



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:37 AM UTC

PDB ID : 6H23 / pdb_00006h23
Title : Crystal structure of the hClpP Y118A mutant with an activating small molecule
Authors : Kick, L.M.; Sieber, S.A.; Schneider, S.
Deposited on : 2018-07-13
Resolution : 3.09 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

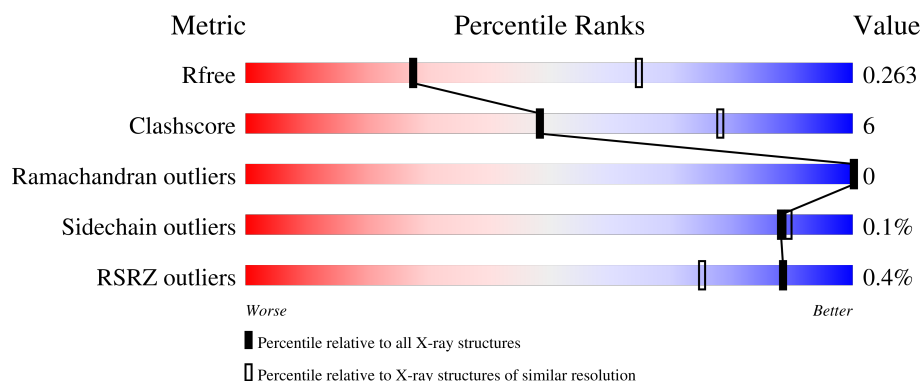
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.09 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}	180053	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	229	 60% 12% 28%
1	B	229	 62% 11% 28%
1	C	229	 62% 10% 28%
1	D	229	 59% 12% 28%
1	E	229	 61% 11% 28%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	229	 63%10%28%
1	G	229	 62%12%26%
1	H	229	 64%9%27%
1	I	229	 56%16%27%
1	J	229	 61%11%28%
1	K	229	 65%7%28%
1	L	229	 63%10%28%
1	M	229	 59%14%28%
1	N	229	 %66%7%27%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18505 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 ATP-dependent Clp protease proteolytic subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1253	796	212	232	13			
1	B	166	Total	C	N	O	S	0	0	0
			1260	801	213	233	13			
1	C	166	Total	C	N	O	S	0	0	0
			1258	799	213	233	13			
1	D	164	Total	C	N	O	S	0	0	0
			1254	796	214	231	13			
1	E	166	Total	C	N	O	S	0	1	0
			1266	804	216	233	13			
1	F	166	Total	C	N	O	S	0	1	0
			1272	807	217	234	14			
1	G	169	Total	C	N	O	S	0	0	0
			1276	810	216	237	13			
1	H	167	Total	C	N	O	S	0	2	0
			1277	811	217	236	13			
1	I	167	Total	C	N	O	S	0	2	0
			1282	813	218	237	14			
1	J	166	Total	C	N	O	S	0	0	0
			1264	802	216	233	13			
1	K	166	Total	C	N	O	S	0	0	0
			1260	799	215	233	13			
1	L	166	Total	C	N	O	S	0	1	0
			1270	806	216	235	13			
1	M	166	Total	C	N	O	S	0	1	0
			1272	807	219	233	13			
1	N	168	Total	C	N	O	S	0	1	0
			1285	815	219	237	14			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	118	ALA	TYR	engineered mutation	UNP Q16740
A	278	TRP	-	expression tag	UNP Q16740
A	279	SER	-	expression tag	UNP Q16740
A	280	HIS	-	expression tag	UNP Q16740
A	281	PRO	-	expression tag	UNP Q16740
A	282	GLN	-	expression tag	UNP Q16740
A	283	PHE	-	expression tag	UNP Q16740
A	284	GLU	-	expression tag	UNP Q16740
A	285	LYS	-	expression tag	UNP Q16740
B	118	ALA	TYR	engineered mutation	UNP Q16740
B	278	TRP	-	expression tag	UNP Q16740
B	279	SER	-	expression tag	UNP Q16740
B	280	HIS	-	expression tag	UNP Q16740
B	281	PRO	-	expression tag	UNP Q16740
B	282	GLN	-	expression tag	UNP Q16740
B	283	PHE	-	expression tag	UNP Q16740
B	284	GLU	-	expression tag	UNP Q16740
B	285	LYS	-	expression tag	UNP Q16740
C	118	ALA	TYR	engineered mutation	UNP Q16740
C	278	TRP	-	expression tag	UNP Q16740
C	279	SER	-	expression tag	UNP Q16740
C	280	HIS	-	expression tag	UNP Q16740
C	281	PRO	-	expression tag	UNP Q16740
C	282	GLN	-	expression tag	UNP Q16740
C	283	PHE	-	expression tag	UNP Q16740
C	284	GLU	-	expression tag	UNP Q16740
C	285	LYS	-	expression tag	UNP Q16740
D	118	ALA	TYR	engineered mutation	UNP Q16740
D	278	TRP	-	expression tag	UNP Q16740
D	279	SER	-	expression tag	UNP Q16740
D	280	HIS	-	expression tag	UNP Q16740
D	281	PRO	-	expression tag	UNP Q16740
D	282	GLN	-	expression tag	UNP Q16740
D	283	PHE	-	expression tag	UNP Q16740
D	284	GLU	-	expression tag	UNP Q16740
D	285	LYS	-	expression tag	UNP Q16740
E	118	ALA	TYR	engineered mutation	UNP Q16740
E	278	TRP	-	expression tag	UNP Q16740
E	279	SER	-	expression tag	UNP Q16740
E	280	HIS	-	expression tag	UNP Q16740
E	281	PRO	-	expression tag	UNP Q16740
E	282	GLN	-	expression tag	UNP Q16740
E	283	PHE	-	expression tag	UNP Q16740

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	284	GLU	-	expression tag	UNP Q16740
E	285	LYS	-	expression tag	UNP Q16740
F	118	ALA	TYR	engineered mutation	UNP Q16740
F	278	TRP	-	expression tag	UNP Q16740
F	279	SER	-	expression tag	UNP Q16740
F	280	HIS	-	expression tag	UNP Q16740
F	281	PRO	-	expression tag	UNP Q16740
F	282	GLN	-	expression tag	UNP Q16740
F	283	PHE	-	expression tag	UNP Q16740
F	284	GLU	-	expression tag	UNP Q16740
F	285	LYS	-	expression tag	UNP Q16740
G	118	ALA	TYR	engineered mutation	UNP Q16740
G	278	TRP	-	expression tag	UNP Q16740
G	279	SER	-	expression tag	UNP Q16740
G	280	HIS	-	expression tag	UNP Q16740
G	281	PRO	-	expression tag	UNP Q16740
G	282	GLN	-	expression tag	UNP Q16740
G	283	PHE	-	expression tag	UNP Q16740
G	284	GLU	-	expression tag	UNP Q16740
G	285	LYS	-	expression tag	UNP Q16740
H	118	ALA	TYR	engineered mutation	UNP Q16740
H	278	TRP	-	expression tag	UNP Q16740
H	279	SER	-	expression tag	UNP Q16740
H	280	HIS	-	expression tag	UNP Q16740
H	281	PRO	-	expression tag	UNP Q16740
H	282	GLN	-	expression tag	UNP Q16740
H	283	PHE	-	expression tag	UNP Q16740
H	284	GLU	-	expression tag	UNP Q16740
H	285	LYS	-	expression tag	UNP Q16740
I	118	ALA	TYR	engineered mutation	UNP Q16740
I	278	TRP	-	expression tag	UNP Q16740
I	279	SER	-	expression tag	UNP Q16740
I	280	HIS	-	expression tag	UNP Q16740
I	281	PRO	-	expression tag	UNP Q16740
I	282	GLN	-	expression tag	UNP Q16740
I	283	PHE	-	expression tag	UNP Q16740
I	284	GLU	-	expression tag	UNP Q16740
I	285	LYS	-	expression tag	UNP Q16740
J	118	ALA	TYR	engineered mutation	UNP Q16740
J	278	TRP	-	expression tag	UNP Q16740
J	279	SER	-	expression tag	UNP Q16740
J	280	HIS	-	expression tag	UNP Q16740

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	281	PRO	-	expression tag	UNP Q16740
J	282	GLN	-	expression tag	UNP Q16740
J	283	PHE	-	expression tag	UNP Q16740
J	284	GLU	-	expression tag	UNP Q16740
J	285	LYS	-	expression tag	UNP Q16740
K	118	ALA	TYR	engineered mutation	UNP Q16740
K	278	TRP	-	expression tag	UNP Q16740
K	279	SER	-	expression tag	UNP Q16740
K	280	HIS	-	expression tag	UNP Q16740
K	281	PRO	-	expression tag	UNP Q16740
K	282	GLN	-	expression tag	UNP Q16740
K	283	PHE	-	expression tag	UNP Q16740
K	284	GLU	-	expression tag	UNP Q16740
K	285	LYS	-	expression tag	UNP Q16740
L	118	ALA	TYR	engineered mutation	UNP Q16740
L	278	TRP	-	expression tag	UNP Q16740
L	279	SER	-	expression tag	UNP Q16740
L	280	HIS	-	expression tag	UNP Q16740
L	281	PRO	-	expression tag	UNP Q16740
L	282	GLN	-	expression tag	UNP Q16740
L	283	PHE	-	expression tag	UNP Q16740
L	284	GLU	-	expression tag	UNP Q16740
L	285	LYS	-	expression tag	UNP Q16740
M	118	ALA	TYR	engineered mutation	UNP Q16740
M	278	TRP	-	expression tag	UNP Q16740
M	279	SER	-	expression tag	UNP Q16740
M	280	HIS	-	expression tag	UNP Q16740
M	281	PRO	-	expression tag	UNP Q16740
M	282	GLN	-	expression tag	UNP Q16740
M	283	PHE	-	expression tag	UNP Q16740
M	284	GLU	-	expression tag	UNP Q16740
M	285	LYS	-	expression tag	UNP Q16740
N	118	ALA	TYR	engineered mutation	UNP Q16740
N	278	TRP	-	expression tag	UNP Q16740
N	279	SER	-	expression tag	UNP Q16740
N	280	HIS	-	expression tag	UNP Q16740
N	281	PRO	-	expression tag	UNP Q16740
N	282	GLN	-	expression tag	UNP Q16740
N	283	PHE	-	expression tag	UNP Q16740
N	284	GLU	-	expression tag	UNP Q16740
N	285	LYS	-	expression tag	UNP Q16740

- Molecule 2 is {N}-(1,3-benzodioxol-5-ylmethyl)-5-[(2-chloranyl-4-fluoranyl-phenyl)methyl]-

FJT

ORTEP diagram of the compound FJT, showing the molecular structure with thermal ellipsoids at the 50% probability level. The structure consists of a 2,3-dihydrobenzofuran moiety linked via an amide bond to a pyrazole ring, which is further connected to a 2-chloro-4-(difluoromethyl)phenyl group. Atoms are labeled with thermal ellipsoids at the 50% probability level. Displacement ellipsoid coefficients are provided in the table below.

Atom	U ¹¹	U ²²	U ³³	U ¹²	U ¹³	U ²³
C01	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C02	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C03	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C04	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C05	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C06	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C07	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C09	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C10	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C13	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C15	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C16	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C17	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C18	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C19	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C20	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C21	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C26	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
C27	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
N08	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
N11	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
N12	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
O14	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
O24	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
O25	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
Cl1	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000
F22	0.0125	0.0125	0.0125	0.0000	0.0000	0.0000

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	B	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	D	1	Total 27	C 18	Cl 1	F 1	N 3	O 4	0	0
2	D	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	E	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	F	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	G	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	H	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	H	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	J	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	K	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	L	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1
2	M	1	Total 54	C 36	Cl 2	F 2	N 6	O 8	0	1

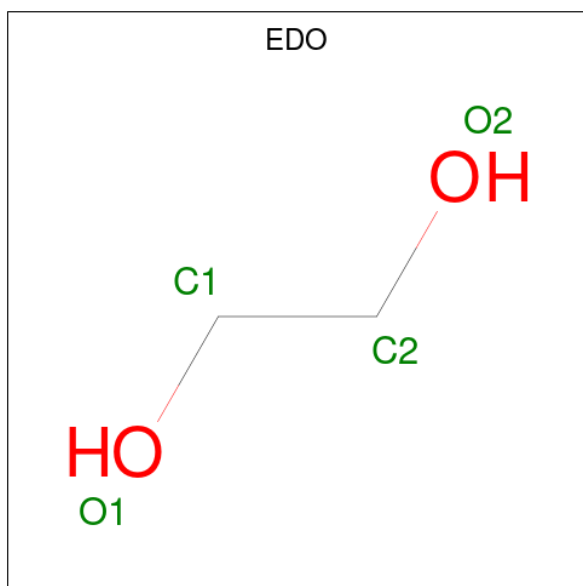


WORLD WIDE
PDB
PROTEIN DATA BANK

Continued from previous page...

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	M	1	Total	C	Cl	F	N	O	0	1
			54	36	2	2	6	8		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	N	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	O	0	0
			1	1		
4	E	2	Total	O	0	0
			2	2		
4	F	2	Total	O	0	0
			2	2		
4	G	2	Total	O	0	0
			2	2		

Continued on next page...

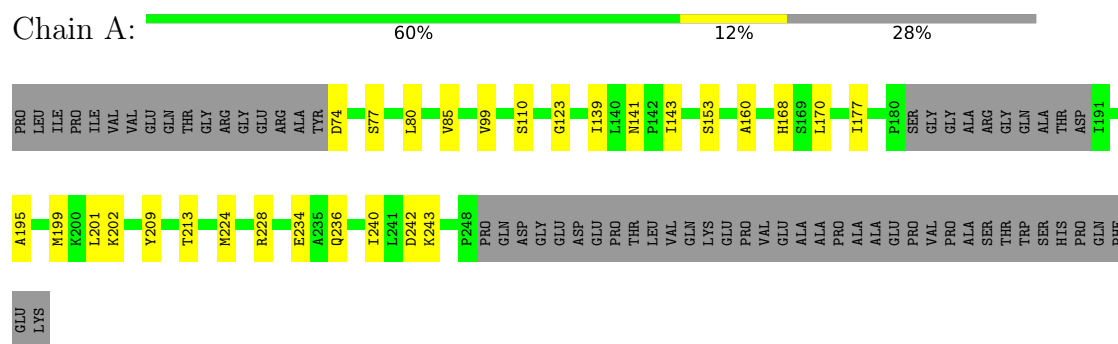
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total 1	O 1	0	0
4	I	1	Total 1	O 1	0	0
4	K	1	Total 1	O 1	0	0
4	N	1	Total 1	O 1	0	0

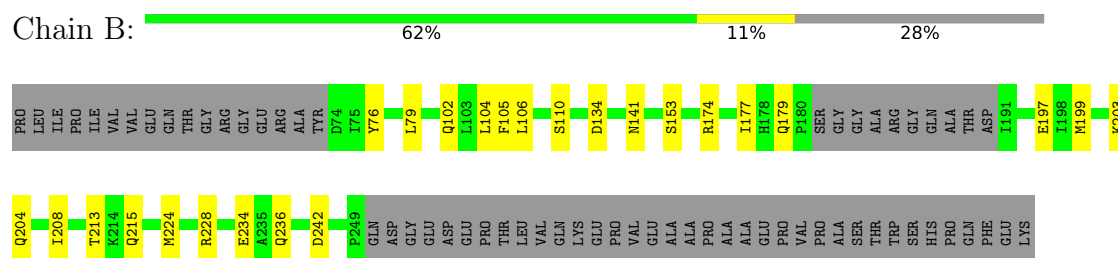
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

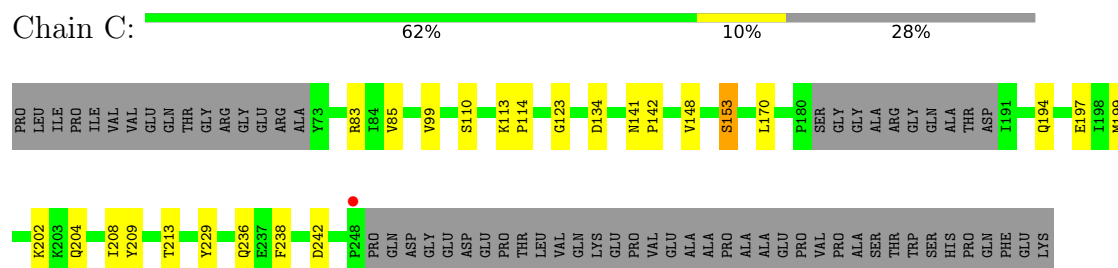
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

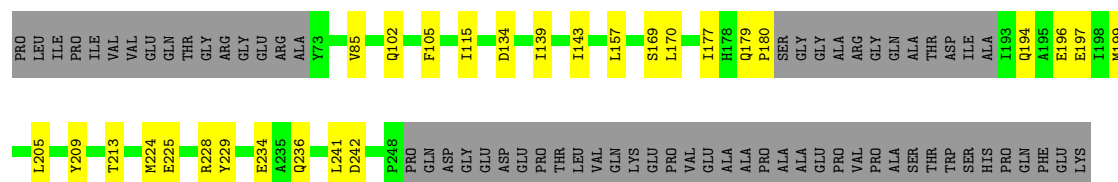


- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



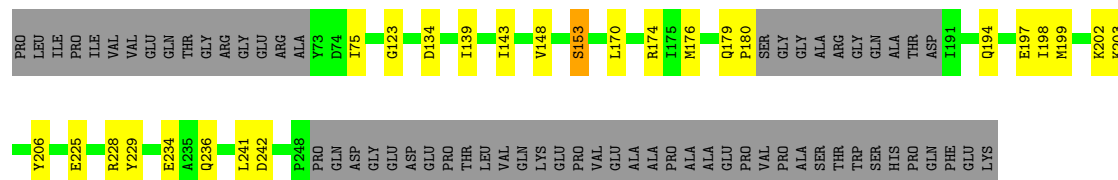
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial





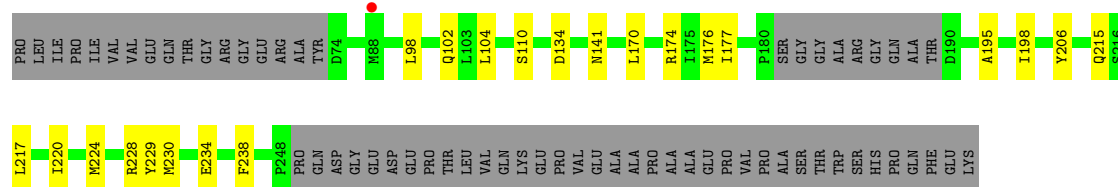
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

