



# Full wwPDB X-ray Structure Validation Report i

Nov 23, 2023 – 01:10 AM JST

PDB ID : 7XYL  
Title : E426Q-glycine-glycylthricin complex  
Authors : Wang, Y.L.; Li, T.L.  
Deposited on : 2022-06-01  
Resolution : 2.10 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 i 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](#) ①) 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 : 2.36  
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) : 2.36

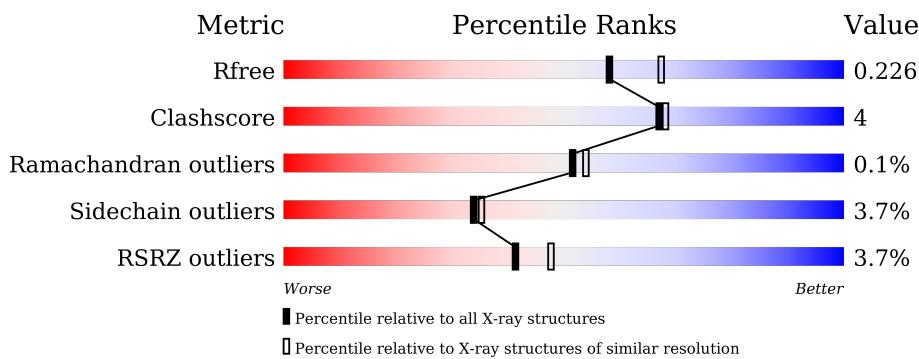
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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.



*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain		
1	G	512	1%	87%	6% • 6%
1	H	512	13%	84%	8% • 6%

## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 32464 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 N-formimidoyl fortimicin A synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C 3654	N 2293	O 661	S 688	12	0	0
1	B	482	Total	C 3654	N 2293	O 661	S 688	12	0	0
1	C	482	Total	C 3654	N 2293	O 661	S 688	12	0	0
1	D	479	Total	C 3636	N 2283	O 658	S 682	13	0	1
1	E	482	Total	C 3662	N 2298	O 662	S 689	13	0	1
1	F	482	Total	C 3662	N 2297	O 662	S 691	12	0	1
1	G	482	Total	C 3654	N 2293	O 661	S 688	12	0	0
1	H	479	Total	C 3636	N 2283	O 658	S 682	13	0	1

There are 176 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP A0A125SXC1
A	-19	GLY	-	expression tag	UNP A0A125SXC1
A	-18	SER	-	expression tag	UNP A0A125SXC1
A	-17	SER	-	expression tag	UNP A0A125SXC1
A	-16	HIS	-	expression tag	UNP A0A125SXC1
A	-15	HIS	-	expression tag	UNP A0A125SXC1
A	-14	HIS	-	expression tag	UNP A0A125SXC1
A	-13	HIS	-	expression tag	UNP A0A125SXC1
A	-12	HIS	-	expression tag	UNP A0A125SXC1
A	-11	HIS	-	expression tag	UNP A0A125SXC1
A	-10	SER	-	expression tag	UNP A0A125SXC1
A	-9	SER	-	expression tag	UNP A0A125SXC1
A	-8	GLY	-	expression tag	UNP A0A125SXC1

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	LEU	-	expression tag	UNP A0A125S2C1
A	-6	VAL	-	expression tag	UNP A0A125S2C1
A	-5	PRO	-	expression tag	UNP A0A125S2C1
A	-4	ARG	-	expression tag	UNP A0A125S2C1
A	-3	GLY	-	expression tag	UNP A0A125S2C1
A	-2	SER	-	expression tag	UNP A0A125S2C1
A	-1	HIS	-	expression tag	UNP A0A125S2C1
A	0	MET	-	expression tag	UNP A0A125S2C1
A	426	GLN	GLU	engineered mutation	UNP A0A125S2C1
B	-20	MET	-	initiating methionine	UNP A0A125S2C1
B	-19	GLY	-	expression tag	UNP A0A125S2C1
B	-18	SER	-	expression tag	UNP A0A125S2C1
B	-17	SER	-	expression tag	UNP A0A125S2C1
B	-16	HIS	-	expression tag	UNP A0A125S2C1
B	-15	HIS	-	expression tag	UNP A0A125S2C1
B	-14	HIS	-	expression tag	UNP A0A125S2C1
B	-13	HIS	-	expression tag	UNP A0A125S2C1
B	-12	HIS	-	expression tag	UNP A0A125S2C1
B	-11	HIS	-	expression tag	UNP A0A125S2C1
B	-10	SER	-	expression tag	UNP A0A125S2C1
B	-9	SER	-	expression tag	UNP A0A125S2C1
B	-8	GLY	-	expression tag	UNP A0A125S2C1
B	-7	LEU	-	expression tag	UNP A0A125S2C1
B	-6	VAL	-	expression tag	UNP A0A125S2C1
B	-5	PRO	-	expression tag	UNP A0A125S2C1
B	-4	ARG	-	expression tag	UNP A0A125S2C1
B	-3	GLY	-	expression tag	UNP A0A125S2C1
B	-2	SER	-	expression tag	UNP A0A125S2C1
B	-1	HIS	-	expression tag	UNP A0A125S2C1
B	0	MET	-	expression tag	UNP A0A125S2C1
B	426	GLN	GLU	engineered mutation	UNP A0A125S2C1
C	-20	MET	-	initiating methionine	UNP A0A125S2C1
C	-19	GLY	-	expression tag	UNP A0A125S2C1
C	-18	SER	-	expression tag	UNP A0A125S2C1
C	-17	SER	-	expression tag	UNP A0A125S2C1
C	-16	HIS	-	expression tag	UNP A0A125S2C1
C	-15	HIS	-	expression tag	UNP A0A125S2C1
C	-14	HIS	-	expression tag	UNP A0A125S2C1
C	-13	HIS	-	expression tag	UNP A0A125S2C1
C	-12	HIS	-	expression tag	UNP A0A125S2C1
C	-11	HIS	-	expression tag	UNP A0A125S2C1
C	-10	SER	-	expression tag	UNP A0A125S2C1

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	-9	SER	-	expression tag	UNP A0A125S2C1
C	-8	GLY	-	expression tag	UNP A0A125S2C1
C	-7	LEU	-	expression tag	UNP A0A125S2C1
C	-6	VAL	-	expression tag	UNP A0A125S2C1
C	-5	PRO	-	expression tag	UNP A0A125S2C1
C	-4	ARG	-	expression tag	UNP A0A125S2C1
C	-3	GLY	-	expression tag	UNP A0A125S2C1
C	-2	SER	-	expression tag	UNP A0A125S2C1
C	-1	HIS	-	expression tag	UNP A0A125S2C1
C	0	MET	-	expression tag	UNP A0A125S2C1
C	426	GLN	GLU	engineered mutation	UNP A0A125S2C1
D	-20	MET	-	initiating methionine	UNP A0A125S2C1
D	-19	GLY	-	expression tag	UNP A0A125S2C1
D	-18	SER	-	expression tag	UNP A0A125S2C1
D	-17	SER	-	expression tag	UNP A0A125S2C1
D	-16	HIS	-	expression tag	UNP A0A125S2C1
D	-15	HIS	-	expression tag	UNP A0A125S2C1
D	-14	HIS	-	expression tag	UNP A0A125S2C1
D	-13	HIS	-	expression tag	UNP A0A125S2C1
D	-12	HIS	-	expression tag	UNP A0A125S2C1
D	-11	HIS	-	expression tag	UNP A0A125S2C1
D	-10	SER	-	expression tag	UNP A0A125S2C1
D	-9	SER	-	expression tag	UNP A0A125S2C1
D	-8	GLY	-	expression tag	UNP A0A125S2C1
D	-7	LEU	-	expression tag	UNP A0A125S2C1
D	-6	VAL	-	expression tag	UNP A0A125S2C1
D	-5	PRO	-	expression tag	UNP A0A125S2C1
D	-4	ARG	-	expression tag	UNP A0A125S2C1
D	-3	GLY	-	expression tag	UNP A0A125S2C1
D	-2	SER	-	expression tag	UNP A0A125S2C1
D	-1	HIS	-	expression tag	UNP A0A125S2C1
D	0	MET	-	expression tag	UNP A0A125S2C1
D	426	GLN	GLU	engineered mutation	UNP A0A125S2C1
E	-20	MET	-	initiating methionine	UNP A0A125S2C1
E	-19	GLY	-	expression tag	UNP A0A125S2C1
E	-18	SER	-	expression tag	UNP A0A125S2C1
E	-17	SER	-	expression tag	UNP A0A125S2C1
E	-16	HIS	-	expression tag	UNP A0A125S2C1
E	-15	HIS	-	expression tag	UNP A0A125S2C1
E	-14	HIS	-	expression tag	UNP A0A125S2C1
E	-13	HIS	-	expression tag	UNP A0A125S2C1
E	-12	HIS	-	expression tag	UNP A0A125S2C1

*Continued on next page...*

*Continued from previous page...*

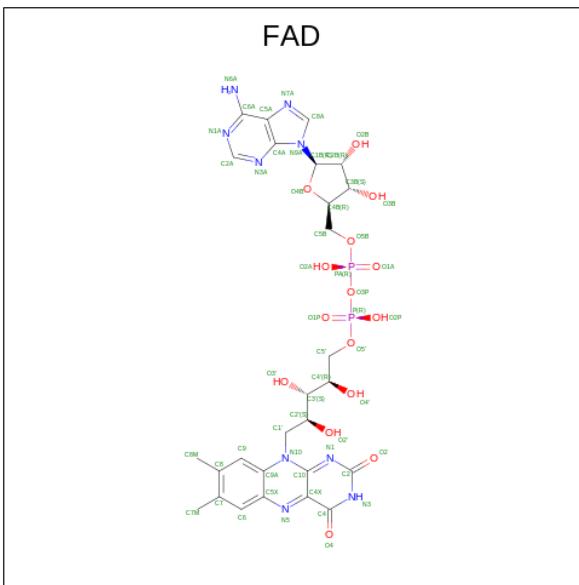
Chain	Residue	Modelled	Actual	Comment	Reference
E	-11	HIS	-	expression tag	UNP A0A125S2C1
E	-10	SER	-	expression tag	UNP A0A125S2C1
E	-9	SER	-	expression tag	UNP A0A125S2C1
E	-8	GLY	-	expression tag	UNP A0A125S2C1
E	-7	LEU	-	expression tag	UNP A0A125S2C1
E	-6	VAL	-	expression tag	UNP A0A125S2C1
E	-5	PRO	-	expression tag	UNP A0A125S2C1
E	-4	ARG	-	expression tag	UNP A0A125S2C1
E	-3	GLY	-	expression tag	UNP A0A125S2C1
E	-2	SER	-	expression tag	UNP A0A125S2C1
E	-1	HIS	-	expression tag	UNP A0A125S2C1
E	0	MET	-	expression tag	UNP A0A125S2C1
E	426	GLN	GLU	engineered mutation	UNP A0A125S2C1
F	-20	MET	-	initiating methionine	UNP A0A125S2C1
F	-19	GLY	-	expression tag	UNP A0A125S2C1
F	-18	SER	-	expression tag	UNP A0A125S2C1
F	-17	SER	-	expression tag	UNP A0A125S2C1
F	-16	HIS	-	expression tag	UNP A0A125S2C1
F	-15	HIS	-	expression tag	UNP A0A125S2C1
F	-14	HIS	-	expression tag	UNP A0A125S2C1
F	-13	HIS	-	expression tag	UNP A0A125S2C1
F	-12	HIS	-	expression tag	UNP A0A125S2C1
F	-11	HIS	-	expression tag	UNP A0A125S2C1
F	-10	SER	-	expression tag	UNP A0A125S2C1
F	-9	SER	-	expression tag	UNP A0A125S2C1
F	-8	GLY	-	expression tag	UNP A0A125S2C1
F	-7	LEU	-	expression tag	UNP A0A125S2C1
F	-6	VAL	-	expression tag	UNP A0A125S2C1
F	-5	PRO	-	expression tag	UNP A0A125S2C1
F	-4	ARG	-	expression tag	UNP A0A125S2C1
F	-3	GLY	-	expression tag	UNP A0A125S2C1
F	-2	SER	-	expression tag	UNP A0A125S2C1
F	-1	HIS	-	expression tag	UNP A0A125S2C1
F	0	MET	-	expression tag	UNP A0A125S2C1
F	426	GLN	GLU	engineered mutation	UNP A0A125S2C1
G	-20	MET	-	initiating methionine	UNP A0A125S2C1
G	-19	GLY	-	expression tag	UNP A0A125S2C1
G	-18	SER	-	expression tag	UNP A0A125S2C1
G	-17	SER	-	expression tag	UNP A0A125S2C1
G	-16	HIS	-	expression tag	UNP A0A125S2C1
G	-15	HIS	-	expression tag	UNP A0A125S2C1
G	-14	HIS	-	expression tag	UNP A0A125S2C1

