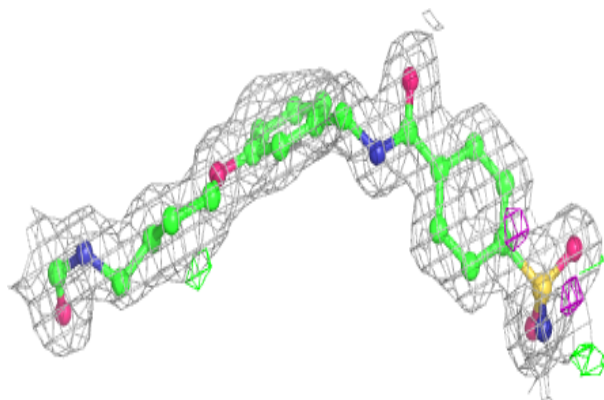


Electron density around 6H0 A 302:

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

**Electron density around 6H0 B 306:**

$2mF_o-DF_c$ (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.