Chain E: 61% 11% 28%



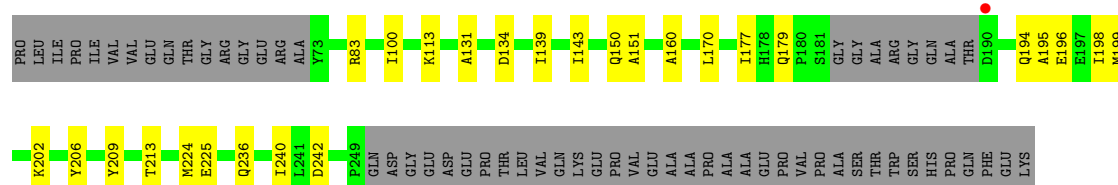
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

Chain F: 63% 10% 28%



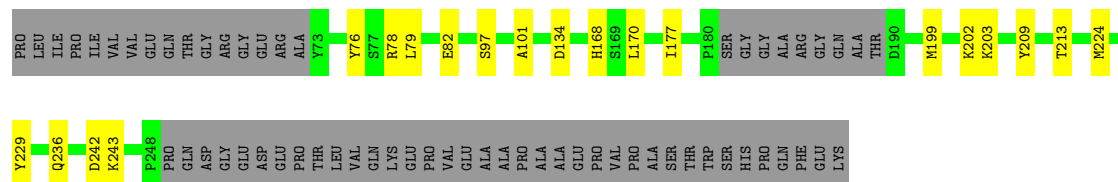
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

Chain G: 62% 12% 26%

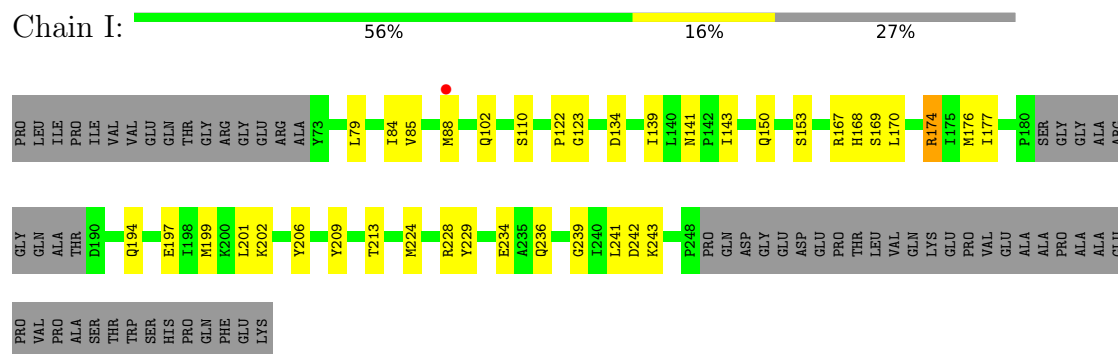


- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

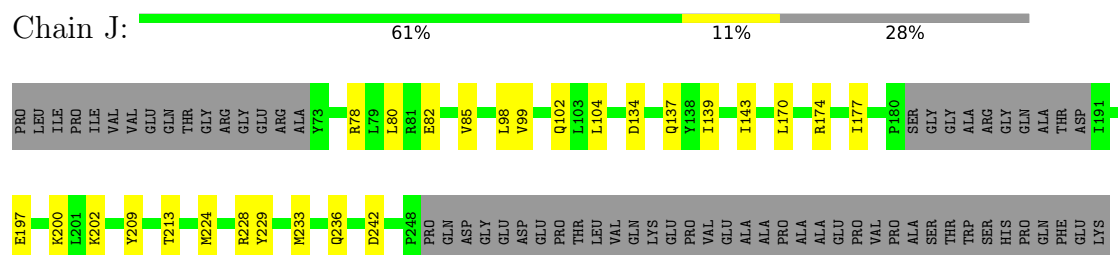
Chain H: 64% 9% 27%



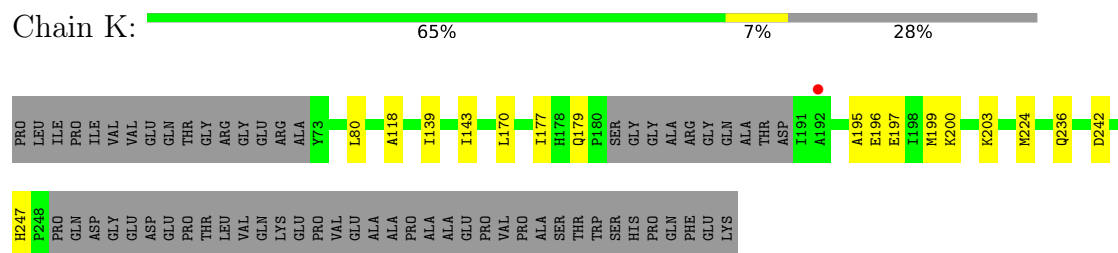
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



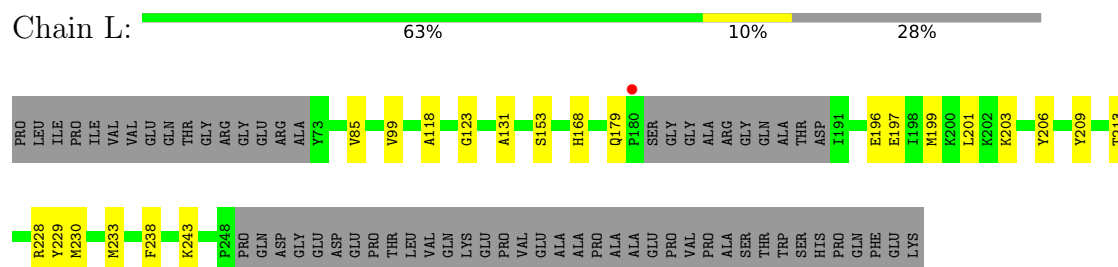
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



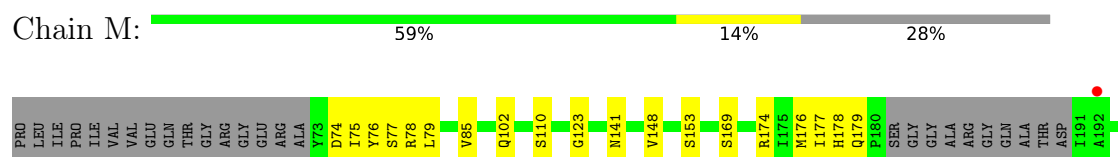
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

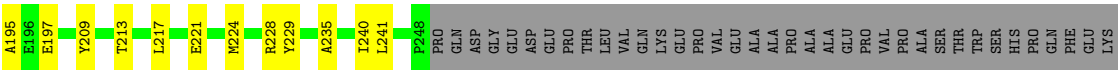


- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

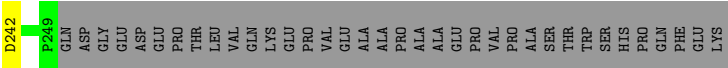


- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial





● Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	115.50Å 97.15Å 127.25Å 90.00° 93.53° 90.00°	Depositor
Resolution (Å)	42.34 – 3.09 42.34 – 3.09	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.34-3.09) 98.9 (42.34-3.09)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 3.07Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.215 , 0.261 0.218 , 0.263	Depositor DCC
R_{free} test set	2572 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	69.1	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18505	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.80% 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: FJT, EDO

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	0.09	0/1275	0.28	0/1728
1	B	0.10	0/1283	0.30	0/1740
1	C	0.10	0/1280	0.33	1/1735 (0.1%)
1	D	0.09	0/1276	0.28	0/1728
1	E	0.10	0/1291	0.34	1/1749 (0.1%)
1	F	0.09	0/1294	0.29	0/1752
1	G	0.10	0/1299	0.31	0/1762
1	H	0.10	0/1305	0.32	0/1768
1	I	0.10	0/1307	0.30	0/1770
1	J	0.10	0/1286	0.31	0/1742
1	K	0.09	0/1282	0.28	0/1738
1	L	0.09	0/1295	0.28	0/1754
1	M	0.10	0/1297	0.29	0/1756
1	N	0.10	0/1308	0.32	0/1772
All	All	0.10	0/18078	0.30	2/24494 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	153	SER	CB-CA-C	-5.69	109.49	117.23
1	E	153	SER	CB-CA-C	-5.34	109.97	117.23

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	1253	0	1259	16	0
1	B	1260	0	1266	17	0
1	C	1258	0	1261	17	0
1	D	1254	0	1265	20	0
1	E	1266	0	1274	24	0
1	F	1272	0	1280	16	0
1	G	1276	0	1275	17	0
1	H	1277	0	1282	14	0
1	I	1282	0	1284	26	0
1	J	1264	0	1272	19	0
1	K	1260	0	1261	15	0
1	L	1270	0	1278	16	0
1	M	1272	0	1285	19	0
1	N	1285	0	1292	12	0
2	A	54	0	0	0	0
2	B	54	0	0	1	0
2	D	81	0	0	0	0
2	E	54	0	0	0	0
2	F	54	0	0	1	0
2	G	54	0	0	0	0
2	H	108	0	0	0	0
2	J	54	0	0	0	0
2	K	54	0	0	2	0
2	L	54	0	0	2	0
2	M	108	0	0	0	0
3	A	4	0	6	2	0
3	E	4	0	6	1	0
3	F	4	0	6	0	0
3	N	4	0	6	0	0
4	D	1	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	K	1	0	0	0	0
4	N	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18505	0	17858	200	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 6.

The worst 5 of 200 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:M:197:GLU:HB3	1:N:174:ARG:HH12	1.48	0.77
1:I:174[A]:ARG:HG3	1:I:174[A]:ARG:HH21	1.52	0.75
1:J:98:LEU:HG	1:J:102:GLN:HE21	1.59	0.66
1:I:236:GLN:NE2	1:I:242:ASP:O	2.29	0.65
1:C:236:GLN:NE2	1:C:242:ASP:O	2.30	0.64

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	161/229 (70%)	157 (98%)	4 (2%)	0	100	100
1	B	162/229 (71%)	158 (98%)	4 (2%)	0	100	100
1	C	162/229 (71%)	158 (98%)	4 (2%)	0	100	100
1	D	160/229 (70%)	156 (98%)	4 (2%)	0	100	100
1	E	163/229 (71%)	159 (98%)	4 (2%)	0	100	100
1	F	163/229 (71%)	159 (98%)	4 (2%)	0	100	100
1	G	165/229 (72%)	160 (97%)	5 (3%)	0	100	100
1	H	165/229 (72%)	161 (98%)	4 (2%)	0	100	100
1	I	165/229 (72%)	160 (97%)	5 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	162/229 (71%)	158 (98%)	4 (2%)	0	100	100
1	K	162/229 (71%)	157 (97%)	5 (3%)	0	100	100
1	L	163/229 (71%)	159 (98%)	4 (2%)	0	100	100
1	M	163/229 (71%)	157 (96%)	6 (4%)	0	100	100
1	N	165/229 (72%)	160 (97%)	5 (3%)	0	100	100
All	All	2281/3206 (71%)	2219 (97%)	62 (3%)	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	136/192 (71%)	136 (100%)	0	100	100
1	B	137/192 (71%)	137 (100%)	0	100	100
1	C	136/192 (71%)	136 (100%)	0	100	100
1	D	137/192 (71%)	137 (100%)	0	100	100
1	E	137/192 (71%)	137 (100%)	0	100	100
1	F	138/192 (72%)	138 (100%)	0	100	100
1	G	138/192 (72%)	138 (100%)	0	100	100
1	H	138/192 (72%)	138 (100%)	0	100	100
1	I	139/192 (72%)	137 (99%)	2 (1%)	59	73
1	J	137/192 (71%)	137 (100%)	0	100	100
1	K	136/192 (71%)	136 (100%)	0	100	100
1	L	138/192 (72%)	138 (100%)	0	100	100
1	M	138/192 (72%)	138 (100%)	0	100	100
1	N	140/192 (73%)	140 (100%)	0	100	100
All	All	1925/2688 (72%)	1923 (100%)	2 (0%)	88	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	174[A]	ARG
1	I	174[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	204	GLN
1	I	168	HIS
1	M	204	GLN
1	I	102	GLN
1	I	179	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

31 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	FJT	D	301	-	30,30,30	2.06	10 (33%)	39,42,42	2.51	13 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FJT	H	302[B]	-	30,30,30	2.08	9 (30%)	39,42,42	2.48	16 (41%)
2	FJT	E	301[A]	-	30,30,30	2.13	10 (33%)	39,42,42	2.60	9 (23%)
3	EDO	E	302	-	3,3,3	0.43	0	2,2,2	0.38	0
2	FJT	D	302[B]	-	30,30,30	2.13	10 (33%)	39,42,42	2.50	12 (30%)
2	FJT	J	301[A]	-	30,30,30	2.11	9 (30%)	39,42,42	2.50	11 (28%)
2	FJT	E	301[B]	-	30,30,30	2.13	10 (33%)	39,42,42	2.70	10 (25%)
2	FJT	F	301[A]	-	30,30,30	2.21	10 (33%)	39,42,42	2.69	12 (30%)
2	FJT	J	301[B]	-	30,30,30	2.12	9 (30%)	39,42,42	2.51	11 (28%)
2	FJT	L	301[A]	-	30,30,30	2.13	10 (33%)	39,42,42	2.56	12 (30%)
3	EDO	F	302	-	3,3,3	0.43	0	2,2,2	0.39	0
2	FJT	A	301[A]	-	30,30,30	2.09	9 (30%)	39,42,42	2.59	15 (38%)
2	FJT	M	301[A]	-	30,30,30	2.18	9 (30%)	39,42,42	2.65	15 (38%)
2	FJT	G	301[A]	-	30,30,30	2.11	10 (33%)	39,42,42	2.53	10 (25%)
3	EDO	A	302	-	3,3,3	0.43	0	2,2,2	0.38	0
2	FJT	F	301[B]	-	30,30,30	2.09	9 (30%)	39,42,42	2.55	12 (30%)
2	FJT	H	301[A]	-	30,30,30	2.12	10 (33%)	39,42,42	2.53	12 (30%)
2	FJT	B	301[A]	-	30,30,30	2.07	9 (30%)	39,42,42	2.43	11 (28%)
2	FJT	L	301[B]	-	30,30,30	2.11	10 (33%)	39,42,42	2.52	9 (23%)
2	FJT	A	301[B]	-	30,30,30	2.11	10 (33%)	39,42,42	2.62	10 (25%)
2	FJT	M	301[B]	-	30,30,30	2.11	10 (33%)	39,42,42	2.69	11 (28%)
2	FJT	G	301[B]	-	30,30,30	2.10	10 (33%)	39,42,42	2.50	13 (33%)
2	FJT	H	301[B]	-	30,30,30	2.13	10 (33%)	39,42,42	2.57	9 (23%)
2	FJT	K	301[A]	-	30,30,30	2.14	9 (30%)	39,42,42	2.56	11 (28%)
2	FJT	B	301[B]	-	30,30,30	2.11	10 (33%)	39,42,42	2.58	12 (30%)
2	FJT	M	302[A]	-	30,30,30	2.11	9 (30%)	39,42,42	2.51	12 (30%)
2	FJT	K	301[B]	-	30,30,30	2.11	10 (33%)	39,42,42	2.54	12 (30%)
2	FJT	H	302[A]	-	30,30,30	2.15	9 (30%)	39,42,42	2.67	12 (30%)
2	FJT	M	302[B]	-	30,30,30	2.11	9 (30%)	39,42,42	2.53	13 (33%)
2	FJT	D	302[A]	-	30,30,30	2.17	9 (30%)	39,42,42	2.71	12 (30%)
3	EDO	N	301	-	3,3,3	0.43	0	2,2,2	0.39	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
2	FJT	D	301	-	-	2/13/19/19	0/4/4/4
2	FJT	H	302[B]	-	-	2/13/19/19	0/4/4/4
2	FJT	E	301[A]	-	-	4/13/19/19	0/4/4/4
3	EDO	E	302	-	-	0/1/1/1	-
2	FJT	D	302[B]	-	-	0/13/19/19	0/4/4/4
2	FJT	J	301[A]	-	-	2/13/19/19	0/4/4/4
2	FJT	E	301[B]	-	-	2/13/19/19	0/4/4/4
2	FJT	F	301[A]	-	-	4/13/19/19	0/4/4/4
2	FJT	J	301[B]	-	-	0/13/19/19	0/4/4/4
2	FJT	L	301[A]	-	-	5/13/19/19	0/4/4/4
3	EDO	F	302	-	-	0/1/1/1	-
2	FJT	A	301[A]	-	-	3/13/19/19	0/4/4/4
2	FJT	M	301[A]	-	-	2/13/19/19	0/4/4/4
2	FJT	G	301[A]	-	-	0/13/19/19	0/4/4/4
3	EDO	A	302	-	-	0/1/1/1	-
2	FJT	F	301[B]	-	-	4/13/19/19	0/4/4/4
2	FJT	H	301[A]	-	-	2/13/19/19	0/4/4/4
2	FJT	B	301[A]	-	-	0/13/19/19	0/4/4/4
2	FJT	L	301[B]	-	-	4/13/19/19	0/4/4/4
2	FJT	A	301[B]	-	-	4/13/19/19	0/4/4/4
2	FJT	M	301[B]	-	-	3/13/19/19	0/4/4/4
2	FJT	G	301[B]	-	-	0/13/19/19	0/4/4/4
2	FJT	H	301[B]	-	-	0/13/19/19	0/4/4/4
2	FJT	K	301[A]	-	-	8/13/19/19	0/4/4/4
2	FJT	B	301[B]	-	-	3/13/19/19	0/4/4/4
2	FJT	M	302[A]	-	-	3/13/19/19	0/4/4/4
2	FJT	K	301[B]	-	-	5/13/19/19	0/4/4/4
2	FJT	H	302[A]	-	-	4/13/19/19	0/4/4/4
2	FJT	M	302[B]	-	-	0/13/19/19	0/4/4/4
2	FJT	D	302[A]	-	-	4/13/19/19	0/4/4/4
3	EDO	N	301	-	-	0/1/1/1	-

The worst 5 of 258 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	301[A]	FJT	C09-N08	7.70	1.46	1.33
2	M	301[A]	FJT	C09-N08	7.54	1.46	1.33
2	H	302[A]	FJT	C09-N08	7.54	1.46	1.33
2	D	302[A]	FJT	C09-N08	7.39	1.46	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	301[B]	FJT	C09-N08	7.37	1.46	1.33

The worst 5 of 317 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301[B]	FJT	O14-C13-C15	9.99	127.68	117.73
2	A	301[B]	FJT	O14-C13-C15	9.72	127.42	117.73
2	M	301[B]	FJT	O14-C13-C15	9.59	127.28	117.73
2	H	301[B]	FJT	O14-C13-C15	9.34	127.04	117.73
2	D	302[A]	FJT	O14-C13-C15	8.89	126.59	117.73