*Continued on next page...*

*Continued from previous page...*

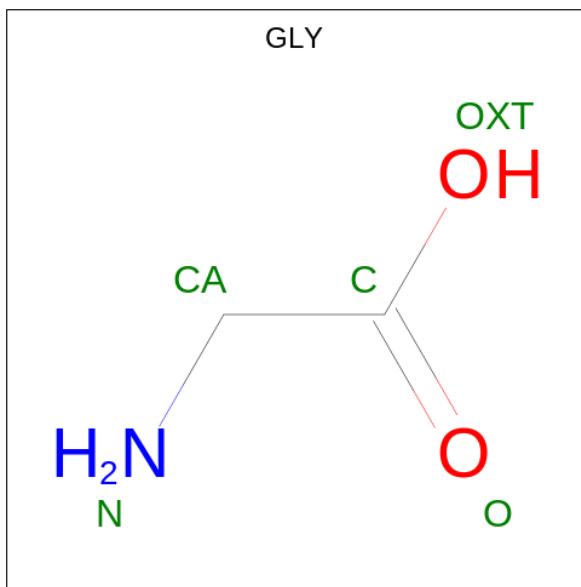
Chain	Residue	Modelled	Actual	Comment	Reference
G	-13	HIS	-	expression tag	UNP A0A125S2C1
G	-12	HIS	-	expression tag	UNP A0A125S2C1
G	-11	HIS	-	expression tag	UNP A0A125S2C1
G	-10	SER	-	expression tag	UNP A0A125S2C1
G	-9	SER	-	expression tag	UNP A0A125S2C1
G	-8	GLY	-	expression tag	UNP A0A125S2C1
G	-7	LEU	-	expression tag	UNP A0A125S2C1
G	-6	VAL	-	expression tag	UNP A0A125S2C1
G	-5	PRO	-	expression tag	UNP A0A125S2C1
G	-4	ARG	-	expression tag	UNP A0A125S2C1
G	-3	GLY	-	expression tag	UNP A0A125S2C1
G	-2	SER	-	expression tag	UNP A0A125S2C1
G	-1	HIS	-	expression tag	UNP A0A125S2C1
G	0	MET	-	expression tag	UNP A0A125S2C1
G	426	GLN	GLU	engineered mutation	UNP A0A125S2C1
H	-20	MET	-	initiating methionine	UNP A0A125S2C1
H	-19	GLY	-	expression tag	UNP A0A125S2C1
H	-18	SER	-	expression tag	UNP A0A125S2C1
H	-17	SER	-	expression tag	UNP A0A125S2C1
H	-16	HIS	-	expression tag	UNP A0A125S2C1
H	-15	HIS	-	expression tag	UNP A0A125S2C1
H	-14	HIS	-	expression tag	UNP A0A125S2C1
H	-13	HIS	-	expression tag	UNP A0A125S2C1
H	-12	HIS	-	expression tag	UNP A0A125S2C1
H	-11	HIS	-	expression tag	UNP A0A125S2C1
H	-10	SER	-	expression tag	UNP A0A125S2C1
H	-9	SER	-	expression tag	UNP A0A125S2C1
H	-8	GLY	-	expression tag	UNP A0A125S2C1
H	-7	LEU	-	expression tag	UNP A0A125S2C1
H	-6	VAL	-	expression tag	UNP A0A125S2C1
H	-5	PRO	-	expression tag	UNP A0A125S2C1
H	-4	ARG	-	expression tag	UNP A0A125S2C1
H	-3	GLY	-	expression tag	UNP A0A125S2C1
H	-2	SER	-	expression tag	UNP A0A125S2C1
H	-1	HIS	-	expression tag	UNP A0A125S2C1
H	0	MET	-	expression tag	UNP A0A125S2C1
H	426	GLN	GLU	engineered mutation	UNP A0A125S2C1

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



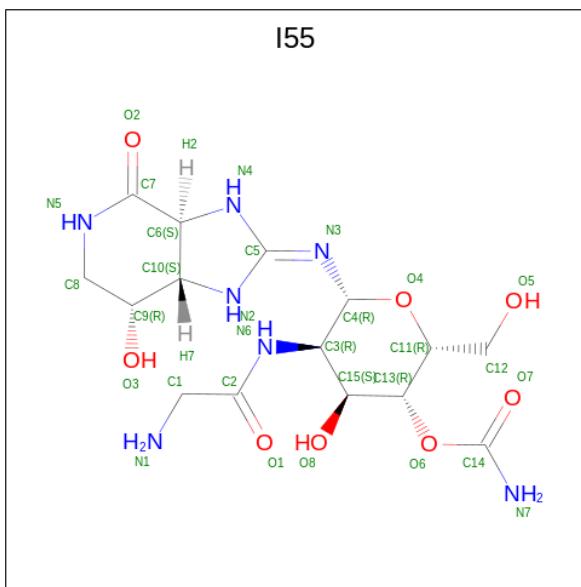
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total		C	N	O	P	
			53	27	9	15	2	0	0
2	B	1	Total		C	N	O	P	
			53	27	9	15	2	0	0
2	C	1	Total		C	N	O	P	
			53	27	9	15	2	0	0
2	D	1	Total		C	N	O	P	
			53	27	9	15	2	0	0
2	E	1	Total		C	N	O	P	
			53	27	9	15	2	0	0
2	F	1	Total		C	N	O	P	
			53	27	9	15	2	0	0
2	G	1	Total		C	N	O	P	
			53	27	9	15	2	0	0
2	H	1	Total		C	N	O	P	
			53	27	9	15	2	0	0

- Molecule 3 is GLYCINE (three-letter code: GLY) (formula: C<sub>2</sub>H<sub>5</sub>NO<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 5 2 1 2	0	0
3	B	1	Total C N O 5 2 1 2	0	0
3	C	1	Total C N O 5 2 1 2	0	0
3	D	1	Total C N O 5 2 1 2	0	0
3	E	1	Total C N O 5 2 1 2	0	0
3	F	1	Total C N O 5 2 1 2	0	0
3	G	1	Total C N O 5 2 1 2	0	0
3	H	1	Total C N O 5 2 1 2	0	0

- Molecule 4 is [(2 {R},3 {R},4 {S},5 {R},6 {R})-6-[( {E})-[(3 {a} {S},7 {R},7 {a} {S})-7-oxidanyl-4-oxidanylidene-3,3 {a},5,6,7,7 {a}-hexahydro-1 {H}-imidazo[4,5-c]pyridin-2-ylidene]amino]-5-(2-azanylethanoylamino)-2-(hydroxymethyl)-4-oxidanyl-oxan-3-yl] carbamate (three-letter code: I55) (formula: C<sub>15</sub>H<sub>25</sub>N<sub>7</sub>O<sub>8</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 30 15 7 8	0	0
4	B	1	Total C N O 30 15 7 8	0	0
4	C	1	Total C N O 30 15 7 8	0	0
4	D	1	Total C N O 30 15 7 8	0	0
4	E	1	Total C N O 30 15 7 8	0	0
4	F	1	Total C N O 30 15 7 8	0	0
4	G	1	Total C N O 30 15 7 8	0	0
4	H	1	Total C N O 30 15 7 8	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	342	Total O 342 342	0	0
5	B	360	Total O 360 360	0	0
5	C	350	Total O 350 350	0	0
5	D	220	Total O 220 220	0	0

Continued on next page...

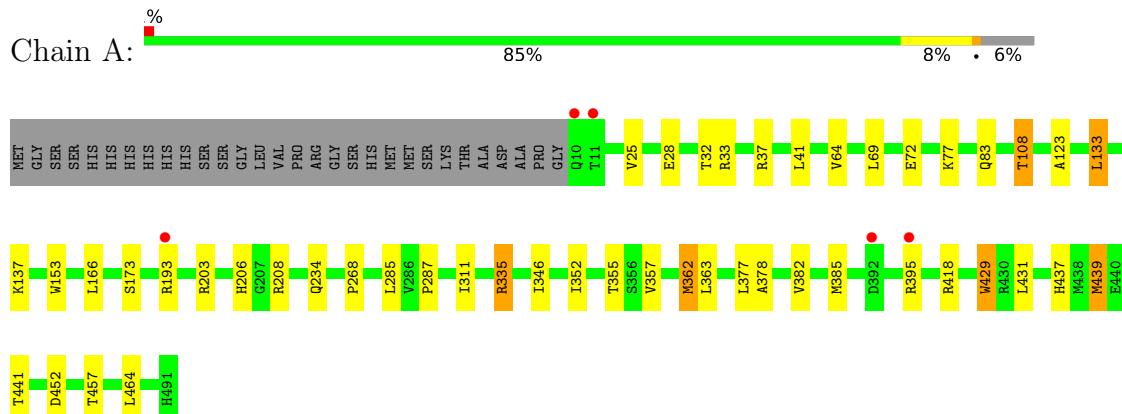
*Continued from previous page...*

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	336	Total O 336 336	0	0
5	F	366	Total O 366 366	0	0
5	G	346	Total O 346 346	0	0
5	H	228	Total O 228 228	0	0

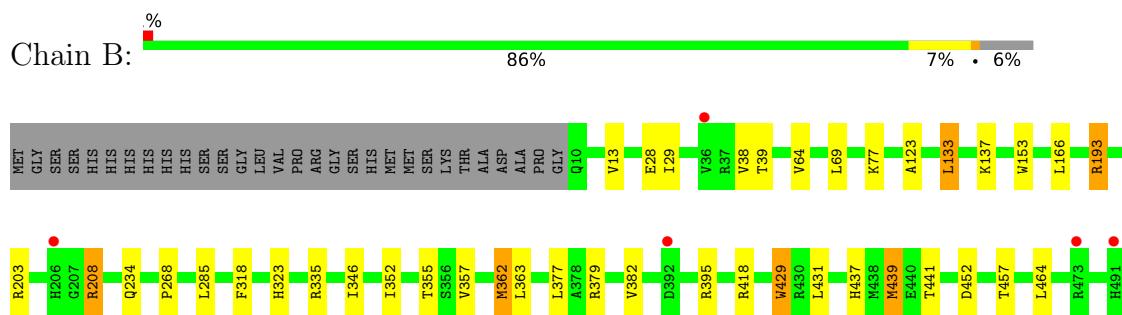
### 3 Residue-property plots

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.