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301[A]	FJT	C13-C15-C16-C17
2	A	301[B]	FJT	N08-C09-C10-N11
2	A	301[B]	FJT	N08-C09-C10-O14
2	D	302[A]	FJT	N08-C09-C10-N11
2	D	302[A]	FJT	N08-C09-C10-O14

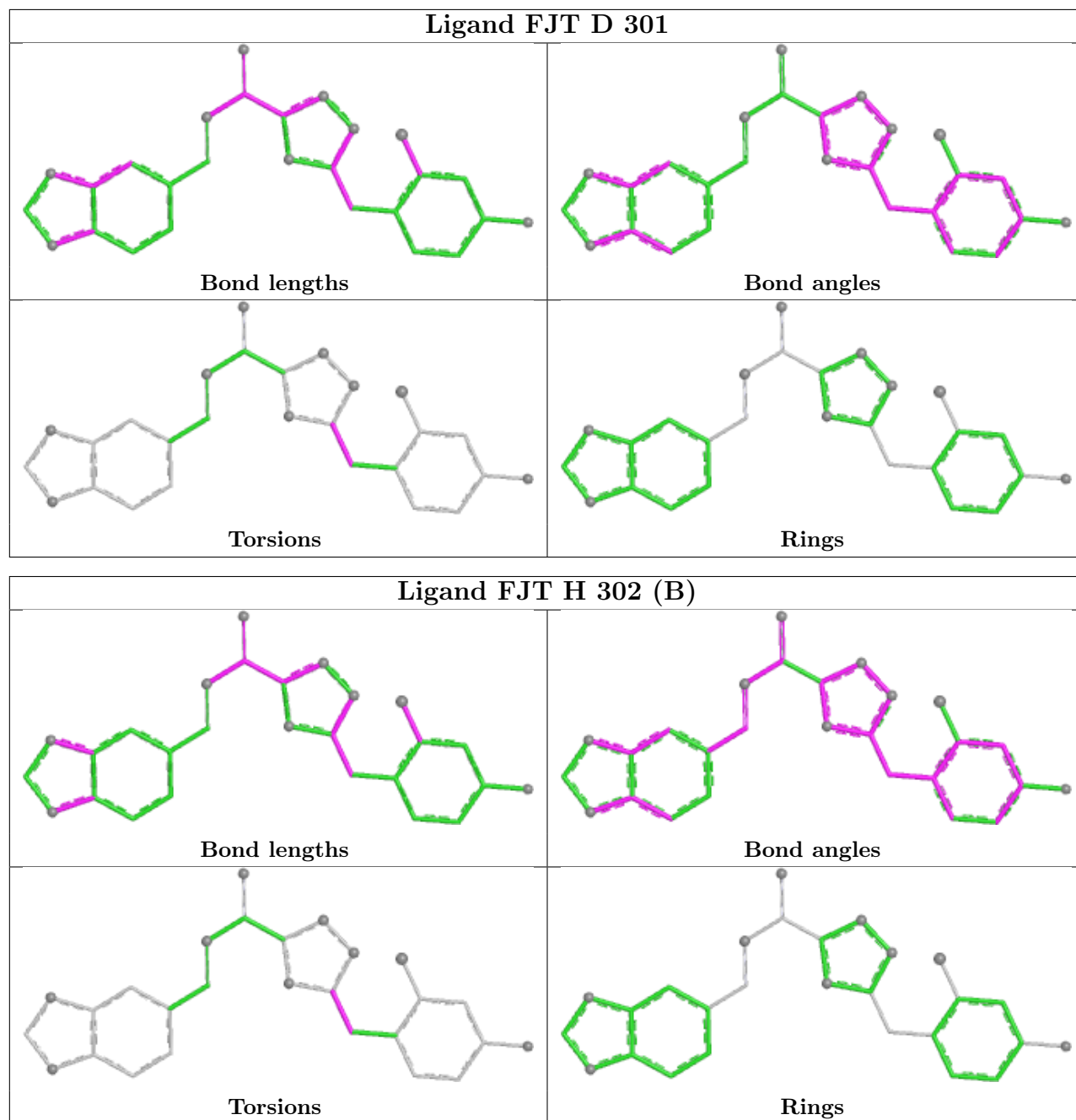
There are no ring outliers.

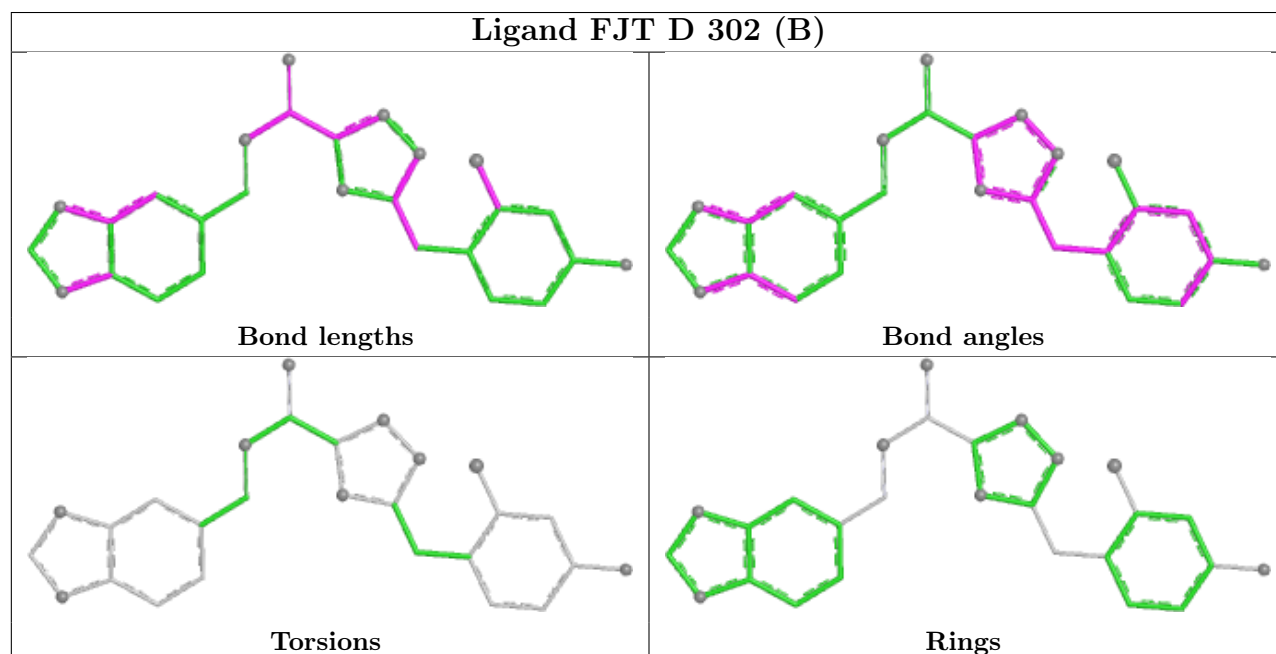
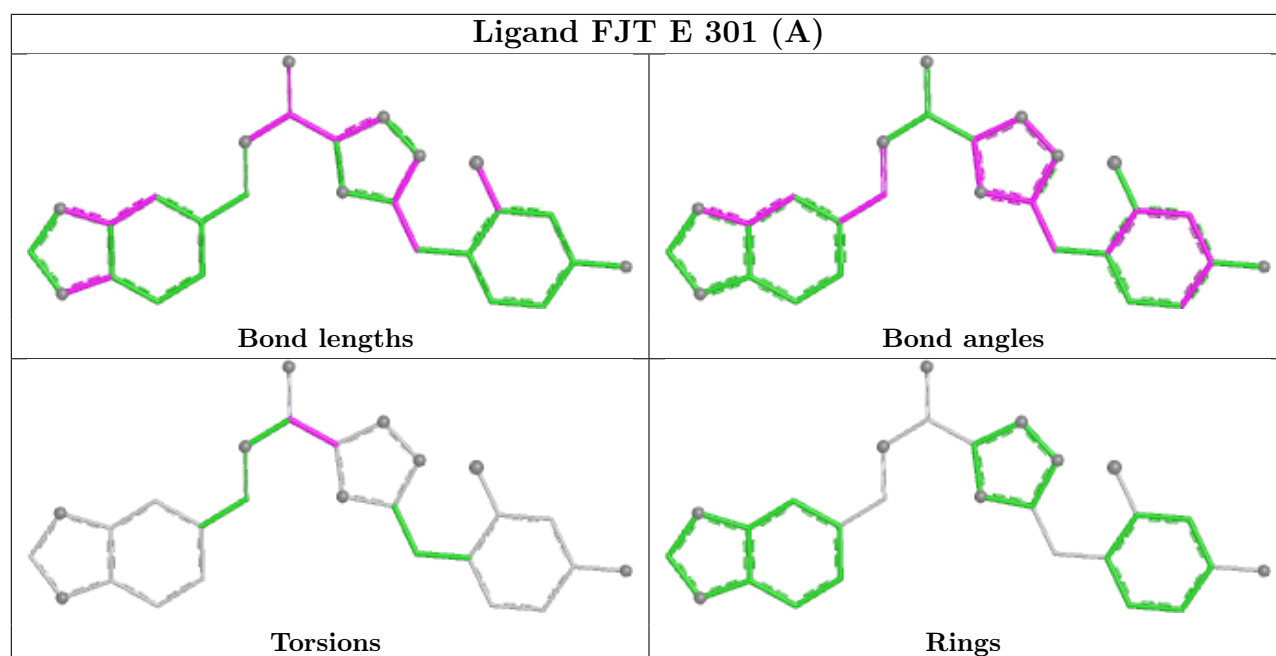
7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	302	EDO	1	0
2	F	301[A]	FJT	1	0
2	L	301[A]	FJT	1	0
3	A	302	EDO	2	0
2	B	301[A]	FJT	1	0
2	L	301[B]	FJT	1	0
2	K	301[B]	FJT	2	0

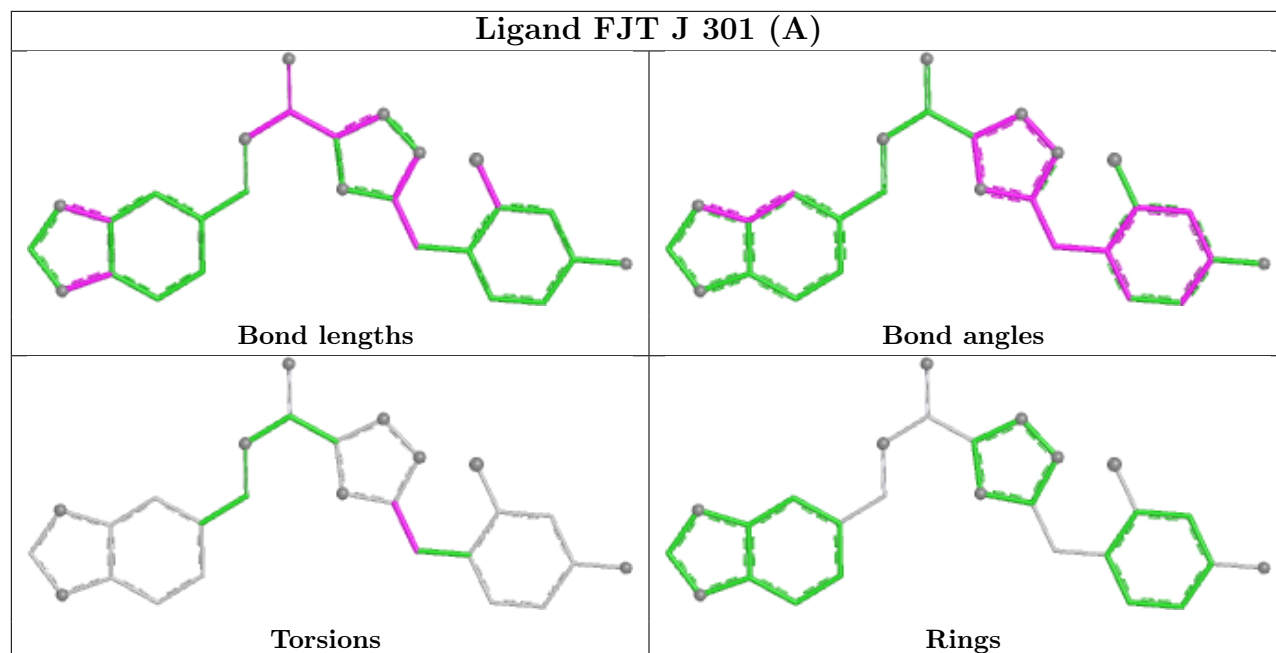
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

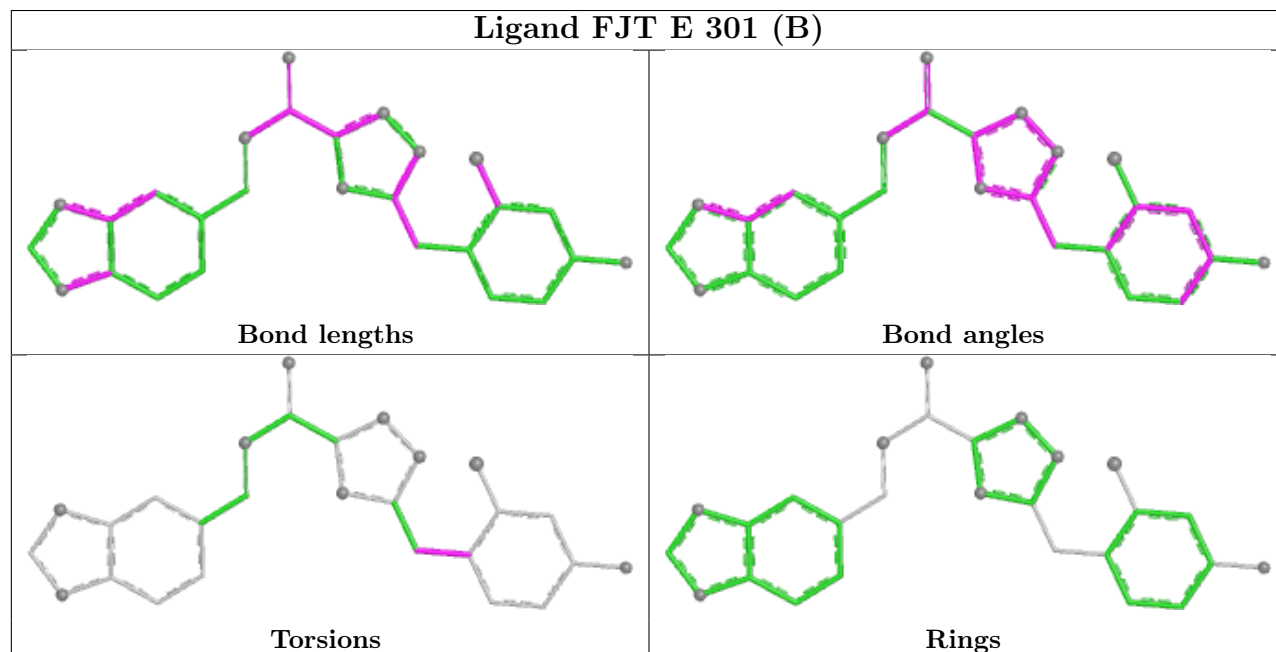


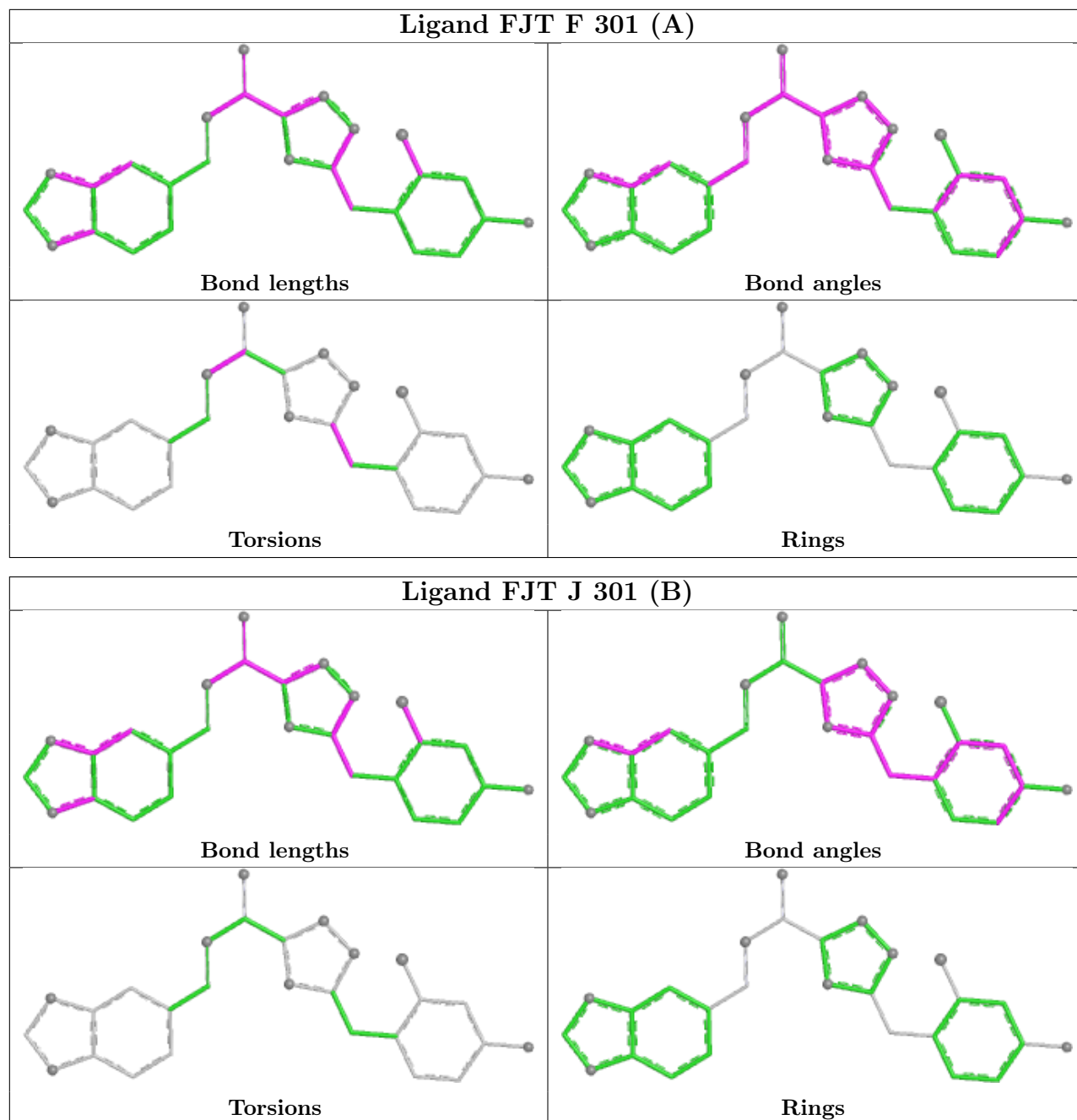


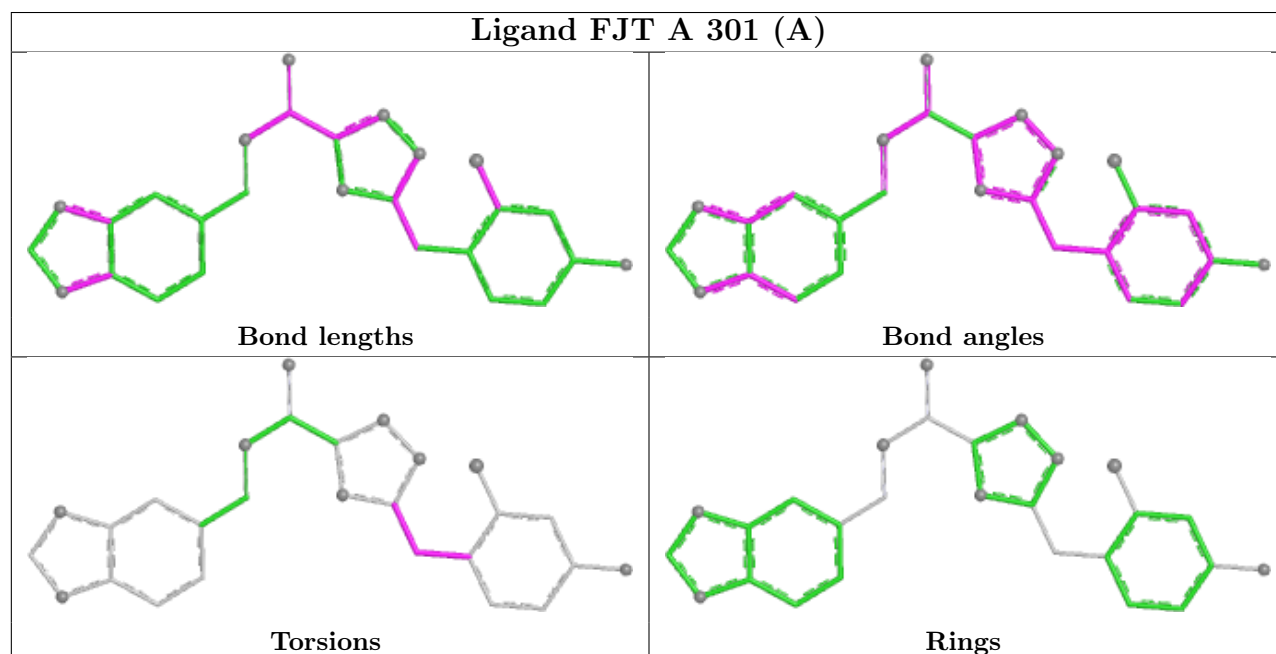
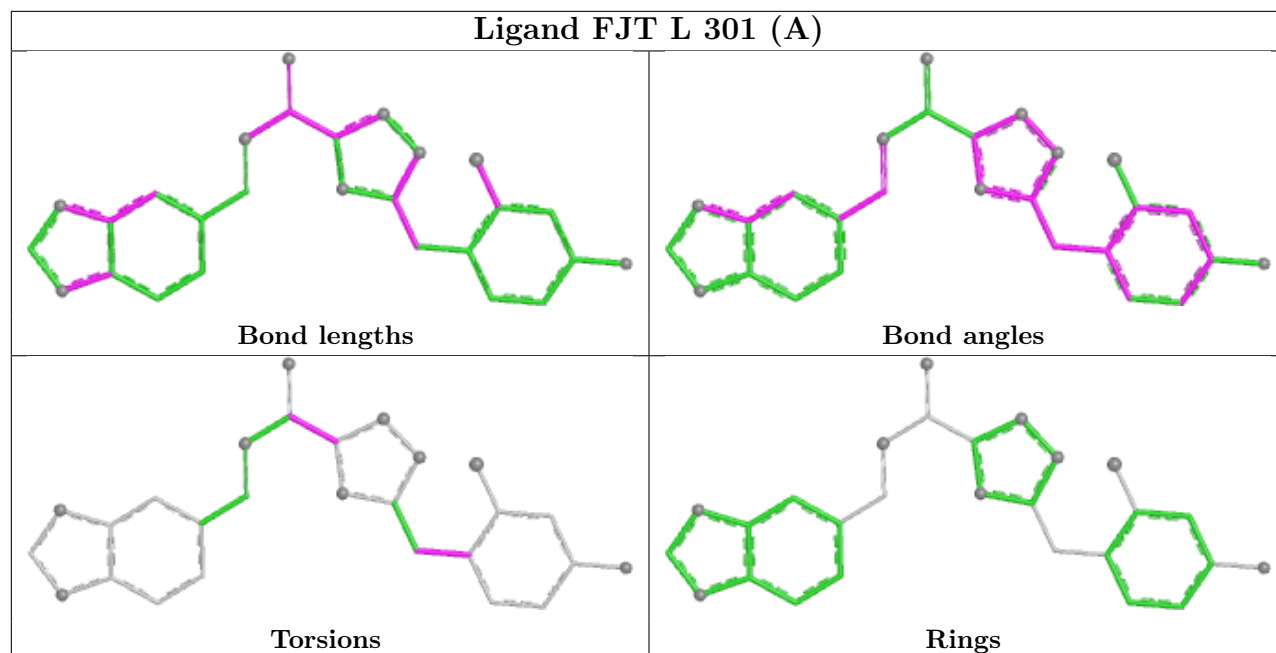
Ligand FJT J 301 (A)



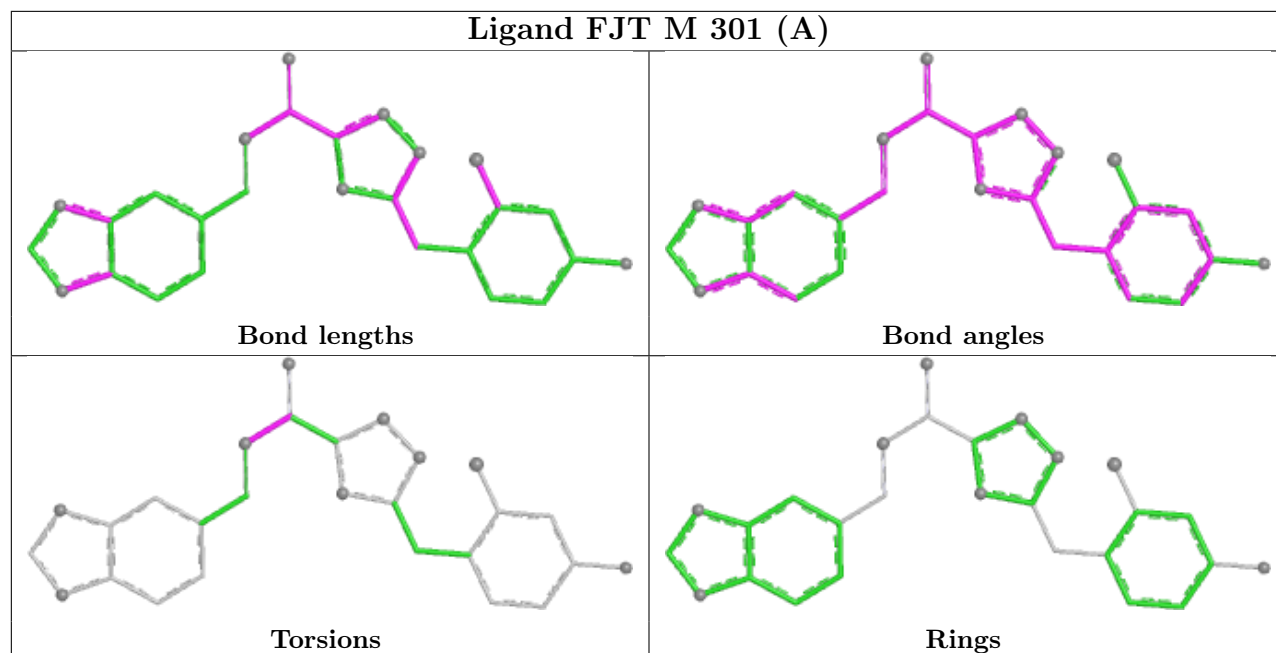
Ligand FJT E 301 (B)



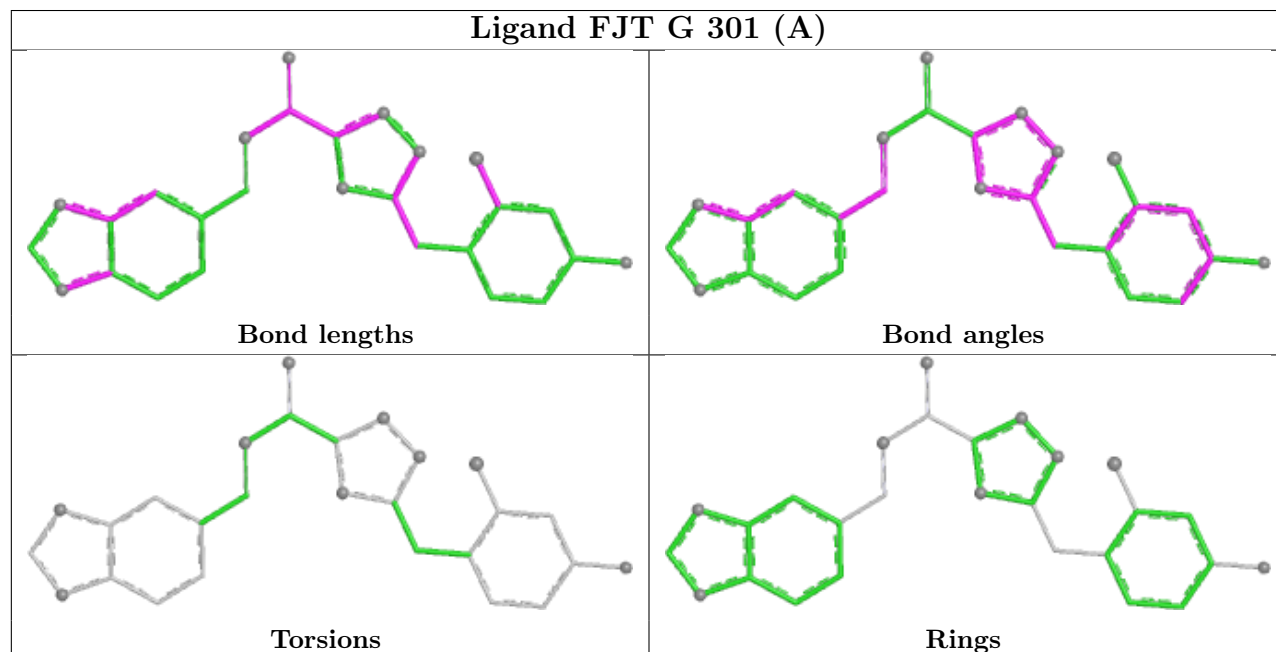




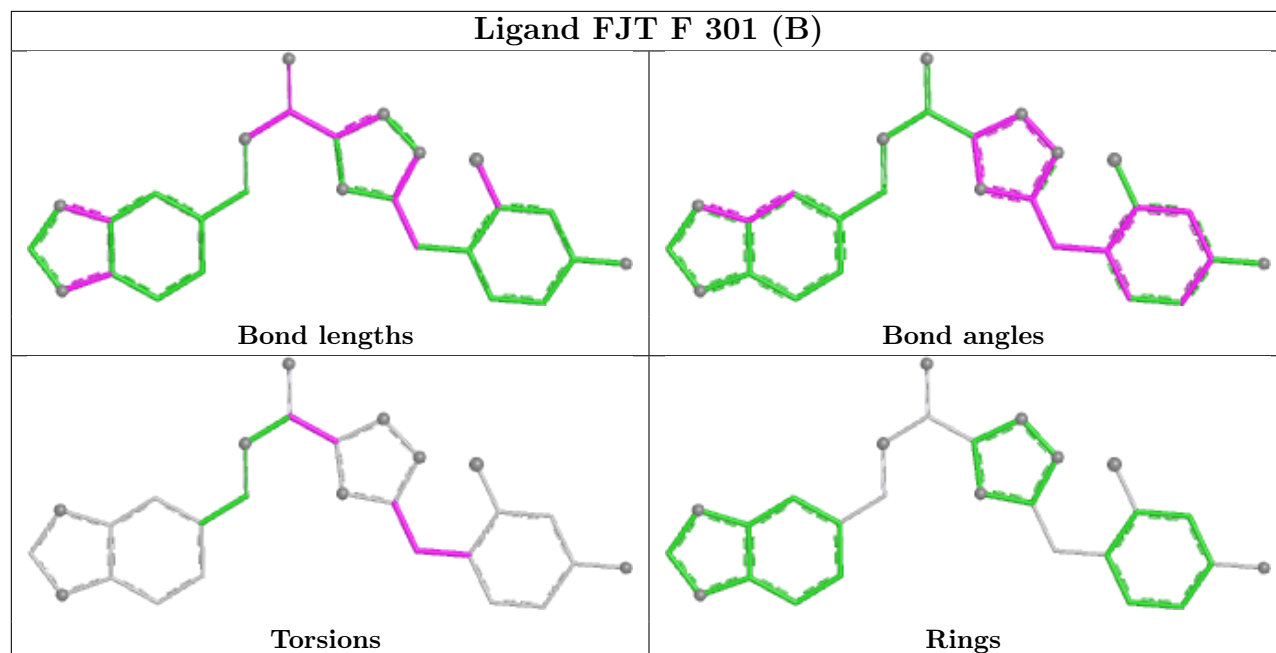
Ligand FJT M 301 (A)



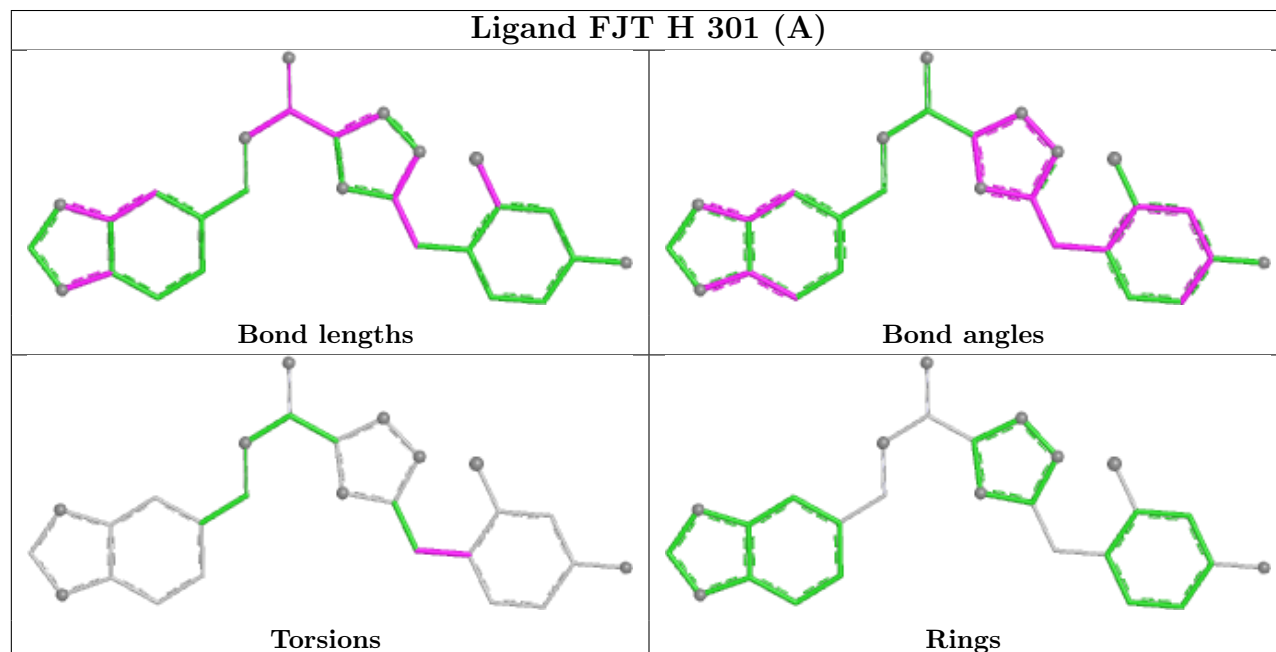
Ligand FJT G 301 (A)

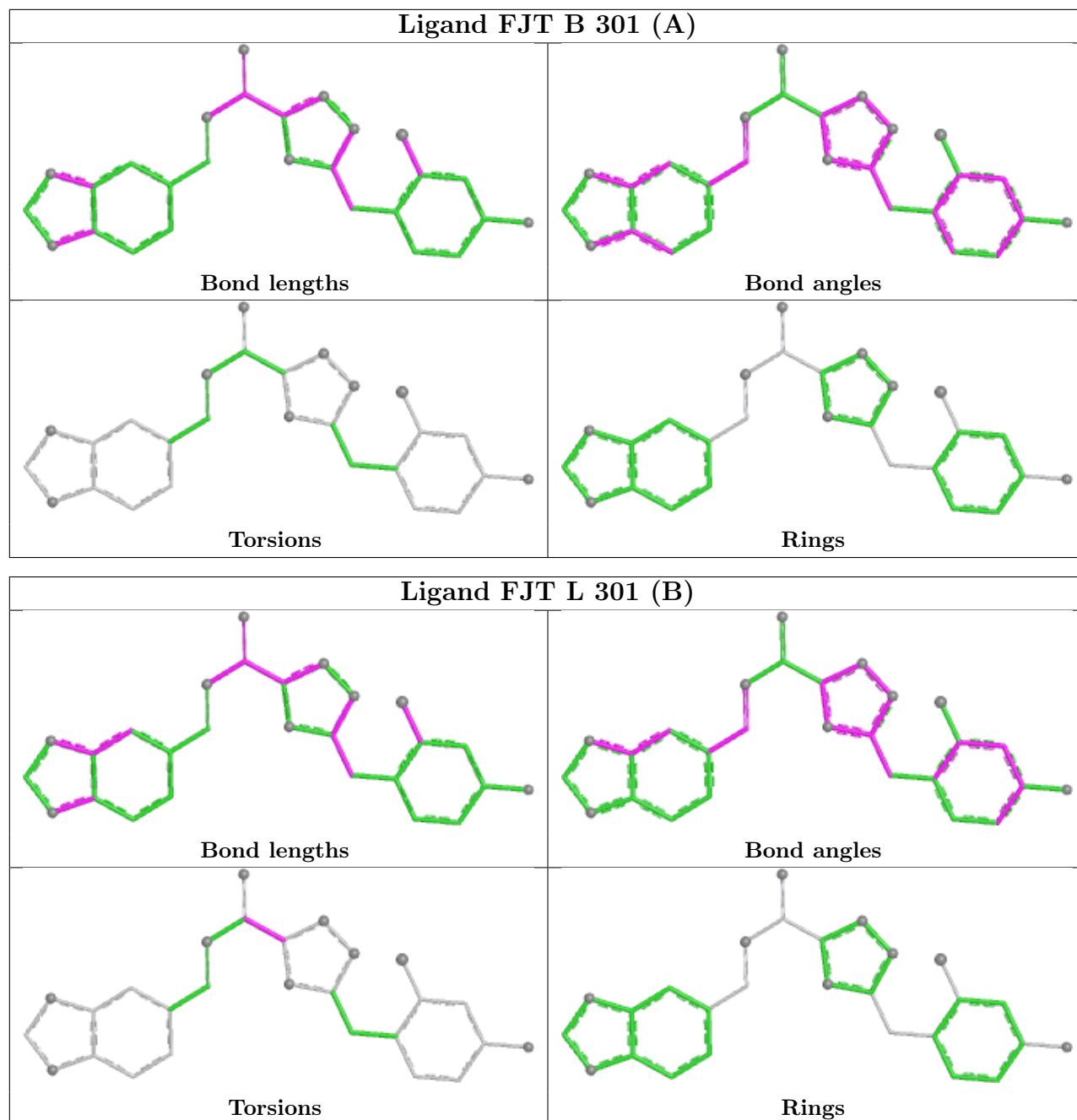


Ligand FJT F 301 (B)