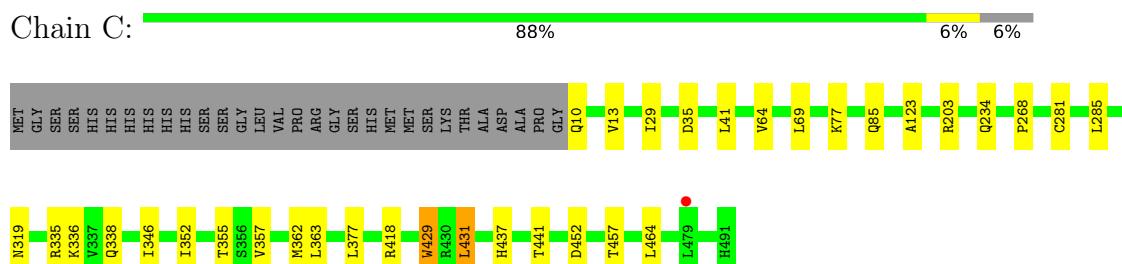
- Molecule 1: N-formimidoyl fortimicin A synthase



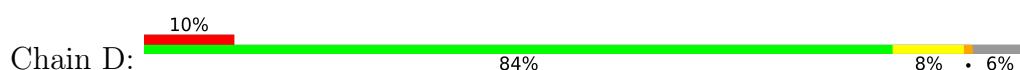
- Molecule 1: N-formimidoyl fortimicin A synthase

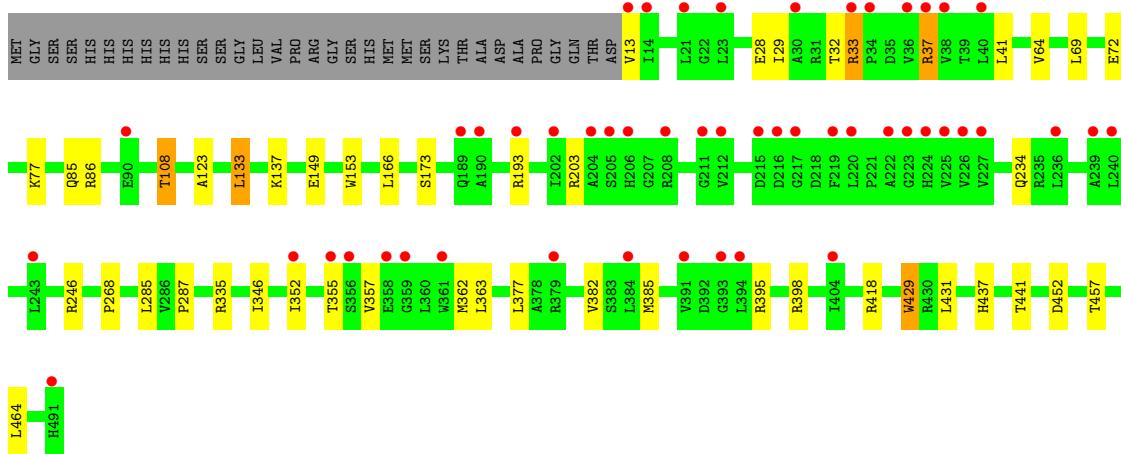


- Molecule 1: N-formimidoyl fortimicin A synthase

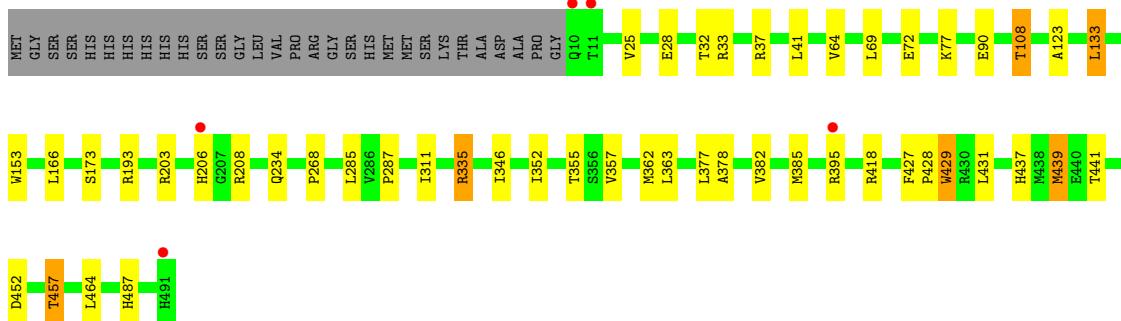
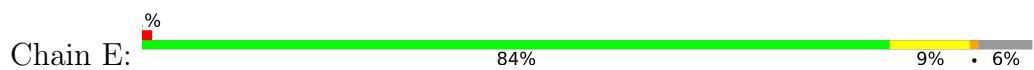


- Molecule 1: N-formimidoyl fortimicin A synthase

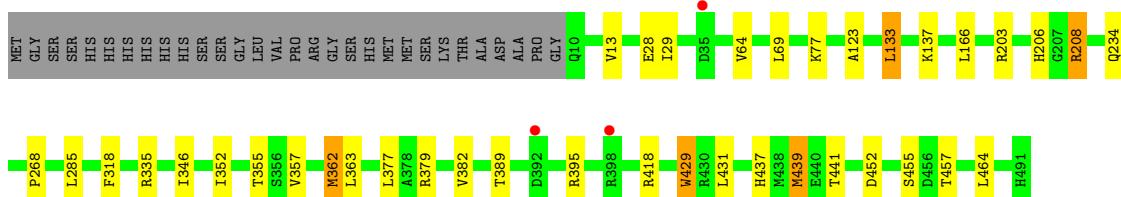
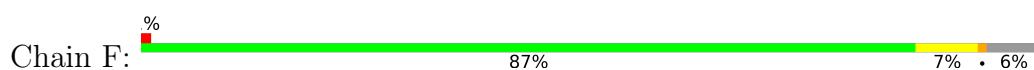




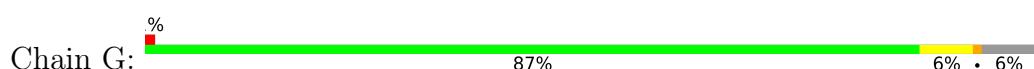
- Molecule 1: N-formimidoyl fortimicin A synthase



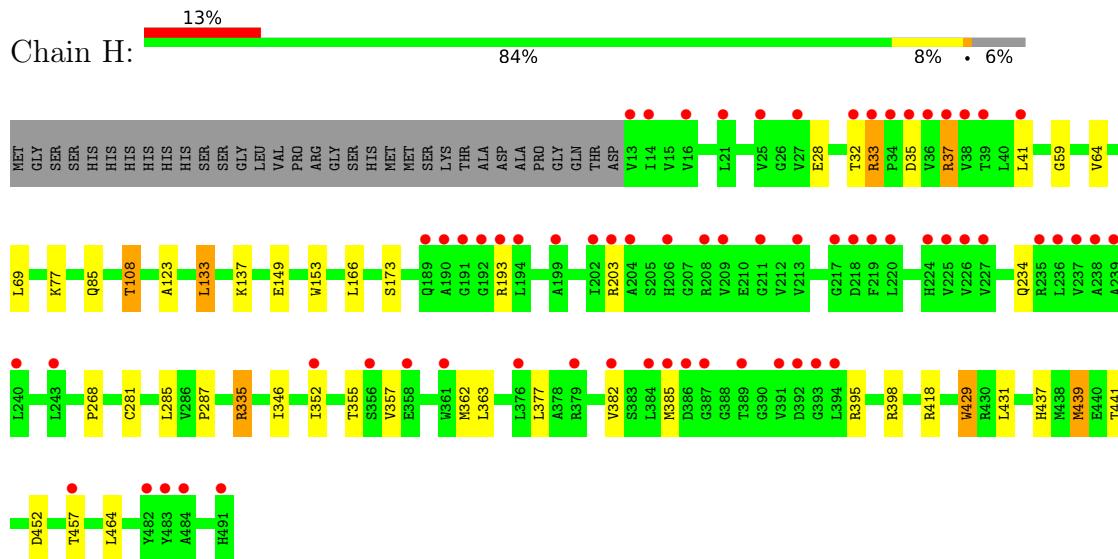
- Molecule 1: N-formimidoyl fortimicin A synthase



- Molecule 1: N-formimidoyl fortimicin A synthase



- Molecule 1: N-formimidoyl fortimicin A synthase



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.38Å 107.37Å 135.04Å 89.98° 89.99° 83.61°	Depositor
Resolution (Å)	28.11 – 2.10 28.10 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.7 (28.11-2.10) 94.7 (28.10-2.10)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	2.88 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
$R$ , $R_{free}$	0.197 , 0.223 0.203 , 0.226	Depositor DCC
$R_{free}$ test set	15925 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.6	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 28.9	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.50$ , $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.480 for -h,-k,l 0.011 for k,h,-l 0.011 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	32464	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $< |L| >$ ,  $< L^2 >$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [\(i\)](#)

### 5.1 Standard geometry [\(i\)](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, I55

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	0.64	0/3737	0.77	0/5092
1	B	0.64	0/3737	0.76	0/5092
1	C	0.66	0/3737	0.77	0/5092
1	D	0.63	0/3719	0.76	0/5067
1	E	0.64	0/3745	0.77	0/5102
1	F	0.64	0/3745	0.76	0/5103
1	G	0.65	0/3737	0.77	0/5092
1	H	0.63	0/3719	0.76	0/5067
All	All	0.64	0/29876	0.76	0/40707

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [\(i\)](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3654	0	3586	33	0
1	B	3654	0	3586	27	0
1	C	3654	0	3586	18	0
1	D	3636	0	3571	30	0
1	E	3662	0	3594	41	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3662	0	3589	35	0
1	G	3654	0	3586	32	0
1	H	3636	0	3571	37	0
2	A	53	0	31	1	0
2	B	53	0	31	0	0
2	C	53	0	31	1	0
2	D	53	0	31	0	0
2	E	53	0	31	1	0
2	F	53	0	31	1	0
2	G	53	0	31	1	0
2	H	53	0	31	2	0
3	A	5	0	2	0	0
3	B	5	0	2	0	0
3	C	5	0	2	0	0
3	D	5	0	2	0	0
3	E	5	0	2	0	0
3	F	5	0	2	0	0
3	G	5	0	2	0	0
3	H	5	0	2	0	0
4	A	30	0	0	0	0
4	B	30	0	0	0	0
4	C	30	0	0	0	0
4	D	30	0	0	0	0
4	E	30	0	0	0	0
4	F	30	0	0	0	0
4	G	30	0	0	0	0
4	H	30	0	0	0	0
5	A	342	0	0	8	0
5	B	360	0	0	2	0
5	C	350	0	0	5	0
5	D	220	0	0	5	0
5	E	336	0	0	5	0
5	F	366	0	0	3	0
5	G	346	0	0	5	0
5	H	228	0	0	4	0
All	All	32464	0	28933	230	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (230) 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:E:439[A]:MET:CE	1:G:439:MET:CE	2.51	0.89
1:F:439:MET:CE	1:H:439:MET:CE	2.52	0.88
1:E:439[A]:MET:HE2	1:G:439:MET:CE	2.05	0.86
1:E:439[A]:MET:HE2	1:G:439:MET:HE2	1.58	0.83
1:E:335:ARG:HG2	5:E:1052:HOH:O	1.79	0.81
1:E:439[A]:MET:CE	1:G:439:MET:HE2	2.08	0.80
1:F:439:MET:CE	1:H:439:MET:HE2	2.10	0.80
1:F:439:MET:HE2	1:H:439:MET:CE	2.14	0.78
1:C:429:TRP:CD1	1:C:431:LEU:HD11	2.22	0.74
1:G:77:LYS:HD2	5:G:1020:HOH:O	1.86	0.74
1:G:429:TRP:CD1	1:G:431:LEU:HD11	2.22	0.74
1:F:439:MET:HE3	1:H:439:MET:CE	2.18	0.74
1:D:382:VAL:HA	1:D:385:MET:HE2	1.71	0.72
1:C:431:LEU:HD12	1:C:431:LEU:N	2.04	0.72
1:F:439:MET:CE	1:H:439:MET:HE3	2.21	0.71
1:G:431:LEU:N	1:G:431:LEU:HD12	2.05	0.71
1:A:382:VAL:HA	1:A:385:MET:HE2	1.71	0.71
1:F:439:MET:HE2	1:H:439:MET:HE2	1.71	0.70
1:E:439[A]:MET:CE	1:G:439:MET:HE3	2.20	0.69
1:H:382:VAL:HA	1:H:385:MET:HE2	1.73	0.69
1:E:382:VAL:HA	1:E:385:MET:HE2	1.76	0.68
1:F:439:MET:HE3	1:H:439:MET:HE2	1.76	0.67
1:E:382:VAL:HA	1:E:385:MET:CE	2.25	0.66
1:H:281[A]:CYS:SG	5:H:981:HOH:O	2.52	0.66
1:A:108:THR:HG22	1:A:173:SER:OG	1.96	0.65
1:D:108:THR:HG22	1:D:173:SER:OG	1.96	0.65
1:A:382:VAL:HA	1:A:385:MET:CE	2.25	0.65
1:H:382:VAL:HA	1:H:385:MET:CE	2.26	0.65
1:H:108:THR:HG22	1:H:173:SER:OG	1.97	0.65
1:D:382:VAL:HA	1:D:385:MET:CE	2.26	0.65
1:E:108:THR:HG22	1:E:173:SER:OG	1.96	0.65
1:A:108:THR:HG21	1:A:287:PRO:O	1.98	0.64
1:D:108:THR:HG21	1:D:287:PRO:O	1.98	0.63
1:F:352:ILE:HD13	1:F:377:LEU:HD22	1.81	0.63
1:E:108:THR:HG21	1:E:287:PRO:O	1.98	0.63
1:E:439[A]:MET:HE2	1:G:439:MET:HE3	1.80	0.62
1:E:439[A]:MET:HE3	1:G:439:MET:CE	2.27	0.62
1:H:108:THR:HG21	1:H:287:PRO:O	1.99	0.62
1:B:352:ILE:HD13	1:B:377:LEU:HD22	1.80	0.62
1:H:32:THR:HG22	1:H:33:ARG:NH1	2.15	0.62
1:C:363:LEU:HD11	1:C:377:LEU:HB3	1.82	0.62
1:C:352:ILE:HD13	1:C:377:LEU:HD22	1.82	0.61