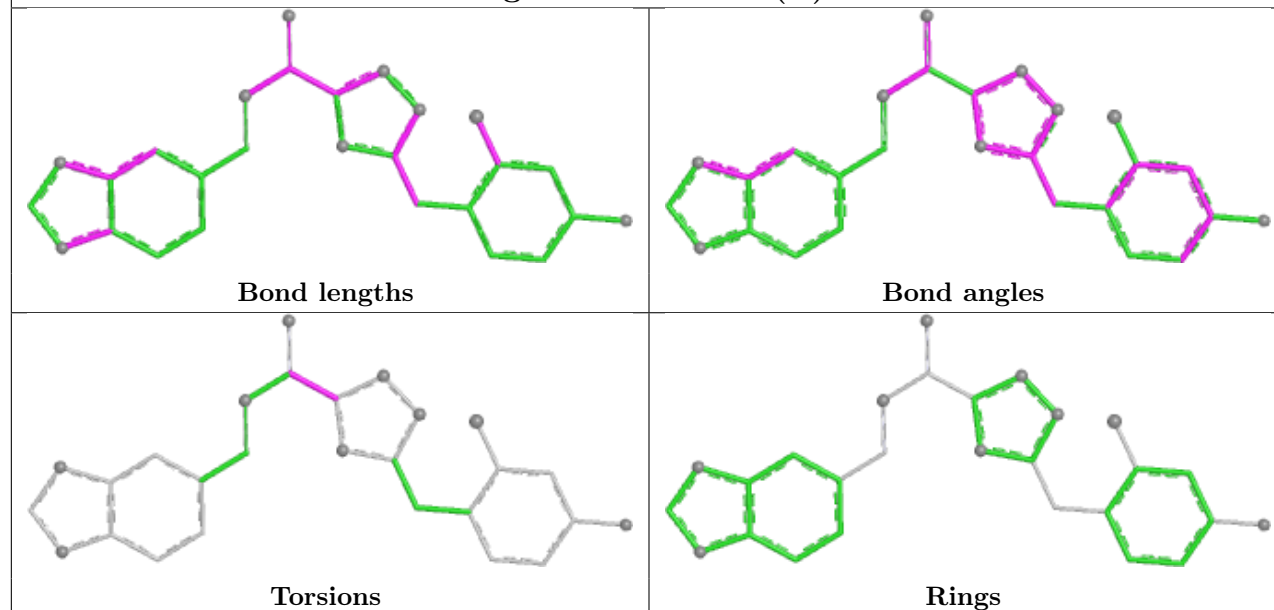


Ligand FJT H 301 (A)

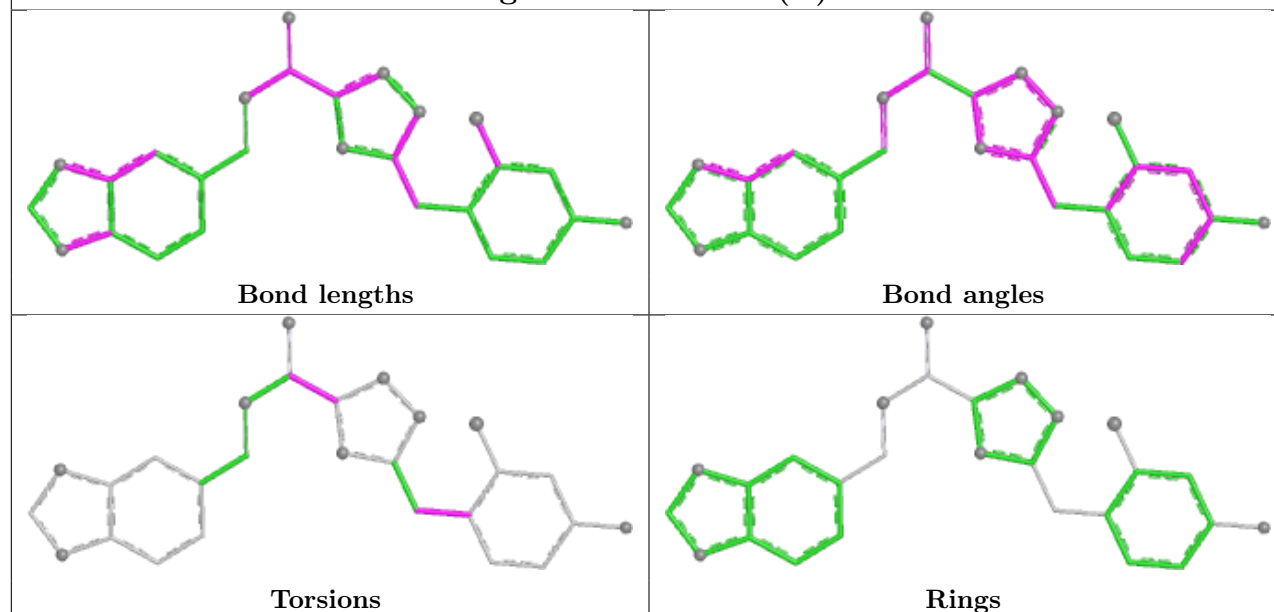


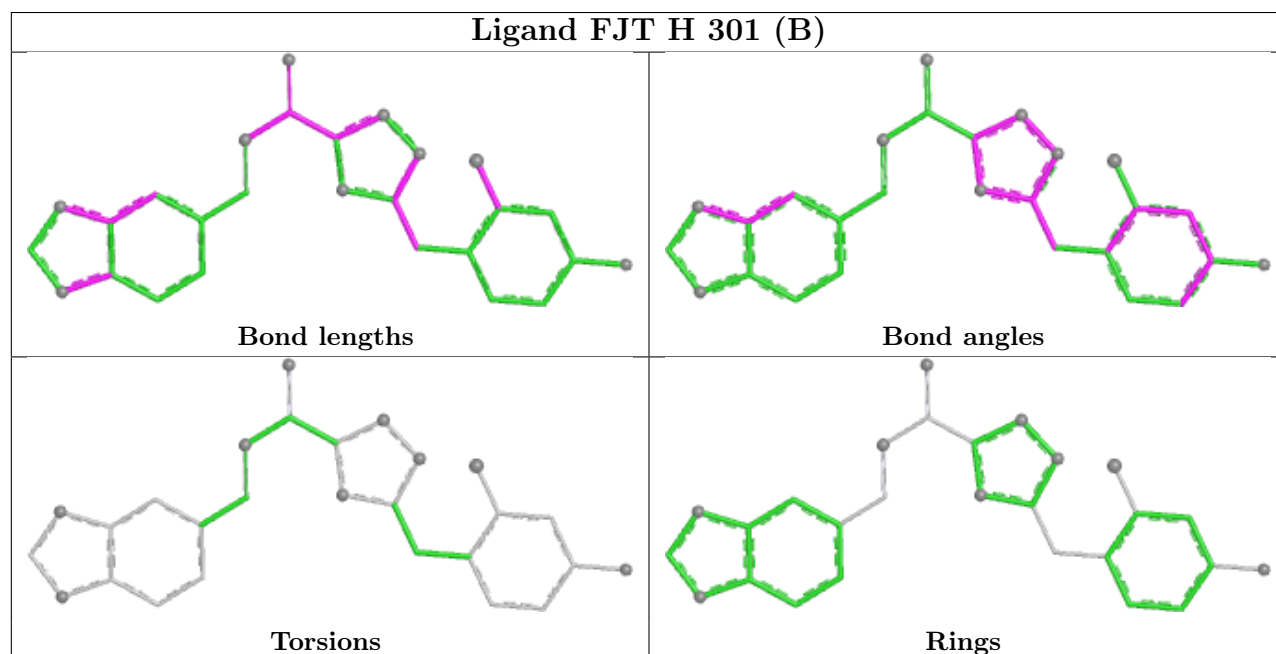
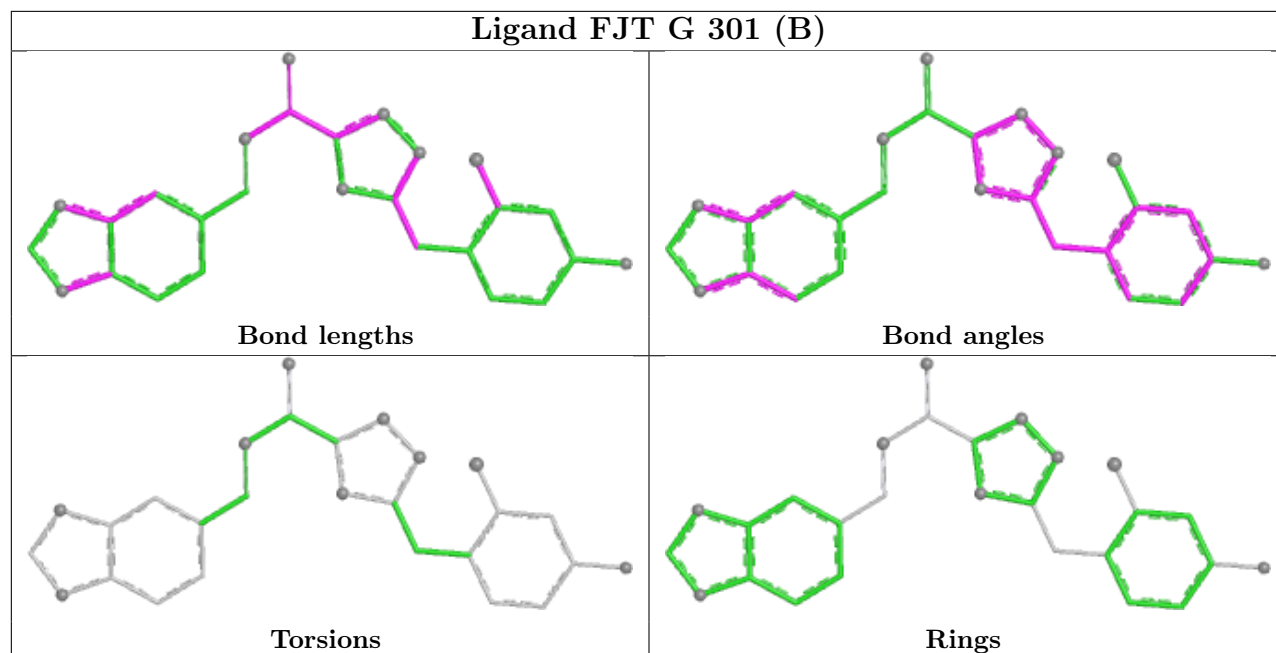


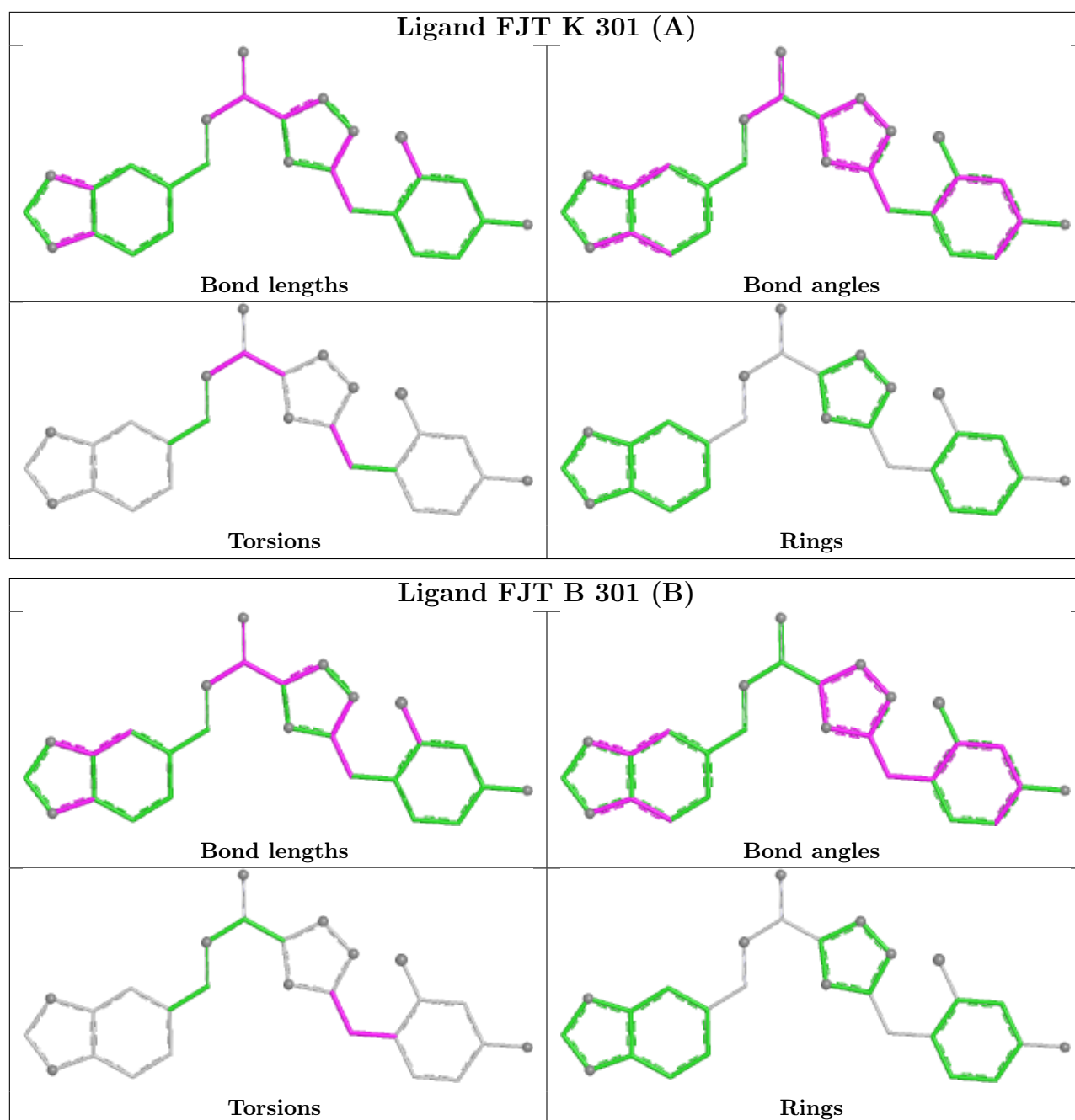
Ligand FJT A 301 (B)



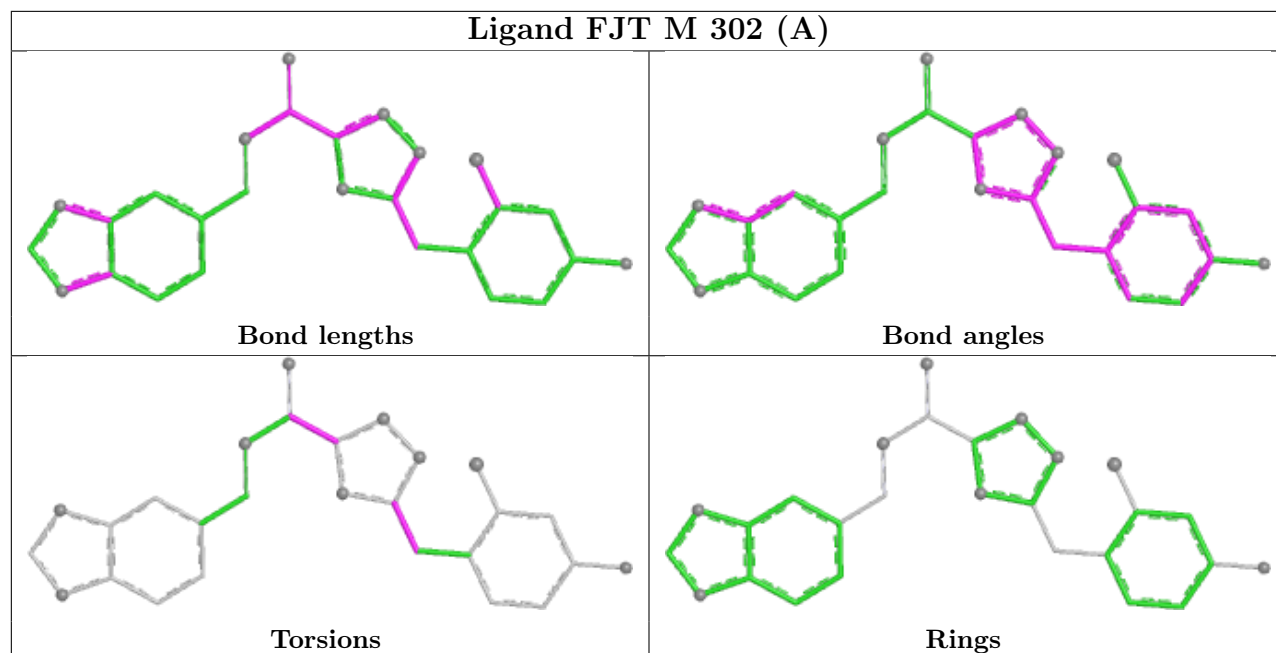
Ligand FJT M 301 (B)



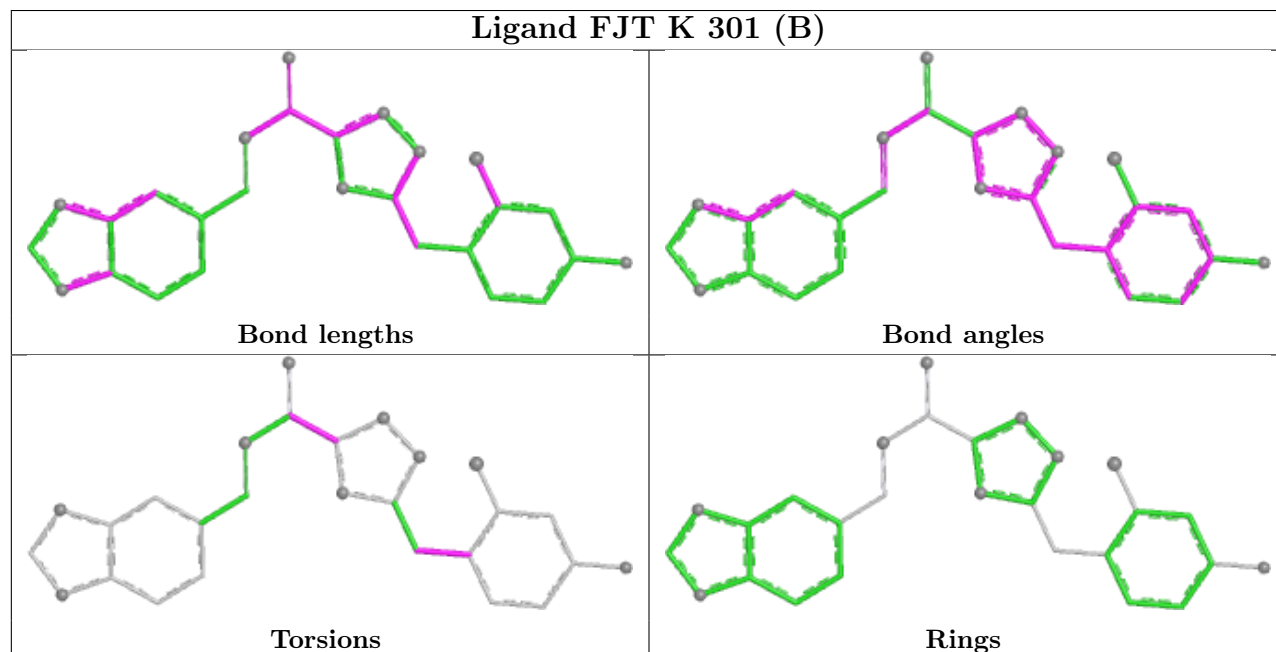


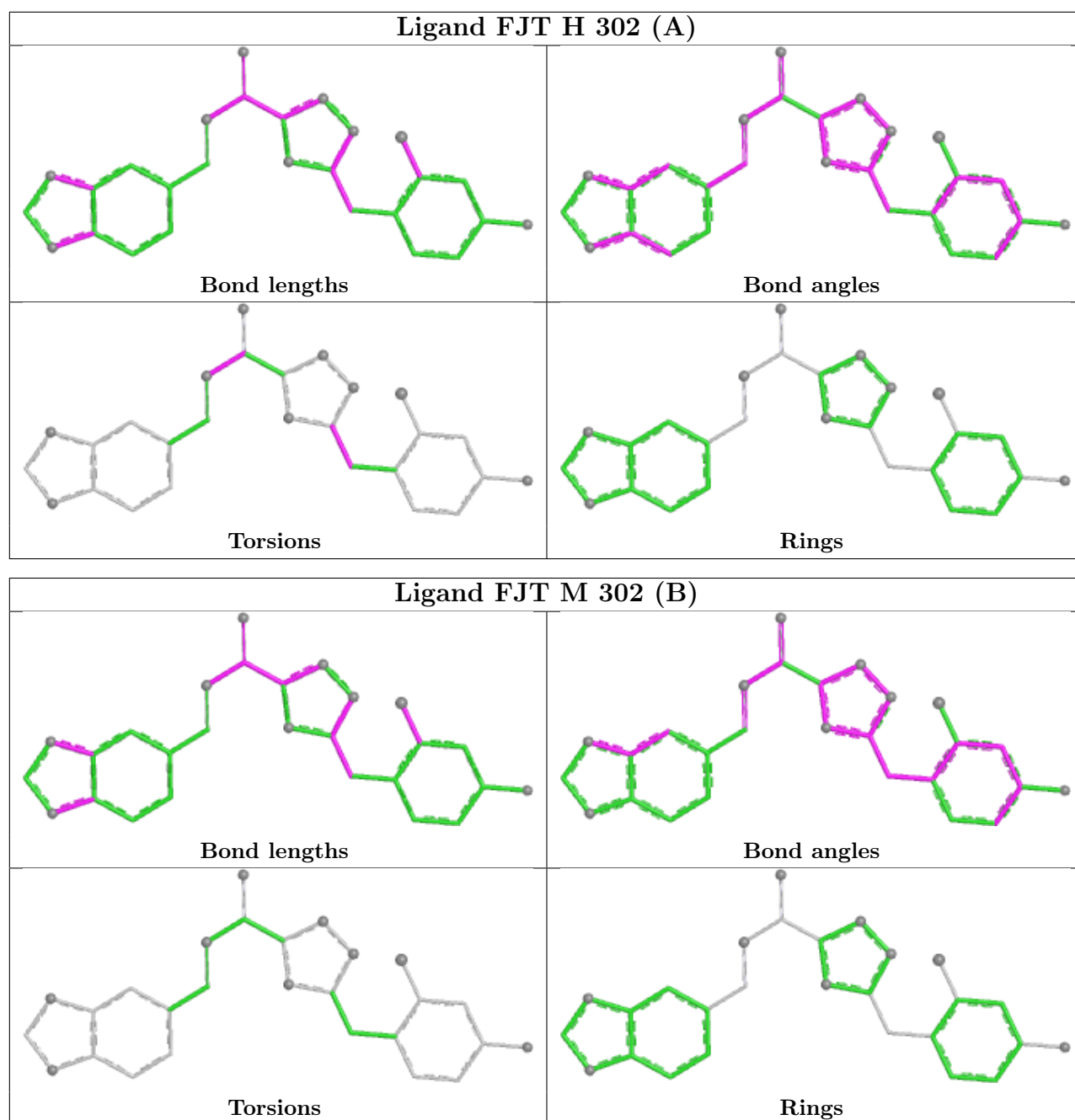


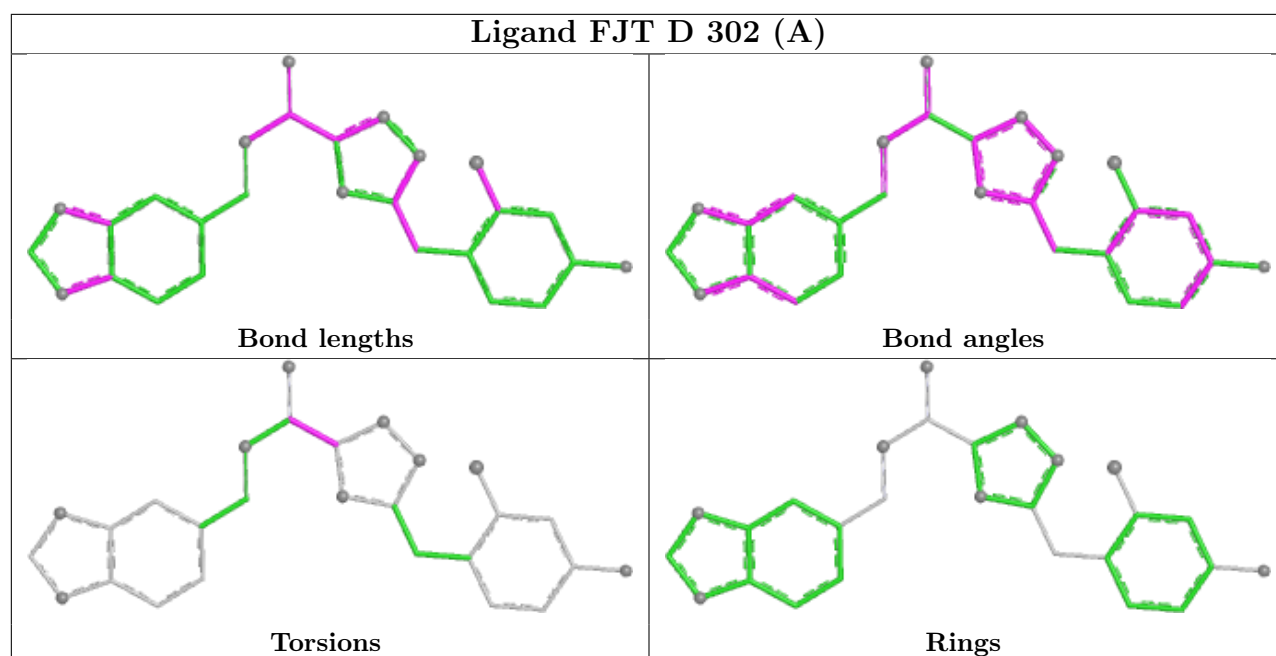
Ligand FJT M 302 (A)



Ligand FJT K 301 (B)







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

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	165/229 (72%)	-0.09	0 100 100	50, 65, 88, 107	0
1	B	166/229 (72%)	0.02	0 100 100	53, 67, 95, 103	0
1	C	166/229 (72%)	-0.00	1 (0%) 85 69	49, 69, 103, 117	0
1	D	164/229 (71%)	-0.16	0 100 100	50, 63, 84, 109	0
1	E	166/229 (72%)	-0.08	0 100 100	29, 59, 82, 110	1 (0%)
1	F	166/229 (72%)	-0.02	1 (0%) 85 69	28, 58, 85, 101	1 (0%)
1	G	169/229 (73%)	-0.04	1 (0%) 85 69	51, 65, 98, 113	0
1	H	167/229 (72%)	-0.01	0 100 100	33, 63, 88, 110	2 (1%)
1	I	167/229 (72%)	-0.12	1 (0%) 85 69	28, 62, 86, 110	2 (1%)
1	J	166/229 (72%)	-0.19	0 100 100	47, 60, 86, 112	0
1	K	166/229 (72%)	-0.11	1 (0%) 85 69	47, 61, 88, 118	0
1	L	166/229 (72%)	-0.20	1 (0%) 85 69	37, 55, 81, 117	1 (0%)
1	M	166/229 (72%)	-0.12	1 (0%) 85 69	32, 62, 86, 111	1 (0%)
1	N	168/229 (73%)	-0.05	2 (1%) 76 55	26, 62, 85, 108	1 (0%)
All	All	2328/3206 (72%)	-0.08	9 (0%) 88 75	26, 63, 91, 118	9 (0%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	88[A]	MET	4.1
1	F	88[A]	MET	3.6
1	K	192	ALA	3.0
1	N	192	ALA	2.9
1	G	190	ASP	2.4

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 oligosaccharides 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
2	FJT	D	302[A]	27/27	0.76	0.20	68,78,81,82	27
2	FJT	D	302[B]	27/27	0.76	0.20	68,77,81,82	27
2	FJT	F	301[A]	27/27	0.82	0.20	70,78,81,82	27
2	FJT	F	301[B]	27/27	0.82	0.20	71,79,81,82	27
2	FJT	H	302[A]	27/27	0.82	0.19	70,81,83,84	27
2	FJT	H	302[B]	27/27	0.82	0.19	69,81,82,83	27
2	FJT	K	301[A]	27/27	0.82	0.19	72,77,81,83	27
2	FJT	K	301[B]	27/27	0.82	0.19	72,77,81,83	27
2	FJT	M	301[A]	27/27	0.83	0.23	66,70,73,74	27
2	FJT	M	301[B]	27/27	0.83	0.23	64,70,74,75	27
2	FJT	L	301[A]	27/27	0.84	0.19	68,77,80,83	27
2	FJT	L	301[B]	27/27	0.84	0.19	68,78,81,84	27
2	FJT	A	301[A]	27/27	0.85	0.21	81,83,85,89	27
2	FJT	A	301[B]	27/27	0.85	0.21	81,83,86,86	27
2	FJT	M	302[A]	27/27	0.85	0.21	63,74,78,79	27
2	FJT	M	302[B]	27/27	0.85	0.21	64,74,79,79	27
3	EDO	E	302	4/4	0.85	0.14	56,57,61,65	0
2	FJT	B	301[B]	27/27	0.86	0.22	82,91,94,96	27
3	EDO	A	302	4/4	0.86	0.14	49,55,60,61	0
2	FJT	B	301[A]	27/27	0.86	0.22	81,92,95,95	27
2	FJT	G	301[A]	27/27	0.87	0.21	79,85,88,90	27
2	FJT	G	301[B]	27/27	0.87	0.21	79,85,88,89	27
3	EDO	F	302	4/4	0.88	0.14	53,58,59,62	0
2	FJT	E	301[B]	27/27	0.89	0.20	62,71,73,76	27
2	FJT	D	301	27/27	0.89	0.15	71,85,89,90	27
2	FJT	E	301[A]	27/27	0.89	0.20	66,71,74,77	27
3	EDO	N	301	4/4	0.89	0.14	59,62,66,67	0

Continued on next page...

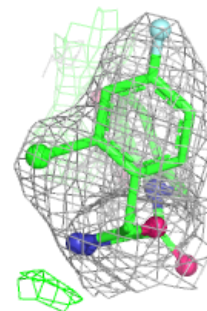
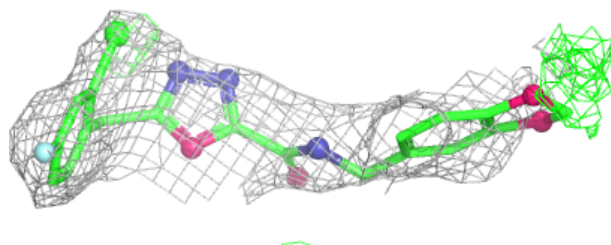
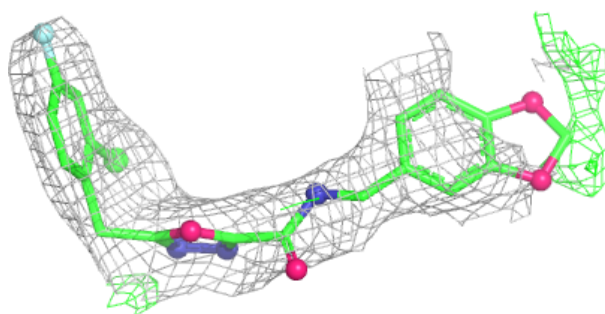
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FJT	H	301[A]	27/27	0.90	0.14	73,79,84,84	27
2	FJT	H	301[B]	27/27	0.90	0.14	71,80,84,84	27
2	FJT	J	301[A]	27/27	0.91	0.18	70,75,81,83	27
2	FJT	J	301[B]	27/27	0.91	0.18	71,75,81,83	27

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.

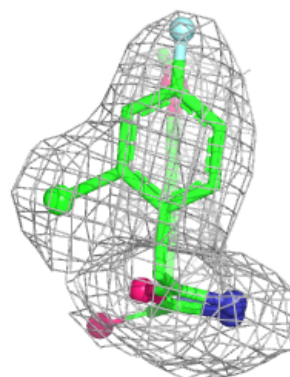
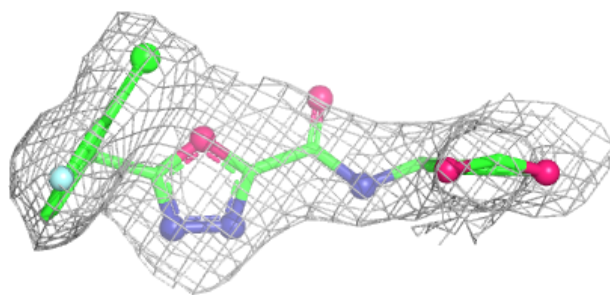
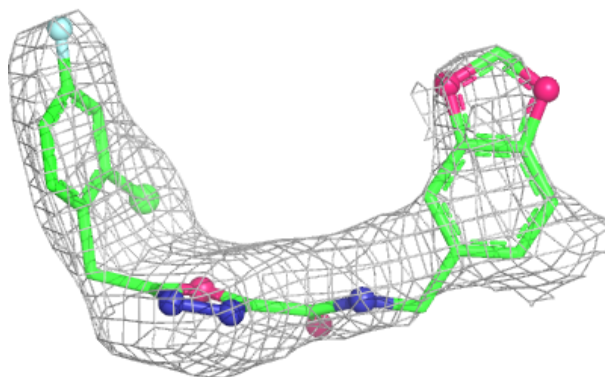
Electron density around FJT D 302 (A):

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

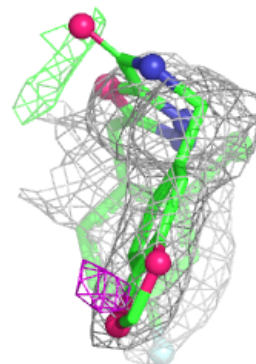
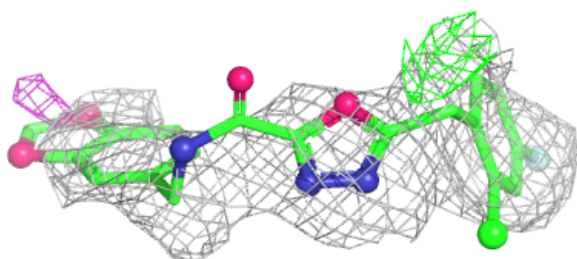
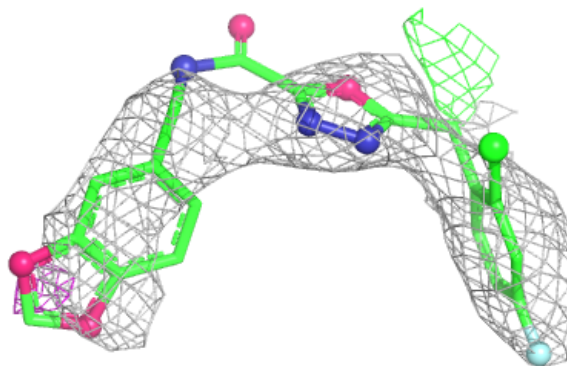


Electron density around FJT D 302 (B):

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

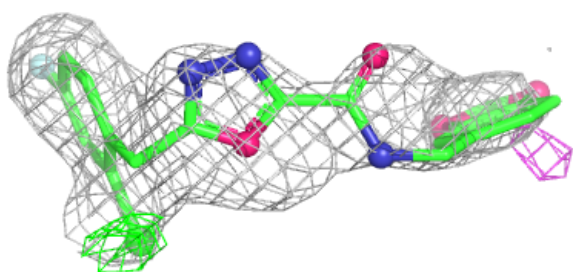
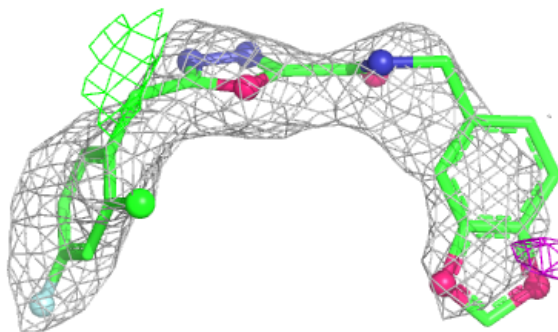
**Electron density around FJT F 301 (A):**