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:363:LEU:HD11	1:G:377:LEU:HB3	1.83	0.60
1:C:429:TRP:CG	1:C:431:LEU:HD11	2.36	0.60
1:G:429:TRP:CG	1:G:431:LEU:HD11	2.36	0.60
1:H:352:ILE:HD13	1:H:377:LEU:HD22	1.83	0.60
1:D:352:ILE:HD13	1:D:377:LEU:HD22	1.83	0.60
1:A:25:VAL:HG23	1:A:378:ALA:HA	1.84	0.60
1:G:352:ILE:HD13	1:G:377:LEU:HD22	1.82	0.60
1:A:346:ILE:HG13	1:A:464:LEU:CD2	2.33	0.59
1:E:346:ILE:HG13	1:E:464:LEU:CD2	2.33	0.59
1:E:123:ALA:HB1	1:E:418:ARG:HD2	1.84	0.58
1:A:123:ALA:HB1	1:A:418:ARG:HD2	1.86	0.58
1:E:25:VAL:HG23	1:E:378:ALA:HA	1.84	0.58
1:B:346:ILE:HG13	1:B:464:LEU:CD2	2.33	0.58
1:B:323:HIS:HE1	5:C:946:HOH:O	1.86	0.58
1:B:38:VAL:HG12	5:B:994:HOH:O	2.02	0.58
1:F:346:ILE:HG13	1:F:464:LEU:CD2	2.34	0.58
1:D:123:ALA:HB1	1:D:418:ARG:HD2	1.87	0.57
1:E:90:GLU:HG2	5:E:813:HOH:O	2.05	0.57
1:C:346:ILE:HG13	1:C:464:LEU:CD2	2.34	0.57
1:G:346:ILE:HG13	1:G:464:LEU:CD2	2.34	0.57
1:E:355:THR:HG22	1:E:357:VAL:H	1.70	0.57
1:H:123:ALA:HB1	1:H:418:ARG:HD2	1.87	0.57
1:D:355:THR:HG22	1:D:357:VAL:H	1.70	0.57
1:F:355:THR:HG22	1:F:357:VAL:H	1.70	0.56
1:H:346:ILE:HG13	1:H:464:LEU:CD2	2.34	0.56
1:H:363:LEU:HD11	1:H:377:LEU:HB3	1.88	0.56
1:F:208:ARG:HG2	1:F:208:ARG:HH11	1.69	0.56
1:D:346:ILE:HG13	1:D:464:LEU:CD2	2.35	0.56
1:D:363:LEU:HD11	1:D:377:LEU:HB3	1.87	0.56
1:H:355:THR:HG22	1:H:357:VAL:H	1.70	0.56
1:A:355:THR:HG22	1:A:357:VAL:H	1.70	0.55
1:F:363:LEU:HD11	1:F:377:LEU:HB3	1.88	0.55
1:B:355:THR:HG22	1:B:357:VAL:H	1.71	0.55
1:C:355:THR:HG22	1:C:357:VAL:H	1.71	0.55
1:G:281:CYS:HB3	5:G:1078:HOH:O	2.05	0.55
1:B:208:ARG:HG2	1:B:208:ARG:HH11	1.70	0.55
1:E:352:ILE:HD13	1:E:377:LEU:HD22	1.89	0.55
1:G:355:THR:HG22	1:G:357:VAL:H	1.71	0.55
1:E:363:LEU:HD11	1:E:377:LEU:HB3	1.89	0.54
1:H:149:GLU:HG3	5:H:828:HOH:O	2.06	0.54
1:A:352:ILE:HD13	1:A:377:LEU:HD22	1.89	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:123:ALA:HB1	1:C:418:ARG:HD2	1.90	0.54
1:B:363:LEU:HD11	1:B:377:LEU:HB3	1.88	0.54
1:E:439[A]:MET:HE3	1:G:439:MET:HE2	1.85	0.54
1:F:439:MET:HE2	1:H:439:MET:HE3	1.83	0.54
1:B:208:ARG:HH11	1:B:208:ARG:CG	2.21	0.54
1:F:431:LEU:HD11	1:H:431:LEU:CD1	2.38	0.54
1:G:123:ALA:HB1	1:G:418:ARG:HD2	1.90	0.53
1:B:431:LEU:HD11	1:D:431:LEU:CD1	2.38	0.53
1:A:335:ARG:NH2	5:A:804:HOH:O	2.41	0.53
1:F:208:ARG:HH11	1:F:208:ARG:CG	2.20	0.53
1:E:437:HIS:O	1:E:441:THR:HG23	2.09	0.53
1:A:32:THR:CG2	5:A:1105:HOH:O	2.56	0.53
1:A:363:LEU:HD11	1:A:377:LEU:HB3	1.89	0.53
1:B:431:LEU:CD1	1:D:431:LEU:HD11	2.40	0.52
1:C:437:HIS:O	1:C:441:THR:HG23	2.09	0.52
1:D:149:GLU:HG3	5:D:854:HOH:O	2.08	0.52
1:G:437:HIS:O	1:G:441:THR:HG23	2.09	0.52
1:E:206:HIS:CE1	5:E:1047:HOH:O	2.63	0.52
1:F:437:HIS:O	1:F:441:THR:HG23	2.09	0.52
1:A:72:GLU:OE2	1:A:72:GLU:HA	2.09	0.52
1:A:437:HIS:O	1:A:441:THR:HG23	2.09	0.52
1:F:431:LEU:CD1	1:H:431:LEU:HD11	2.39	0.52
1:H:395:ARG:O	1:H:398:ARG:HG3	2.10	0.52
1:A:268:PRO:HG3	1:A:285:LEU:HD22	1.92	0.52
1:D:437:HIS:O	1:D:441:THR:HG23	2.10	0.52
1:F:268:PRO:HG3	1:F:285:LEU:HD22	1.92	0.51
1:G:281:CYS:CB	5:G:1078:HOH:O	2.58	0.51
1:B:431:LEU:HD11	1:D:431:LEU:HD11	1.92	0.51
1:E:72:GLU:OE2	1:E:72:GLU:HA	2.09	0.51
1:B:437:HIS:O	1:B:441:THR:HG23	2.10	0.51
1:C:268:PRO:HG3	1:C:285:LEU:HD22	1.92	0.51
1:F:123:ALA:HB1	1:F:418:ARG:HD2	1.93	0.51
1:H:437:HIS:O	1:H:441:THR:HG23	2.10	0.51
1:B:123:ALA:HB1	1:B:418:ARG:HD2	1.92	0.51
1:B:268:PRO:HG3	1:B:285:LEU:HD22	1.93	0.51
1:E:268:PRO:HG3	1:E:285:LEU:HD22	1.93	0.51
1:D:108:THR:CG2	1:D:287:PRO:O	2.60	0.50
1:D:86:ARG:HD2	1:F:206:HIS:O	2.11	0.50
1:D:395:ARG:O	1:D:398:ARG:HG3	2.12	0.50
1:H:335:ARG:HD3	5:H:965:HOH:O	2.12	0.50
1:H:268:PRO:HG3	1:H:285:LEU:HD22	1.94	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:268:PRO:HG3	1:G:285:LEU:HD22	1.93	0.49
1:A:108:THR:CG2	1:A:287:PRO:O	2.60	0.49
1:E:108:THR:CG2	1:E:287:PRO:O	2.60	0.49
1:F:431:LEU:HD11	1:H:431:LEU:HD11	1.92	0.49
1:H:108:THR:CG2	1:H:287:PRO:O	2.59	0.49
1:H:59:GLY:O	5:H:801:HOH:O	2.20	0.49
2:H:701:FAD:N1	2:H:701:FAD:O2'	2.43	0.48
1:D:268:PRO:HG3	1:D:285:LEU:HD22	1.94	0.48
1:E:208:ARG:HG2	5:E:826:HOH:O	2.13	0.48
1:A:32:THR:HG21	5:A:1105:HOH:O	2.14	0.48
1:B:39:THR:HG23	1:B:193:ARG:HD2	1.96	0.48
1:F:379:ARG:HD3	5:F:1062:HOH:O	2.14	0.48
1:A:37:ARG:HG2	1:A:193:ARG:HH12	1.79	0.47
1:A:429:TRP:CZ3	1:A:439:MET:HE1	2.50	0.47
1:G:101:ALA:N	5:G:801:HOH:O	2.34	0.47
1:E:429:TRP:CZ3	1:E:439[A]:MET:HE1	2.49	0.47
1:B:429:TRP:CZ3	1:B:439:MET:HE1	2.50	0.47
1:C:35:ASP:HA	5:C:1085:HOH:O	2.15	0.47
1:H:32:THR:HG22	1:H:33:ARG:CZ	2.46	0.46
1:H:429:TRP:CZ3	1:H:439:MET:HE1	2.50	0.46
1:G:13:VAL:HG11	1:G:29:ILE:HD13	1.97	0.46
1:G:90:GLU:HG2	5:G:1040:HOH:O	2.14	0.46
1:F:429:TRP:CZ3	1:F:439:MET:HE1	2.51	0.46
1:B:431:LEU:CD1	1:D:431:LEU:CD1	2.94	0.45
1:F:431:LEU:CD1	1:H:431:LEU:CD1	2.94	0.45
1:A:311:ILE:HG23	1:B:318:PHE:HB3	1.99	0.45
1:C:13:VAL:HG11	1:C:29:ILE:HD13	1.97	0.45
1:E:64:VAL:HG13	1:E:69:LEU:HD22	1.98	0.45
1:D:33:ARG:NH2	5:D:806:HOH:O	2.48	0.45
1:E:37:ARG:HG2	1:E:193:ARG:HH12	1.80	0.45
1:D:32:THR:HG21	5:D:806:HOH:O	2.17	0.45
1:F:133:LEU:HD13	1:F:166:LEU:HD22	1.99	0.44
1:F:64:VAL:HG13	1:F:69:LEU:HD22	1.99	0.44
1:A:64:VAL:HG13	1:A:69:LEU:HD22	1.97	0.44
1:A:206:HIS:CE1	5:A:1018:HOH:O	2.70	0.44
1:D:28:GLU:HB3	1:D:382:VAL:HG21	2.00	0.44
1:E:32:THR:HG22	1:E:33:ARG:HG2	1.99	0.44
1:E:133:LEU:HD13	1:E:166:LEU:HD22	2.00	0.44
1:F:362:MET:HE2	1:F:362:MET:HB2	1.94	0.44
1:B:64:VAL:HG13	1:B:69:LEU:HD22	1.99	0.44
1:B:133:LEU:HD13	1:B:166:LEU:HD22	2.00	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:701:FAD:H9	2:E:701:FAD:H1'2	1.74	0.44
1:A:133:LEU:HD13	1:A:166:LEU:HD22	2.00	0.44
1:C:281:CYS:CB	5:C:1081:HOH:O	2.65	0.44
1:E:346:ILE:HG13	1:E:464:LEU:HD21	2.00	0.44
1:G:64:VAL:HG13	1:G:69:LEU:HD22	2.00	0.44
1:B:429:TRP:CG	1:B:431:LEU:HD13	2.53	0.43
1:D:72:GLU:OE2	1:F:389:THR:HG22	2.18	0.43
1:A:28:GLU:HB3	1:A:382:VAL:HG21	2.01	0.43
1:A:429:TRP:CG	1:A:431:LEU:HD13	2.53	0.43
1:A:208:ARG:NH2	5:A:823:HOH:O	2.51	0.43
1:H:64:VAL:HG13	1:H:69:LEU:HD22	2.01	0.43
1:D:37:ARG:HG3	1:D:193:ARG:HH12	1.84	0.43
1:G:429:TRP:CZ3	1:G:439:MET:HE1	2.53	0.43
1:H:429:TRP:CG	1:H:431:LEU:HD13	2.54	0.43
1:B:133:LEU:O	1:B:137:LYS:HD3	2.18	0.43
1:D:64:VAL:HG13	1:D:69:LEU:HD22	2.00	0.43
1:E:429:TRP:CG	1:E:431:LEU:HD13	2.54	0.43
1:F:133:LEU:O	1:F:137:LYS:HD3	2.18	0.43
2:H:701:FAD:H1'2	2:H:701:FAD:H9	1.74	0.43
1:A:346:ILE:HG13	1:A:464:LEU:HD21	2.00	0.43
1:B:28:GLU:HB3	1:B:382:VAL:HG21	2.01	0.43
1:D:429:TRP:CG	1:D:431:LEU:HD13	2.54	0.43
1:F:429:TRP:CG	1:F:431:LEU:HD13	2.53	0.43
1:F:13:VAL:HG11	1:F:29:ILE:HD13	2.02	0.42
2:C:701:FAD:H9	2:C:701:FAD:H1'2	1.76	0.42
1:F:28:GLU:HB3	1:F:382:VAL:HG21	2.01	0.42
1:C:336:LYS:HE3	1:C:338:GLN:HG2	2.02	0.42
1:A:32:THR:HG22	1:A:33:ARG:HG2	2.02	0.42
1:E:311:ILE:HG23	1:F:318:PHE:HB3	2.00	0.42
1:H:133:LEU:HD13	1:H:166:LEU:HD22	2.01	0.42
1:B:13:VAL:HG11	1:B:29:ILE:HD13	2.01	0.42
1:H:28:GLU:HB3	1:H:382:VAL:HG21	2.00	0.42
1:C:10:GLN:HA	5:C:949:HOH:O	2.19	0.42
1:E:28:GLU:HB3	1:E:382:VAL:HG21	2.01	0.42
1:G:363:LEU:HD12	1:G:363:LEU:HA	1.90	0.42
2:G:701:FAD:H9	2:G:701:FAD:H1'2	1.78	0.42
1:D:32:THR:CG2	5:D:806:HOH:O	2.68	0.42
1:E:439[B]:MET:CE	1:G:439:MET:HA	2.50	0.42
1:D:133:LEU:HD13	1:D:166:LEU:HD22	2.01	0.42
1:E:133:LEU:HD12	1:E:133:LEU:HA	1.91	0.41
1:F:137:LYS:HE2	5:F:1125:HOH:O	2.20	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:439[B]:MET:HE1	1:G:439:MET:HA	2.01	0.41
1:A:362:MET:HE2	1:A:362:MET:HB2	1.92	0.41
1:C:429:TRP:CD2	1:C:431:LEU:HD11	2.55	0.41
1:B:379:ARG:HD3	5:B:1037:HOH:O	2.21	0.41
1:A:137:LYS:HD2	1:A:137:LYS:HA	1.94	0.41
1:C:64:VAL:HG13	1:C:69:LEU:HD22	2.01	0.41
1:G:431:LEU:N	1:G:431:LEU:CD1	2.81	0.41
1:H:37:ARG:HG3	1:H:193:ARG:HH12	1.85	0.41
1:B:208:ARG:CG	1:B:208:ARG:NH1	2.84	0.41
1:B:362:MET:HE2	1:B:362:MET:HB2	1.93	0.41
1:C:281:CYS:HB3	5:C:1081:HOH:O	2.20	0.41
2:F:701:FAD:H1'2	2:F:701:FAD:H9	1.74	0.41
1:A:32:THR:HG22	5:A:1105:HOH:O	2.19	0.41
1:E:457:THR:HG21	1:E:487:HIS:CD2	2.56	0.41
1:A:83:GLN:NE2	5:A:803:HOH:O	2.37	0.40
1:E:206:HIS:HE1	5:E:1047:HOH:O	2.03	0.40
1:F:455:SER:HA	5:F:1095:HOH:O	2.21	0.40
1:G:429:TRP:CD2	1:G:431:LEU:HD11	2.55	0.40
1:G:457:THR:HG21	1:G:487:HIS:CD2	2.57	0.40
1:A:464:LEU:HB2	5:A:1077:HOH:O	2.21	0.40
2:A:701:FAD:H1'2	2:A:701:FAD:H9	1.77	0.40
1:E:427:PHE:N	1:E:428:PRO:HA	2.37	0.40
1:D:13:VAL:HG11	1:D:29:ILE:HD13	2.04	0.40
1:D:246:ARG:HD2	5:D:905:HOH:O	2.21	0.40

There are no symmetry-related clashes.

### 5.3 Torsion angles [\(i\)](#)

#### 5.3.1 Protein backbone [\(i\)](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	480/512 (94%)	468 (98%)	11 (2%)	1 (0%)	47 49

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	480/512 (94%)	468 (98%)	11 (2%)	1 (0%)	47 49
1	C	480/512 (94%)	468 (98%)	12 (2%)	0	100 100
1	D	478/512 (93%)	466 (98%)	11 (2%)	1 (0%)	47 49
1	E	481/512 (94%)	469 (98%)	11 (2%)	1 (0%)	47 49
1	F	481/512 (94%)	469 (98%)	12 (2%)	0	100 100
1	G	480/512 (94%)	468 (98%)	12 (2%)	0	100 100
1	H	478/512 (93%)	466 (98%)	11 (2%)	1 (0%)	47 49
All	All	3838/4096 (94%)	3742 (98%)	91 (2%)	5 (0%)	51 54

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	TRP
1	B	153	TRP
1	D	153	TRP
1	E	153	TRP
1	H	153	TRP

### 5.3.2 Protein sidechains [\(i\)](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	376/400 (94%)	363 (96%)	13 (4%)	36 38
1	B	376/400 (94%)	363 (96%)	13 (4%)	36 38
1	C	376/400 (94%)	364 (97%)	12 (3%)	39 41
1	D	374/400 (94%)	359 (96%)	15 (4%)	31 32
1	E	377/400 (94%)	363 (96%)	14 (4%)	34 35
1	F	377/400 (94%)	365 (97%)	12 (3%)	39 41
1	G	376/400 (94%)	360 (96%)	16 (4%)	29 29
1	H	374/400 (94%)	357 (96%)	17 (4%)	27 27

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3006/3200 (94%)	2894 (96%)	112 (4%)	34 35

All (112) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LEU
1	A	77	LYS
1	A	108	THR
1	A	133	LEU
1	A	203	ARG
1	A	234	GLN
1	A	335	ARG
1	A	362	MET
1	A	395	ARG
1	A	429	TRP
1	A	439	MET
1	A	452	ASP
1	A	457	THR
1	B	77	LYS
1	B	133	LEU
1	B	193	ARG
1	B	203	ARG
1	B	208	ARG
1	B	234	GLN
1	B	335	ARG
1	B	362	MET
1	B	395	ARG
1	B	429	TRP
1	B	439	MET
1	B	452	ASP
1	B	457	THR
1	C	41	LEU
1	C	77	LYS
1	C	85	GLN
1	C	203	ARG
1	C	234	GLN
1	C	319	ASN
1	C	335	ARG
1	C	362	MET
1	C	429	TRP
1	C	431	LEU
1	C	452	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	457	THR
1	D	33	ARG
1	D	37	ARG
1	D	41	LEU
1	D	77	LYS
1	D	85	GLN
1	D	108	THR
1	D	133	LEU
1	D	137	LYS
1	D	203	ARG
1	D	234	GLN
1	D	335	ARG
1	D	362	MET
1	D	429	TRP
1	D	452	ASP
1	D	457	THR
1	E	41	LEU
1	E	77	LYS
1	E	108	THR
1	E	133	LEU
1	E	203	ARG
1	E	234	GLN
1	E	335	ARG
1	E	362	MET
1	E	395	ARG
1	E	429	TRP
1	E	439[A]	MET
1	E	439[B]	MET
1	E	452	ASP
1	E	457	THR
1	F	77	LYS
1	F	133	LEU
1	F	203	ARG
1	F	208	ARG
1	F	234	GLN
1	F	335	ARG
1	F	362	MET
1	F	395	ARG
1	F	429	TRP
1	F	439	MET
1	F	452	ASP
1	F	457	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	G	10	GLN
1	G	41	LEU
1	G	77	LYS
1	G	85	GLN
1	G	90	GLU
1	G	203	ARG
1	G	234	GLN
1	G	319	ASN
1	G	335	ARG
1	G	362	MET
1	G	429	TRP
1	G	431	LEU
1	G	439	MET
1	G	452	ASP
1	G	457	THR
1	G	473	ARG
1	H	33	ARG
1	H	35	ASP
1	H	37	ARG
1	H	41	LEU
1	H	77	LYS
1	H	85	GLN
1	H	108	THR
1	H	133	LEU
1	H	137	LYS
1	H	203	ARG
1	H	234	GLN
1	H	335	ARG
1	H	362	MET
1	H	429	TRP
1	H	439	MET
1	H	452	ASP
1	H	457	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	234	GLN
1	A	245	HIS
1	A	487	HIS
1	B	10	GLN
1	B	234	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	323	HIS
1	B	487	HIS
1	C	234	GLN
1	C	245	HIS
1	C	487	HIS
1	D	234	GLN
1	E	234	GLN
1	E	245	HIS
1	E	487	HIS
1	F	10	GLN
1	F	83	GLN
1	F	234	GLN
1	F	487	HIS
1	G	10	GLN
1	G	234	GLN
1	G	245	HIS
1	G	487	HIS
1	H	234	GLN
1	H	319	ASN

### 5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [\(i\)](#)

24 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	FAD	D	701	-	53,58,58	0.70	0	68,89,89	0.83	1 (1%)
2	FAD	H	701	-	53,58,58	0.71	0	68,89,89	0.81	1 (1%)
4	I55	G	1156	-	28,32,32	0.80	1 (3%)	31,46,46	1.13	2 (6%)
4	I55	A	1147	-	28,32,32	1.03	1 (3%)	31,46,46	1.49	2 (6%)
3	GLY	E	703	-	4,4,4	0.76	0	3,4,4	1.24	0
3	GLY	G	703	-	4,4,4	1.22	1 (25%)	3,4,4	0.80	0
4	I55	D	1023	-	28,32,32	0.79	1 (3%)	31,46,46	1.00	1 (3%)
3	GLY	A	703	-	4,4,4	0.95	0	3,4,4	1.13	0
4	I55	H	1037	-	28,32,32	0.74	1 (3%)	31,46,46	0.96	2 (6%)
3	GLY	C	703	-	4,4,4	1.16	1 (25%)	3,4,4	0.92	0
3	GLY	D	703	-	4,4,4	0.76	0	3,4,4	2.25	2 (66%)
3	GLY	F	703	-	4,4,4	1.27	0	3,4,4	0.77	0
2	FAD	G	701	-	53,58,58	0.76	1 (1%)	68,89,89	0.90	4 (5%)
2	FAD	A	701	-	53,58,58	0.69	0	68,89,89	0.87	3 (4%)
4	I55	F	1181	-	28,32,32	1.00	1 (3%)	31,46,46	1.15	2 (6%)
2	FAD	E	701	-	53,58,58	0.76	1 (1%)	68,89,89	0.93	4 (5%)
4	I55	C	1153	-	28,32,32	0.82	1 (3%)	31,46,46	1.18	2 (6%)
4	I55	E	1140	-	28,32,32	1.10	1 (3%)	31,46,46	1.21	2 (6%)
2	FAD	F	701	-	53,58,58	0.76	1 (1%)	68,89,89	0.88	2 (2%)
3	GLY	B	703	-	4,4,4	1.26	0	3,4,4	0.72	0
4	I55	B	1164	-	28,32,32	1.02	1 (3%)	31,46,46	1.19	3 (9%)
2	FAD	C	701	-	53,58,58	0.70	0	68,89,89	0.90	3 (4%)
2	FAD	B	701	-	53,58,58	0.73	1 (1%)	68,89,89	0.90	2 (2%)
3	GLY	H	703	-	4,4,4	0.81	0	3,4,4	2.02	1 (33%)

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	FAD	D	701	-	-	2/30/50/50	0/6/6/6
2	FAD	H	701	-	-	2/30/50/50	0/6/6/6
4	I55	G	1156	-	-	3/14/61/61	0/3/3/3