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

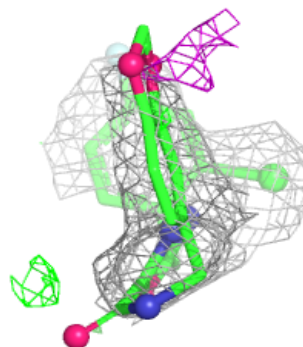
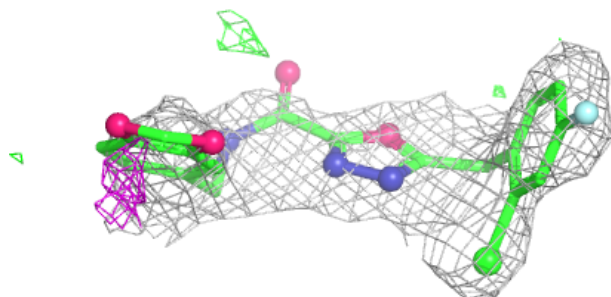
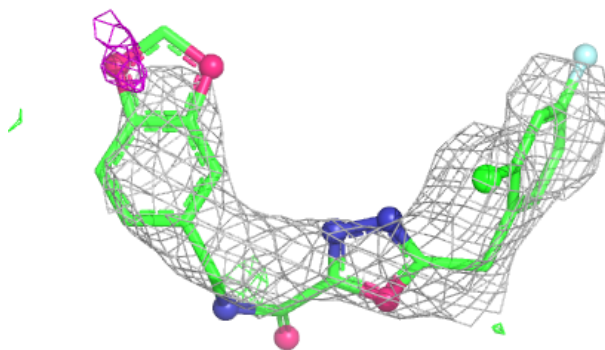


Electron density around FJT F 301 (B):

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

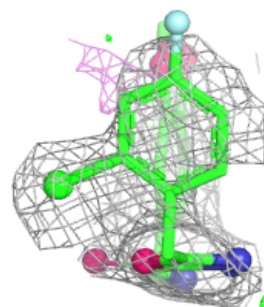
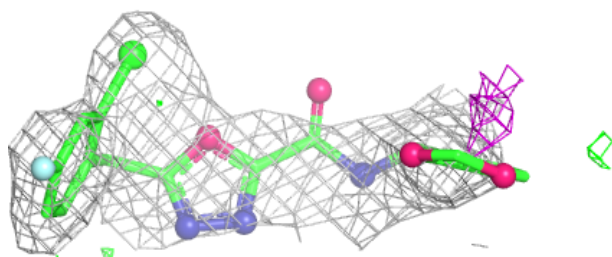
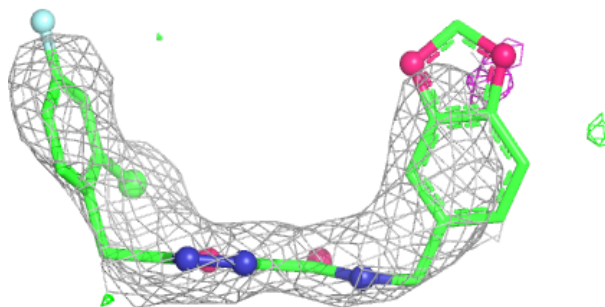
**Electron density around FJT H 302 (A):**

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

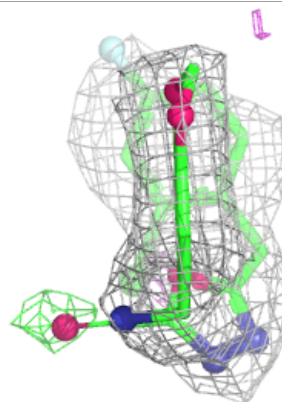
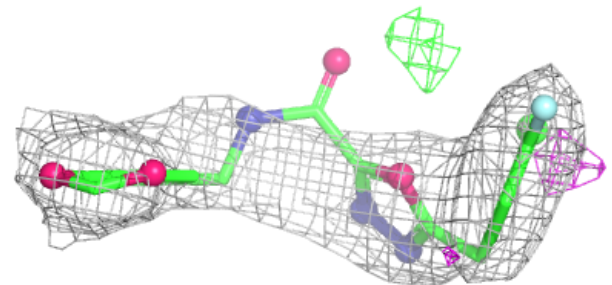
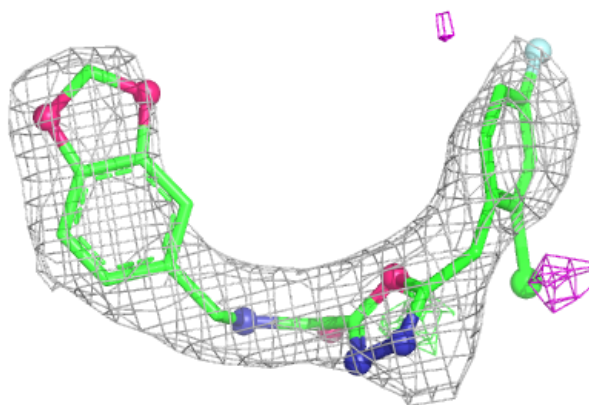


Electron density around FJT H 302 (B):

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

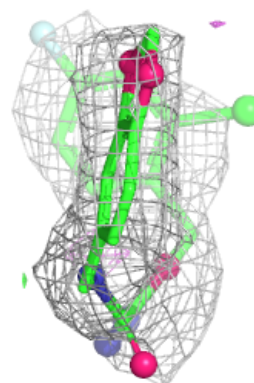
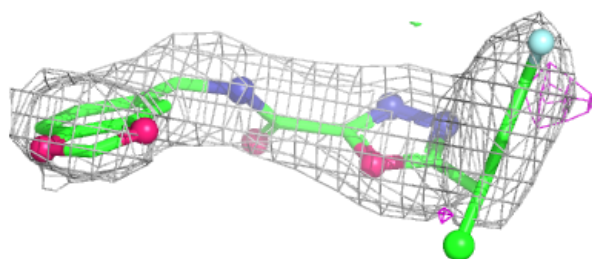
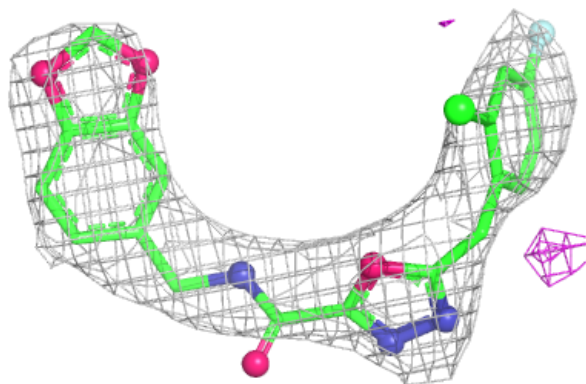
**Electron density around FJT K 301 (A):**

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

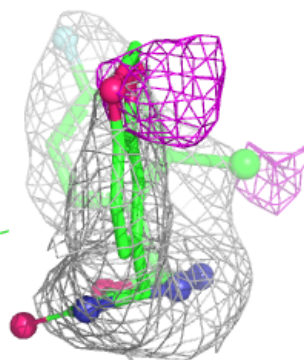
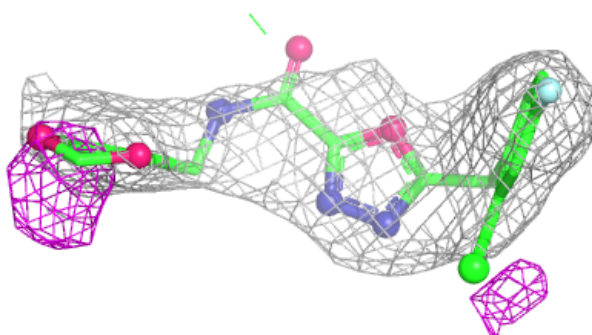
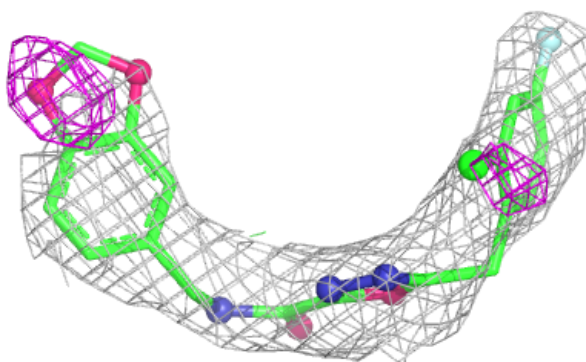


Electron density around FJT K 301 (B):

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

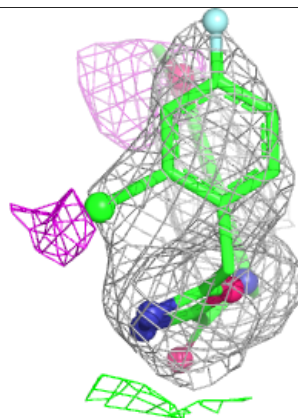
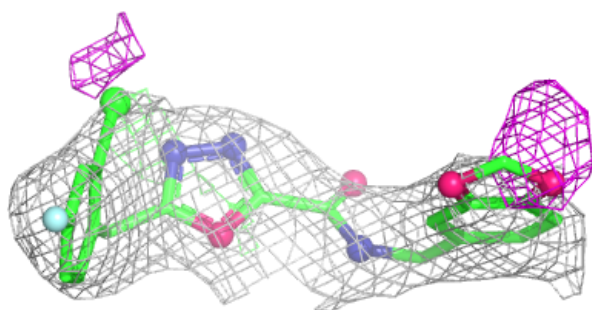
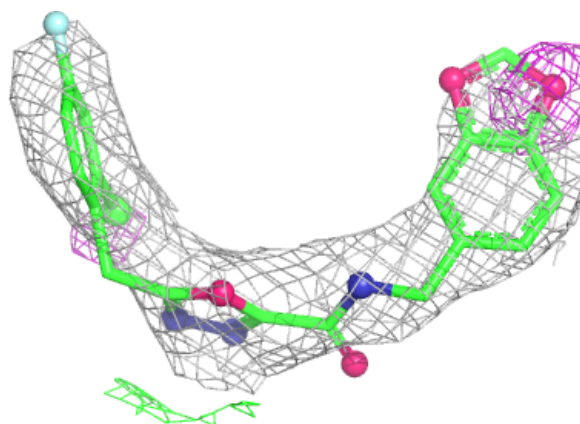
**Electron density around FJT M 301 (A):**

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

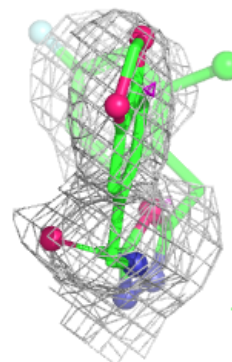
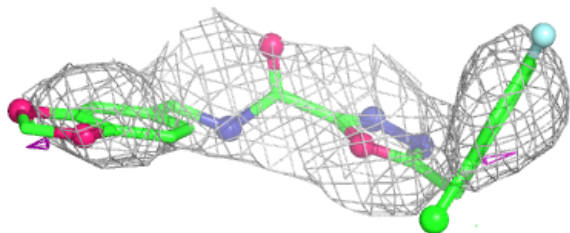
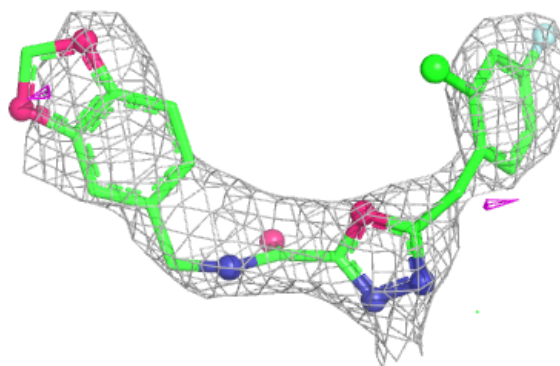


Electron density around FJT M 301 (B):

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

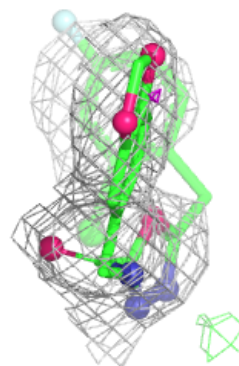
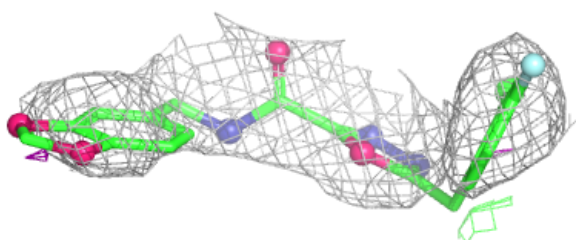
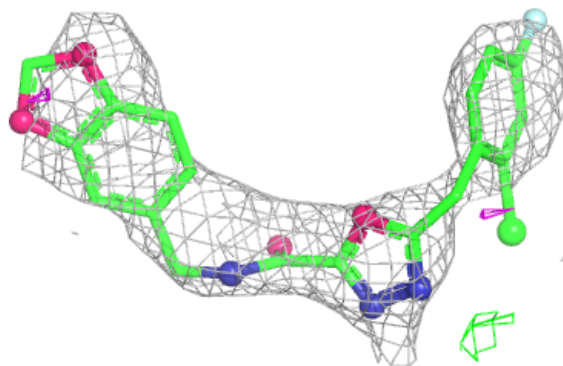
**Electron density around FJT L 301 (A):**

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

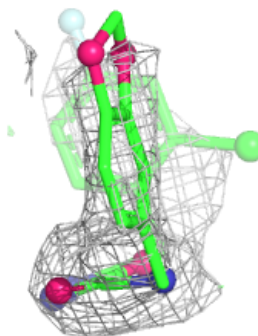
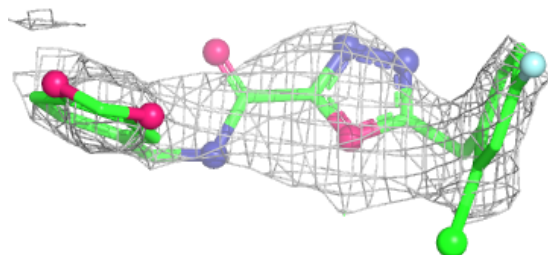
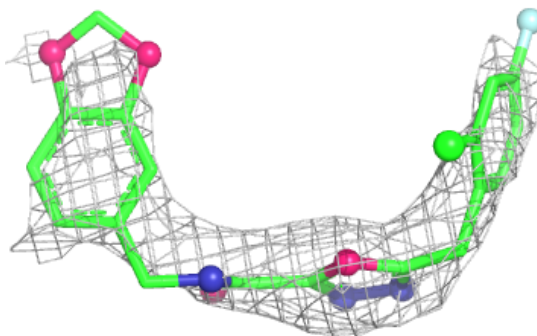


Electron density around FJT L 301 (B):

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

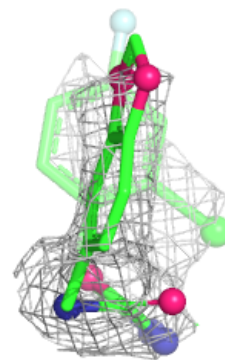
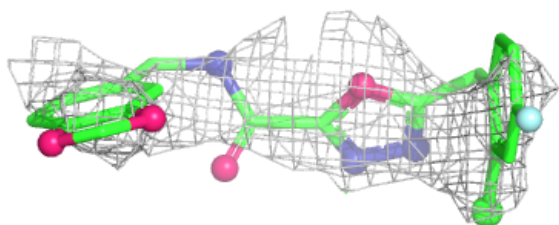
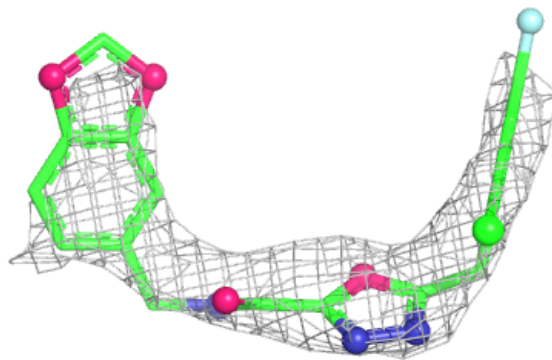
**Electron density around FJT A 301 (A):**

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

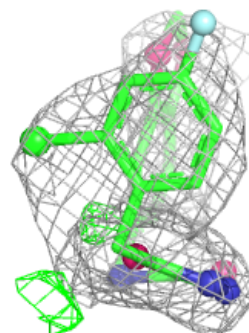
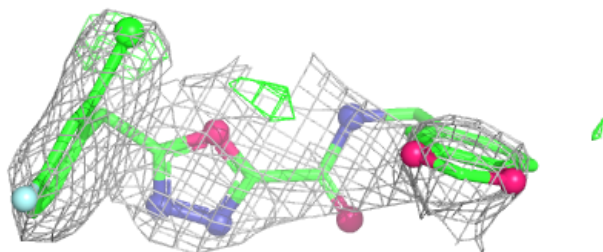
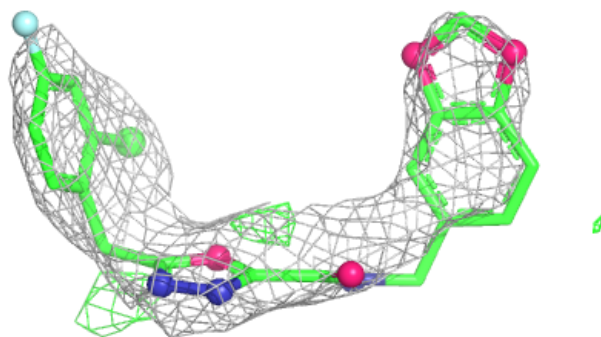


Electron density around FJT A 301 (B):

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

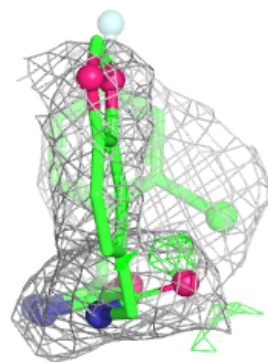
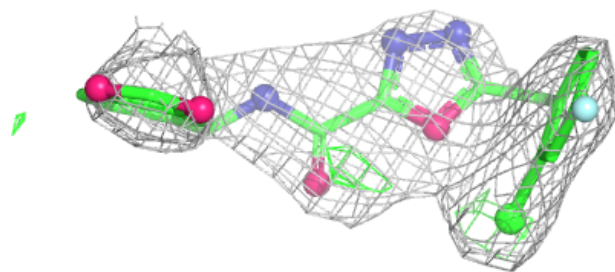
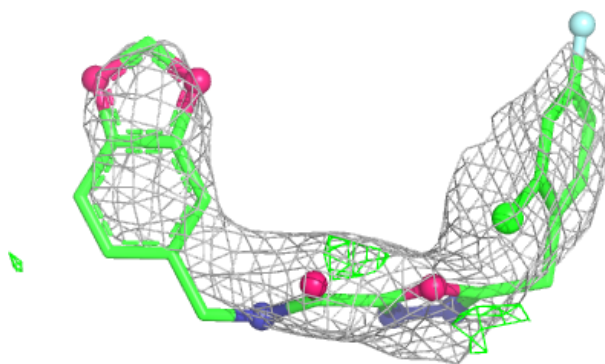
**Electron density around FJT M 302 (A):**