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	I55	A	1147	-	-	0/14/61/61	0/3/3/3
3	GLY	E	703	-	-	0/2/2/2	-
3	GLY	G	703	-	-	0/2/2/2	-
4	I55	D	1023	-	-	1/14/61/61	0/3/3/3
3	GLY	A	703	-	-	0/2/2/2	-
4	I55	H	1037	-	-	1/14/61/61	0/3/3/3
3	GLY	C	703	-	-	0/2/2/2	-
3	GLY	D	703	-	-	0/2/2/2	-
3	GLY	F	703	-	-	0/2/2/2	-
2	FAD	G	701	-	-	3/30/50/50	0/6/6/6
2	FAD	A	701	-	-	1/30/50/50	0/6/6/6
4	I55	F	1181	-	-	1/14/61/61	0/3/3/3
2	FAD	E	701	-	-	1/30/50/50	0/6/6/6
4	I55	C	1153	-	-	3/14/61/61	0/3/3/3
4	I55	E	1140	-	-	0/14/61/61	0/3/3/3
2	FAD	F	701	-	-	2/30/50/50	0/6/6/6
3	GLY	B	703	-	-	0/2/2/2	-
4	I55	B	1164	-	-	1/14/61/61	0/3/3/3
2	FAD	C	701	-	-	3/30/50/50	0/6/6/6
2	FAD	B	701	-	-	2/30/50/50	0/6/6/6
3	GLY	H	703	-	-	0/2/2/2	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1140	I55	C4-C3	-5.01	1.50	1.53
4	B	1164	I55	C4-C3	-4.61	1.50	1.53
4	F	1181	I55	C4-C3	-4.55	1.50	1.53
4	A	1147	I55	C4-C3	-4.49	1.50	1.53
4	C	1153	I55	C4-C3	-3.23	1.51	1.53
4	D	1023	I55	C4-C3	-3.19	1.51	1.53
4	G	1156	I55	C4-C3	-3.17	1.51	1.53
4	H	1037	I55	C4-C3	-3.04	1.51	1.53
2	E	701	FAD	C1'-C2'	-2.60	1.49	1.52
2	G	701	FAD	C1'-C2'	-2.49	1.49	1.52
2	F	701	FAD	O2'-C2'	-2.23	1.38	1.43
3	G	703	GLY	OXT-C	-2.17	1.23	1.30
3	C	703	GLY	OXT-C	-2.05	1.23	1.30
2	B	701	FAD	C1'-C2'	-2.04	1.49	1.52

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1147	I55	C10-N6-C5	-7.22	105.63	112.56
4	E	1140	I55	C10-N6-C5	-5.53	107.25	112.56
4	B	1164	I55	C10-N6-C5	-5.00	107.77	112.56
4	C	1153	I55	C10-N6-C5	-4.59	108.16	112.56
4	F	1181	I55	C10-N6-C5	-4.47	108.27	112.56
4	G	1156	I55	C10-N6-C5	-4.05	108.68	112.56
4	D	1023	I55	C10-N6-C5	-3.75	108.97	112.56
4	H	1037	I55	C10-N6-C5	-3.20	109.50	112.56
2	B	701	FAD	C4'-C3'-C2'	3.00	119.61	113.36
3	D	703	GLY	OXT-C-CA	2.94	125.13	113.45
2	E	701	FAD	C4'-C3'-C2'	2.91	119.41	113.36
2	F	701	FAD	O2A-PA-O1A	2.86	126.40	112.24
2	F	701	FAD	C4'-C3'-C2'	2.81	119.20	113.36
2	B	701	FAD	O2A-PA-O1A	2.71	125.66	112.24
3	H	703	GLY	OXT-C-CA	2.64	123.96	113.45
4	C	1153	I55	C6-C7-N5	-2.62	114.96	118.19
2	A	701	FAD	C5A-C6A-N6A	2.61	124.33	120.35
2	E	701	FAD	C5A-C6A-N6A	2.58	124.28	120.35
2	G	701	FAD	C4'-C3'-C2'	2.58	118.72	113.36
2	E	701	FAD	O2A-PA-O1A	2.57	124.94	112.24
2	A	701	FAD	O2A-PA-O1A	2.47	124.43	112.24
4	G	1156	I55	C6-C7-N5	-2.43	115.19	118.19
2	A	701	FAD	C4'-C3'-C2'	2.40	118.36	113.36
2	C	701	FAD	C4'-C3'-C2'	2.39	118.33	113.36
4	F	1181	I55	C9-C8-N5	2.39	112.30	109.83
2	C	701	FAD	C5A-C6A-N6A	2.36	123.93	120.35
2	G	701	FAD	C5A-C6A-N6A	2.25	123.78	120.35
4	A	1147	I55	C9-C8-N5	2.24	112.15	109.83
3	D	703	GLY	OXT-C-O	-2.19	117.84	123.30
4	B	1164	I55	C9-C8-N5	2.16	112.06	109.83
2	D	701	FAD	C5A-C6A-N6A	2.15	123.61	120.35
4	H	1037	I55	C6-C7-N5	-2.09	115.61	118.19
2	H	701	FAD	C5A-C6A-N6A	2.09	123.53	120.35
2	C	701	FAD	C4-N3-C2	-2.06	121.84	125.64
2	E	701	FAD	O4'-C4'-C3'	2.06	114.10	109.10
4	B	1164	I55	C6-C7-N5	-2.03	115.68	118.19
2	G	701	FAD	C4X-C4-N3	2.03	118.35	113.19
2	G	701	FAD	C4-N3-C2	-2.02	121.91	125.64
4	E	1140	I55	C9-C8-N5	2.01	111.92	109.83

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1153	I55	N1-C1-C2-O1
4	C	1153	I55	N1-C1-C2-N2
2	G	701	FAD	O4B-C4B-C5B-O5B
2	C	701	FAD	O4B-C4B-C5B-O5B
4	G	1156	I55	N1-C1-C2-O1
2	D	701	FAD	C2'-C1'-N10-C10
2	H	701	FAD	C2'-C1'-N10-C10
4	G	1156	I55	N1-C1-C2-N2
2	B	701	FAD	O4B-C4B-C5B-O5B
2	F	701	FAD	O4B-C4B-C5B-O5B
4	B	1164	I55	C15-C13-O6-C14
4	C	1153	I55	C15-C13-O6-C14
4	D	1023	I55	C15-C13-O6-C14
4	F	1181	I55	C15-C13-O6-C14
4	G	1156	I55	C15-C13-O6-C14
4	H	1037	I55	C15-C13-O6-C14
2	A	701	FAD	O4B-C4B-C5B-O5B
2	E	701	FAD	O4B-C4B-C5B-O5B
2	C	701	FAD	C2'-C1'-N10-C10
2	D	701	FAD	O4B-C4B-C5B-O5B
2	H	701	FAD	O4B-C4B-C5B-O5B
2	G	701	FAD	C3B-C4B-C5B-O5B
2	C	701	FAD	C3B-C4B-C5B-O5B
2	B	701	FAD	C3B-C4B-C5B-O5B
2	F	701	FAD	C3B-C4B-C5B-O5B
2	G	701	FAD	C2'-C1'-N10-C10

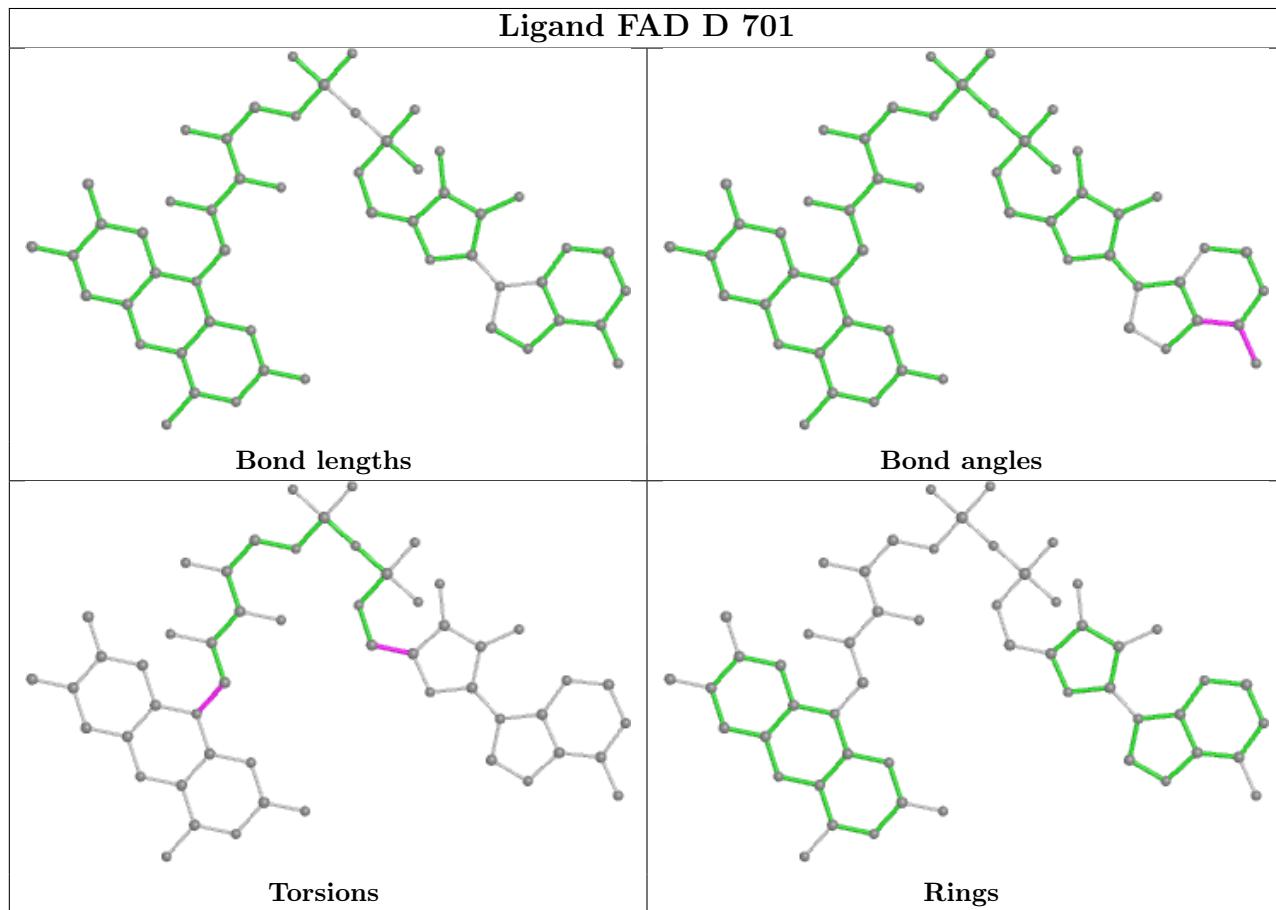
There are no ring outliers.

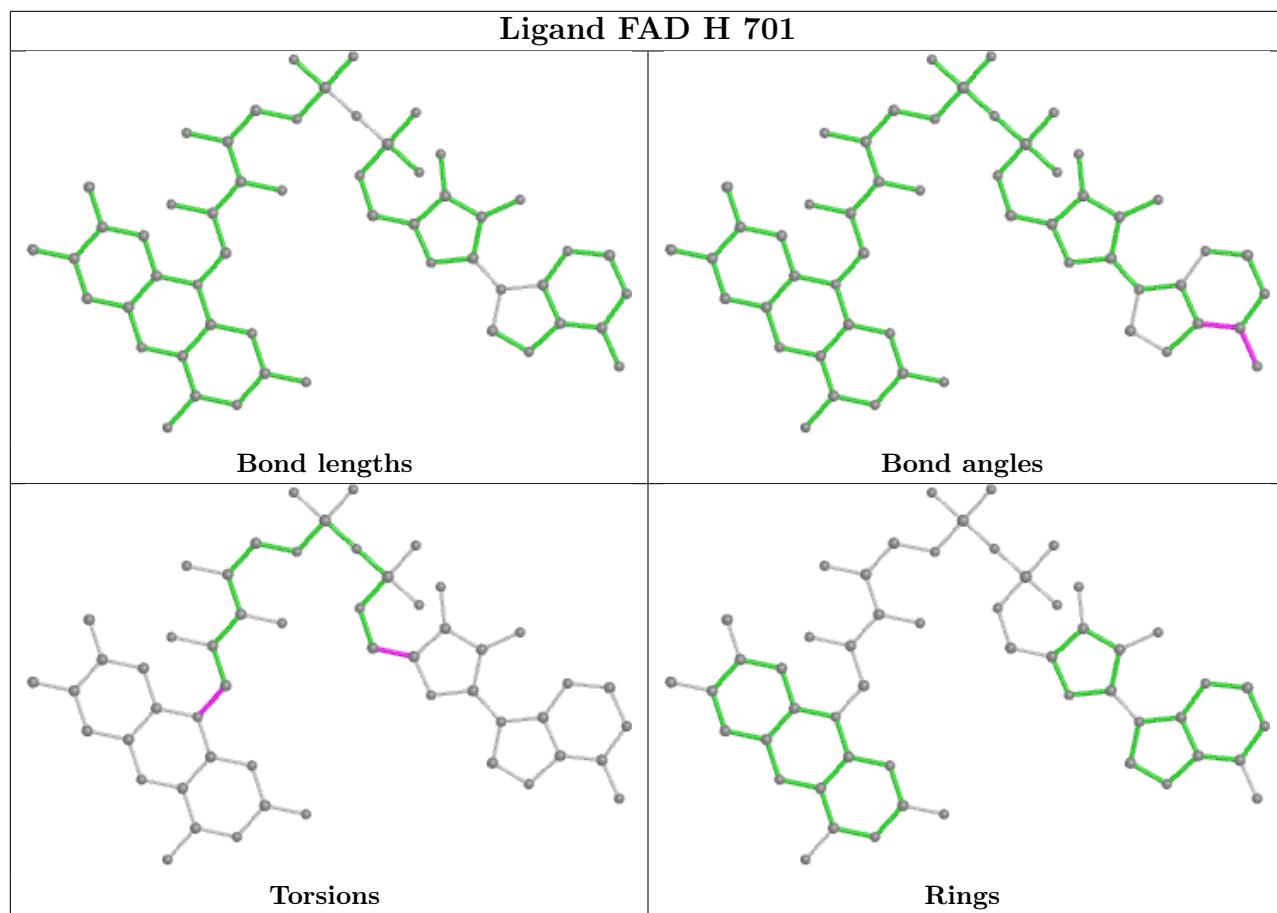
6 monomers are involved in 7 short contacts:

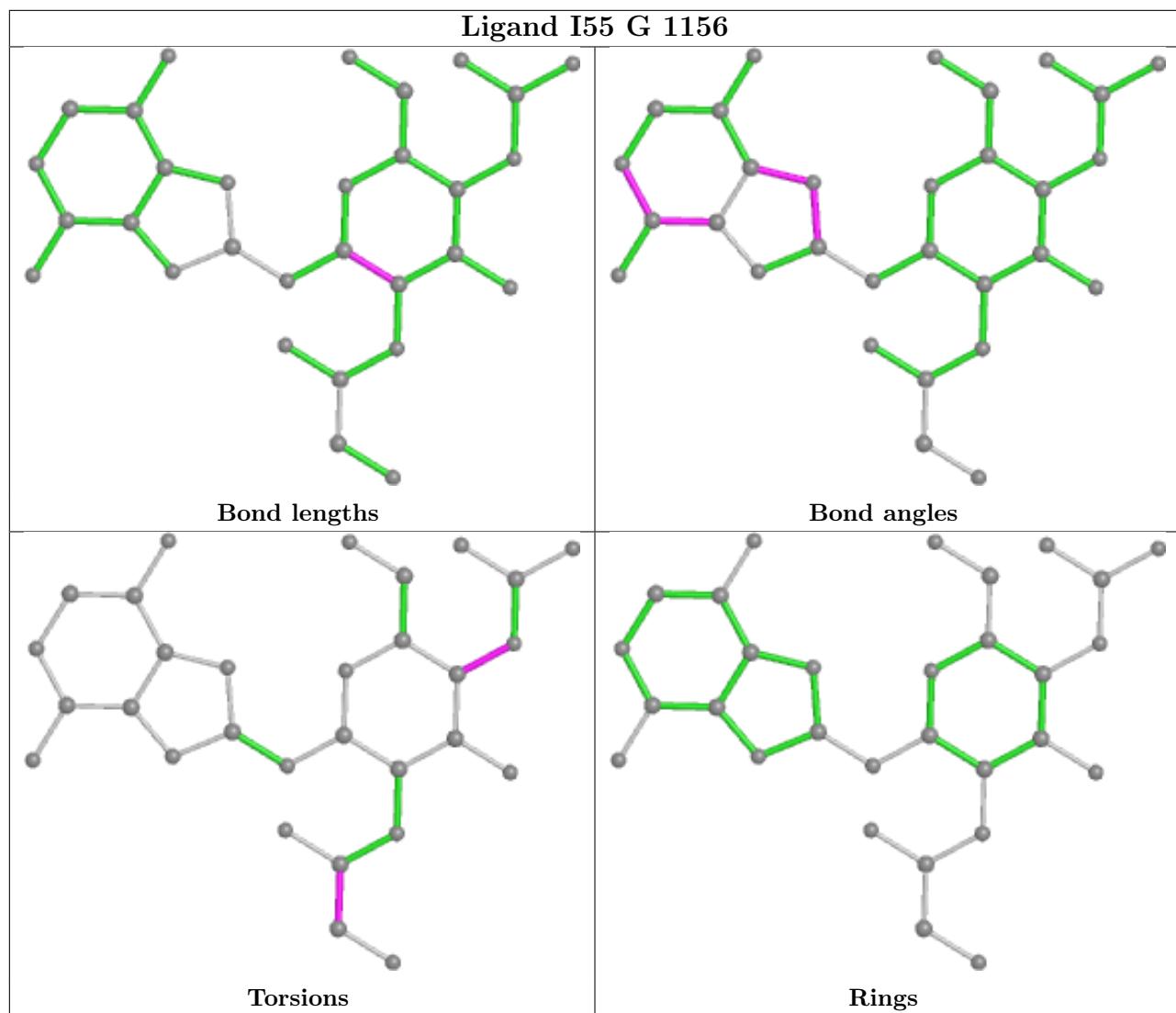
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	701	FAD	2	0
2	G	701	FAD	1	0
2	A	701	FAD	1	0
2	E	701	FAD	1	0
2	F	701	FAD	1	0
2	C	701	FAD	1	0

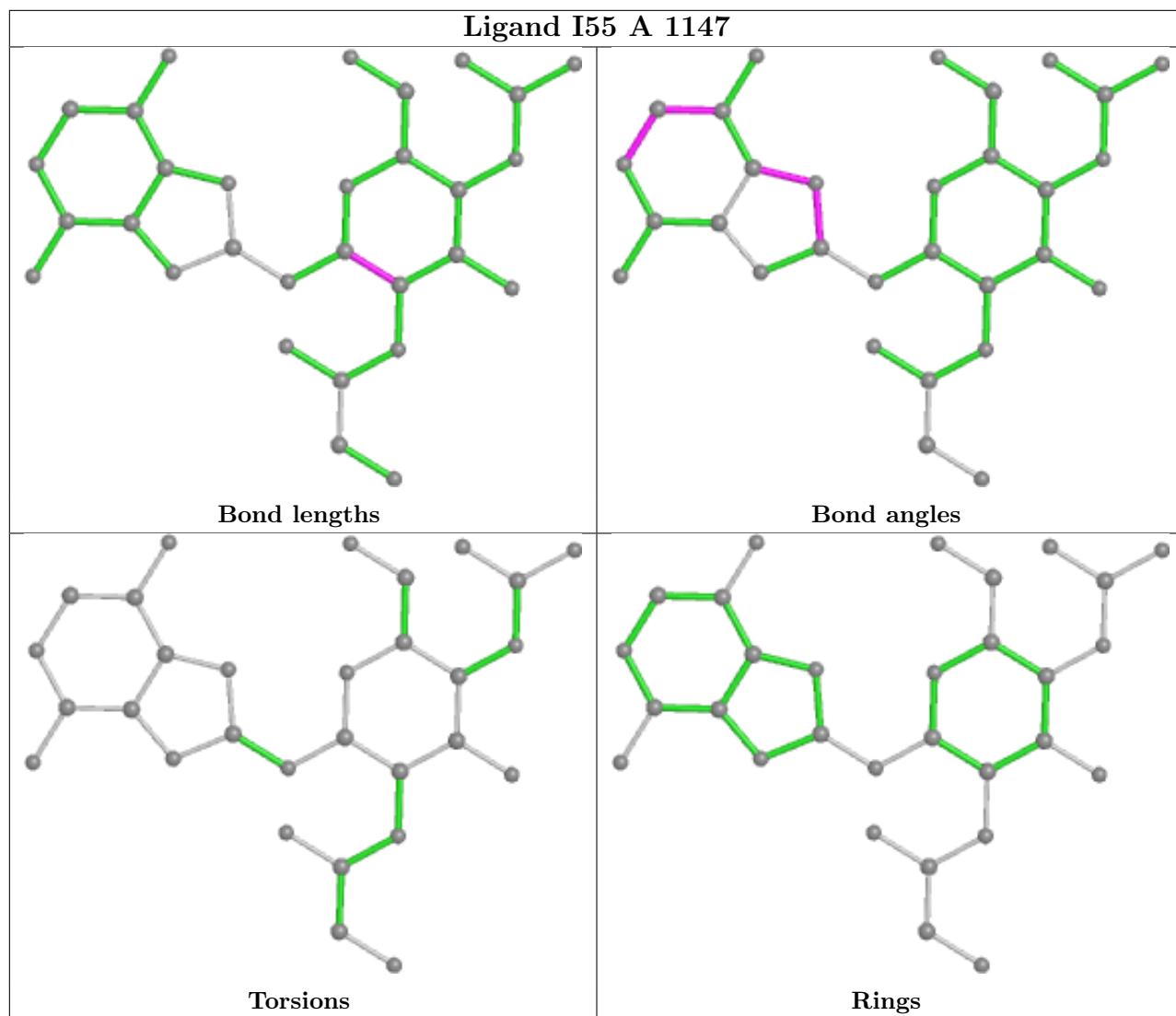
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

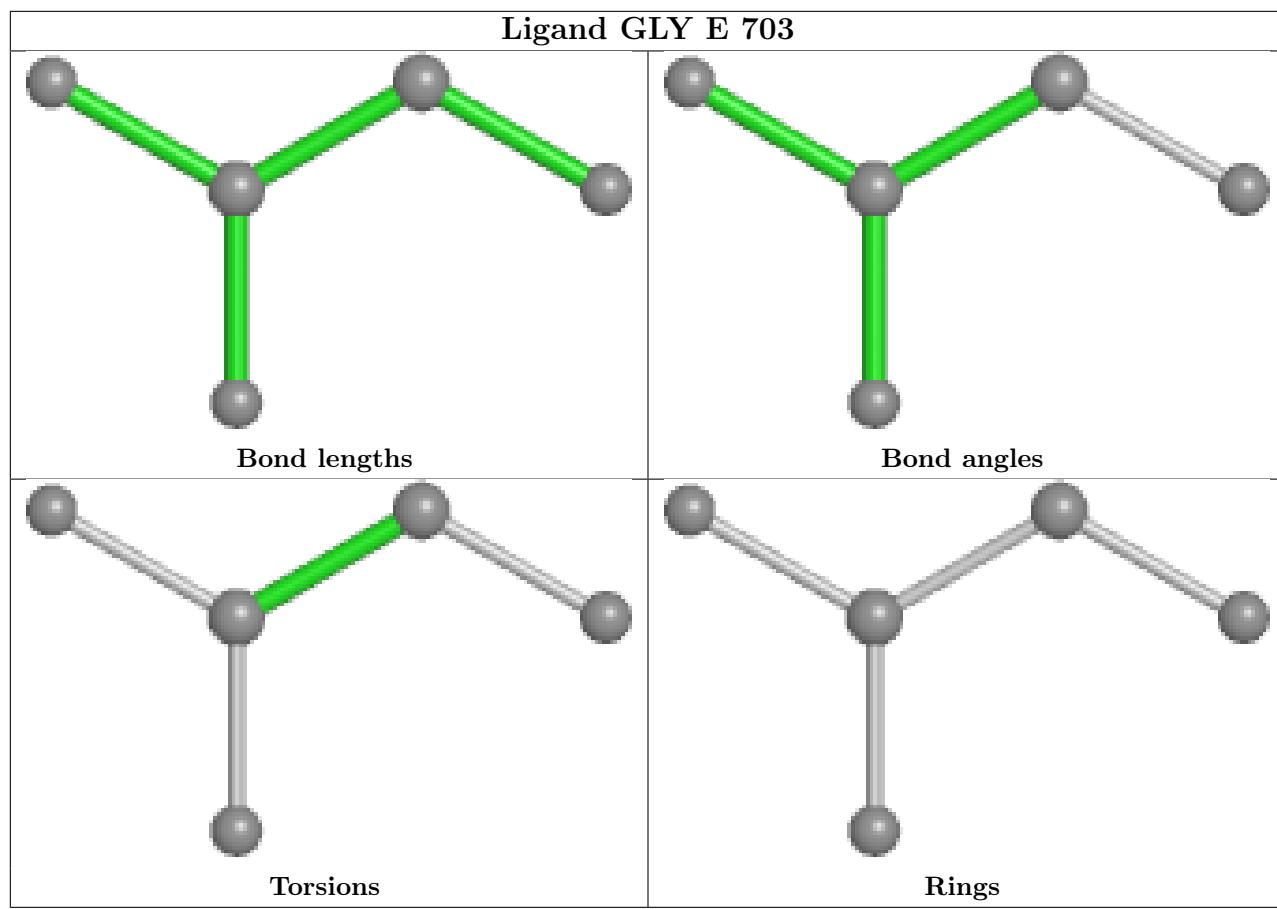
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