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

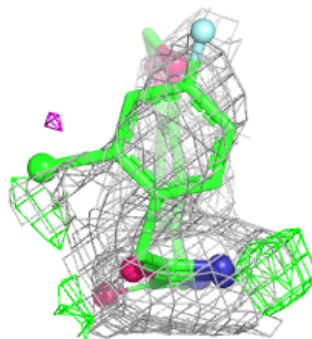
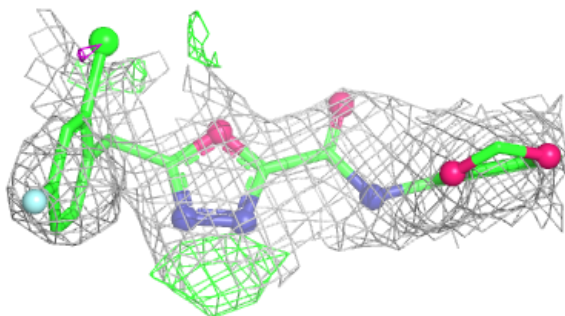
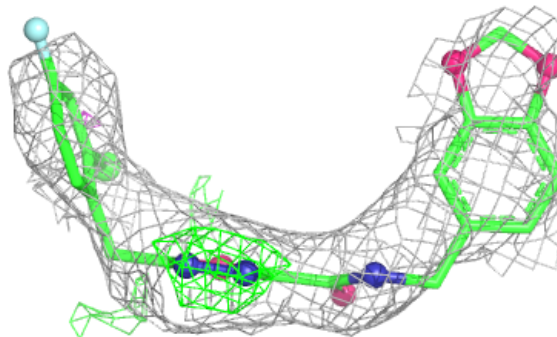


Electron density around FJT M 302 (B):

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

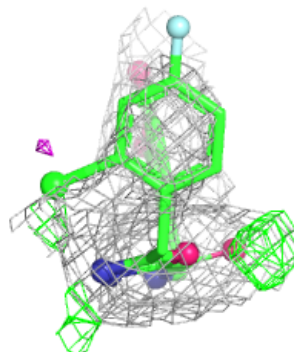
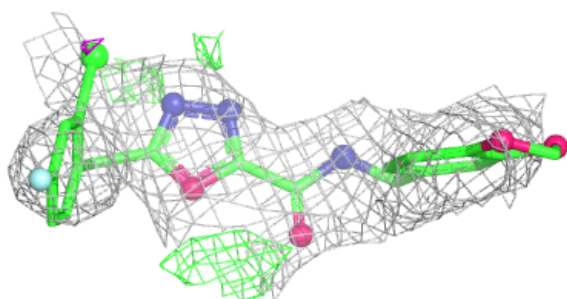
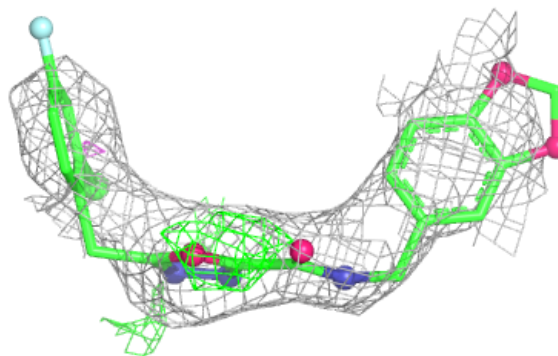
**Electron density around FJT B 301 (B):**

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

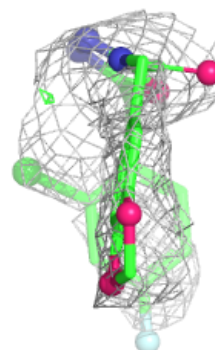
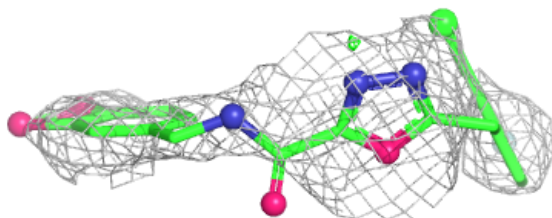
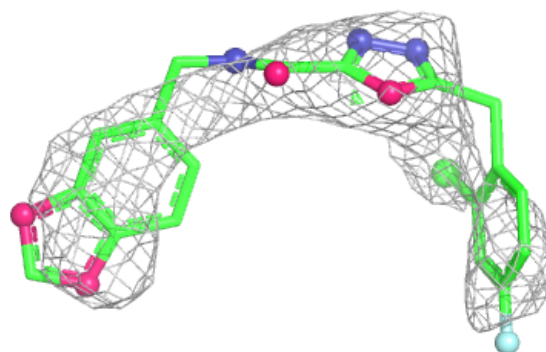


Electron density around FJT B 301 (A):

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

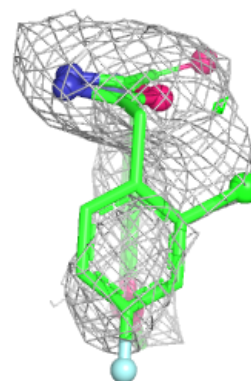
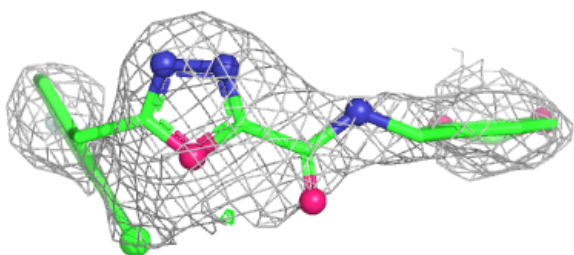
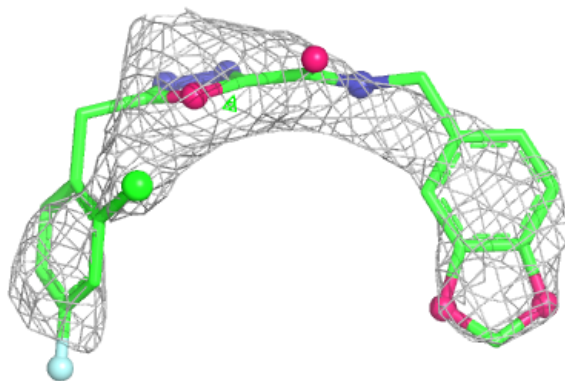
**Electron density around FJT G 301 (A):**

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

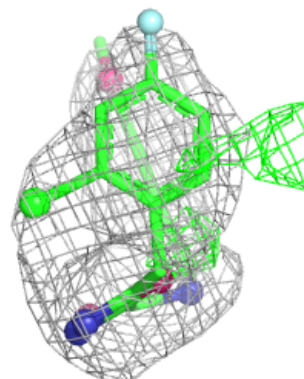
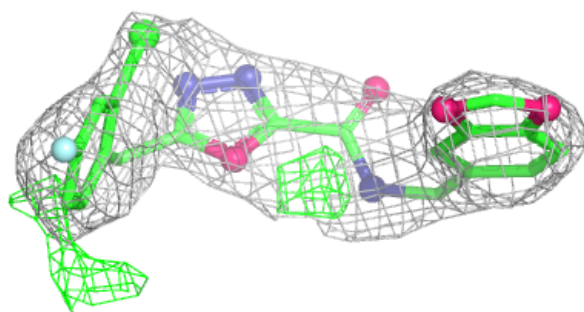
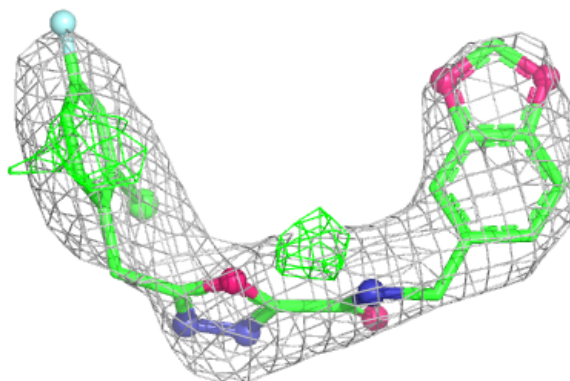


Electron density around FJT G 301 (B):

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

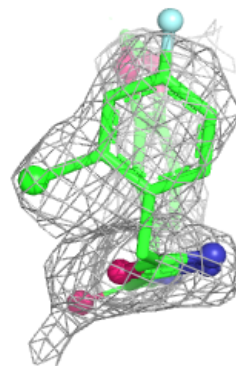
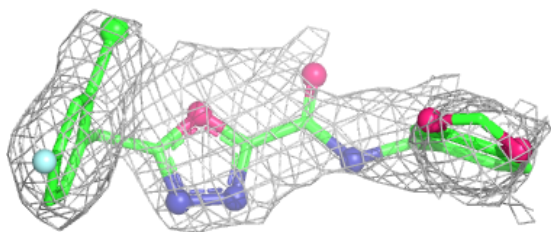
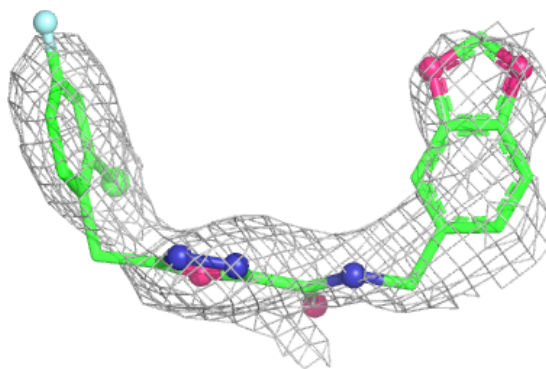
**Electron density around FJT E 301 (B):**

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

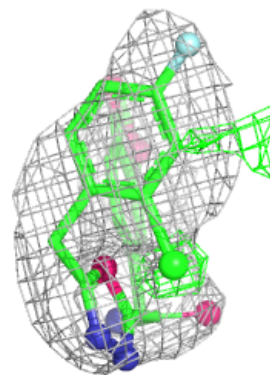
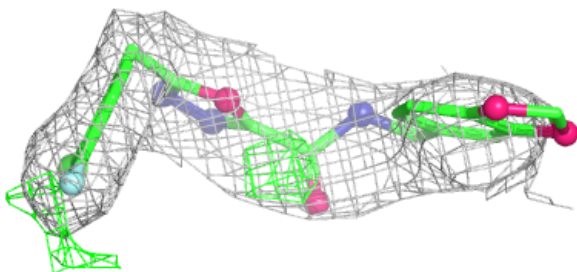
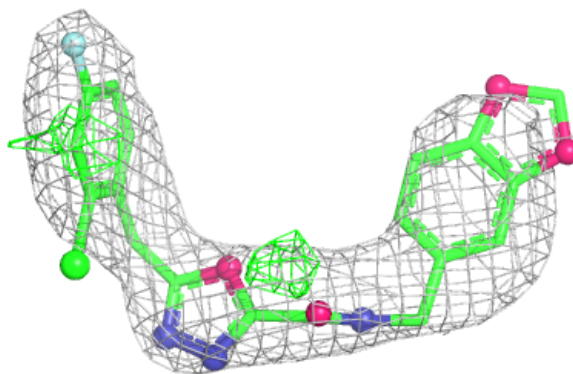


Electron density around FJT D 301:

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

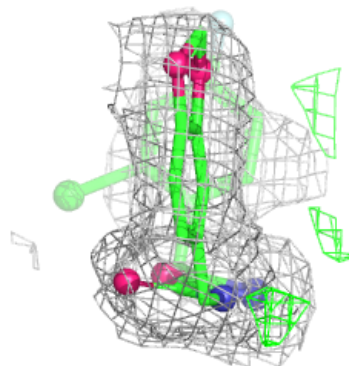
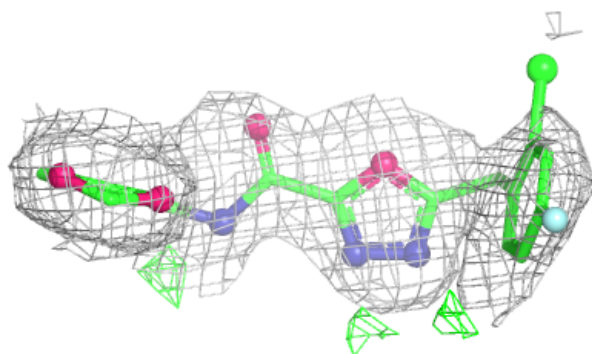
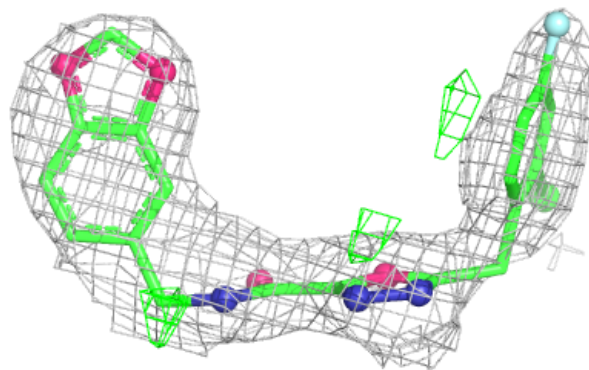
**Electron density around FJT E 301 (A):**

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

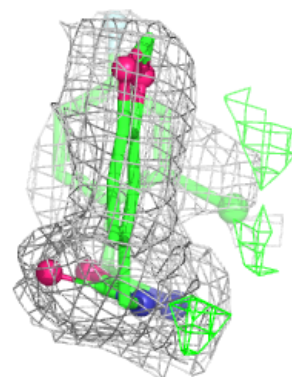
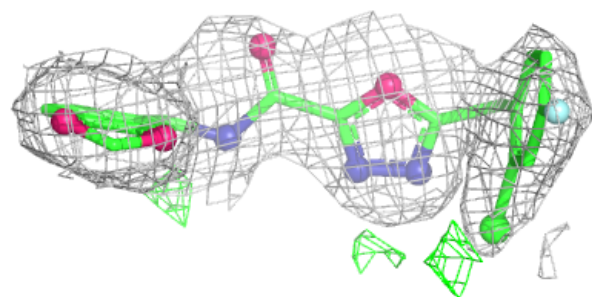
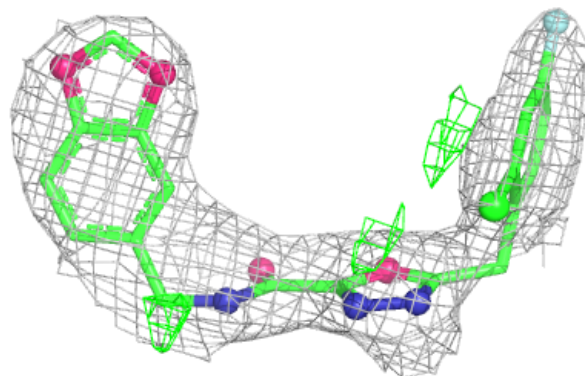


Electron density around FJT H 301 (A):

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

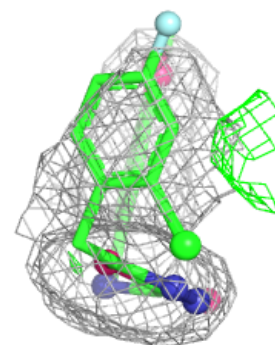
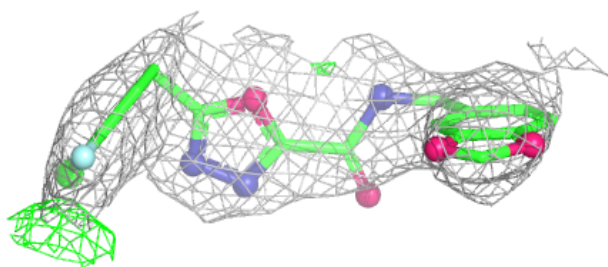
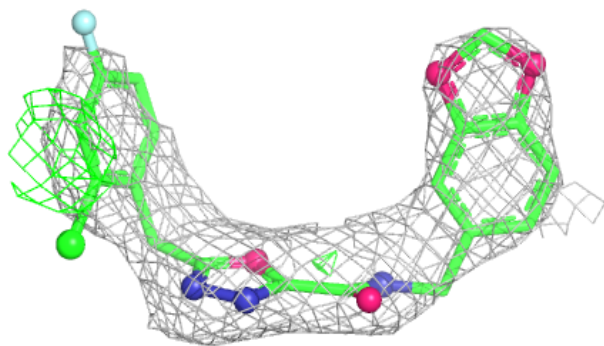
**Electron density around FJT H 301 (B):**

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

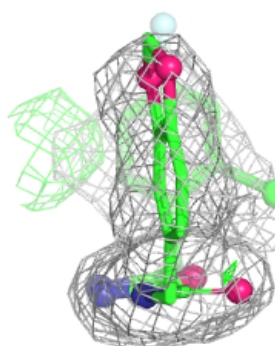
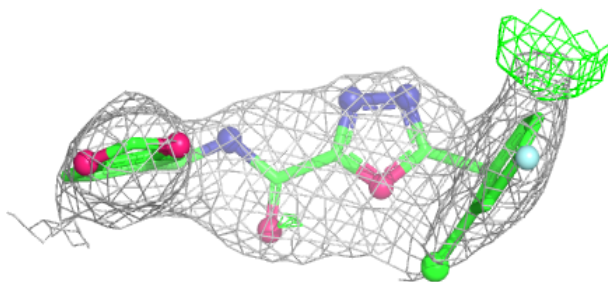
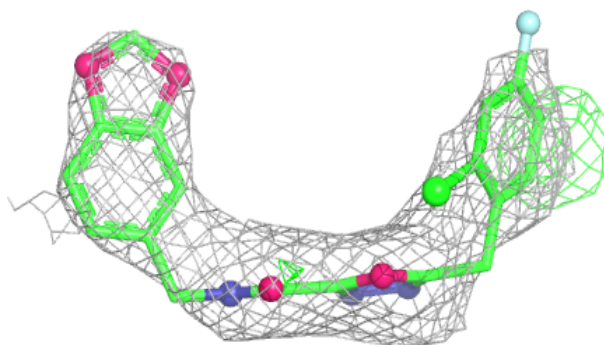


Electron density around FJT J 301 (A):

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

**Electron density around FJT J 301 (B):**

$2mF_o - DF_c$ (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.