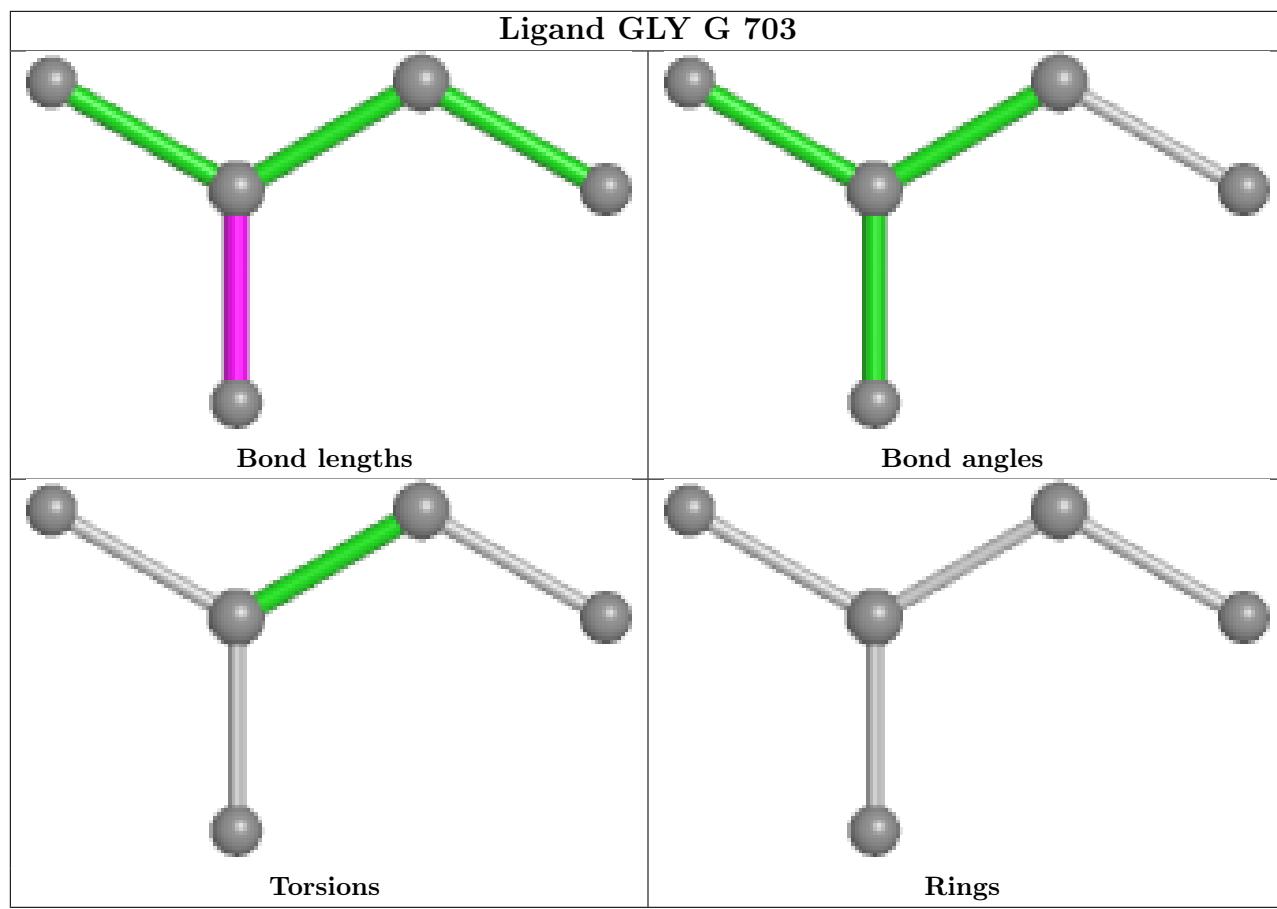


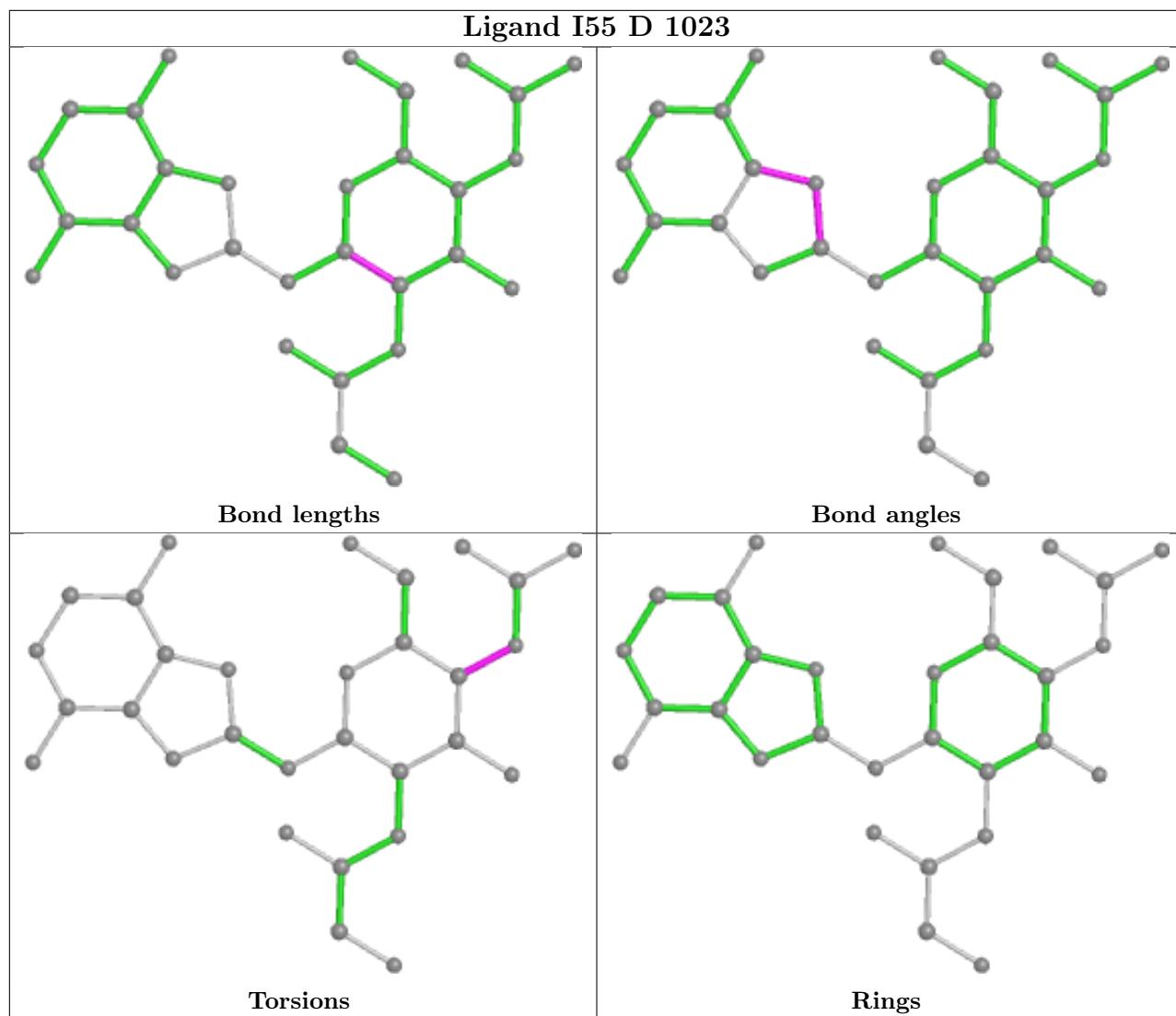


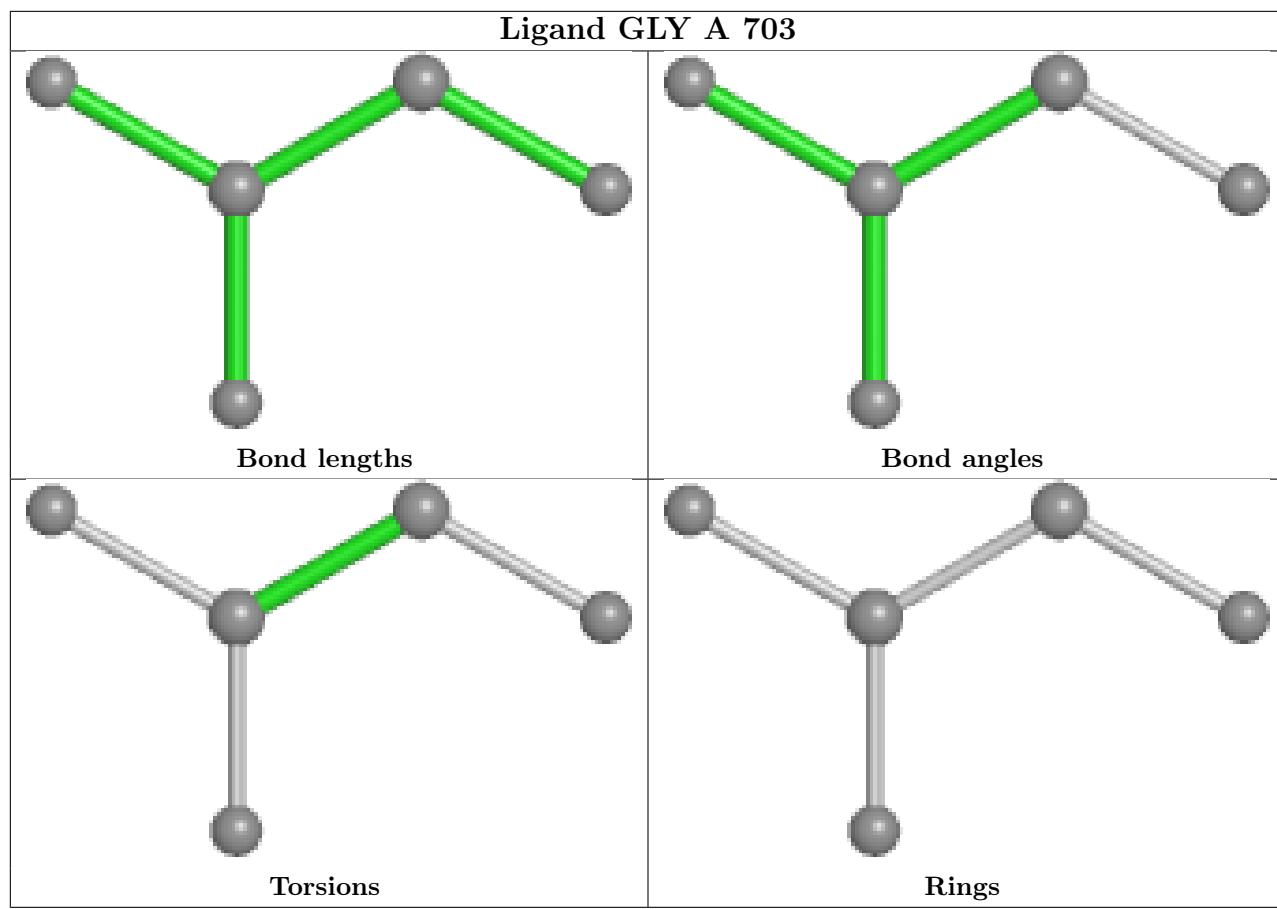


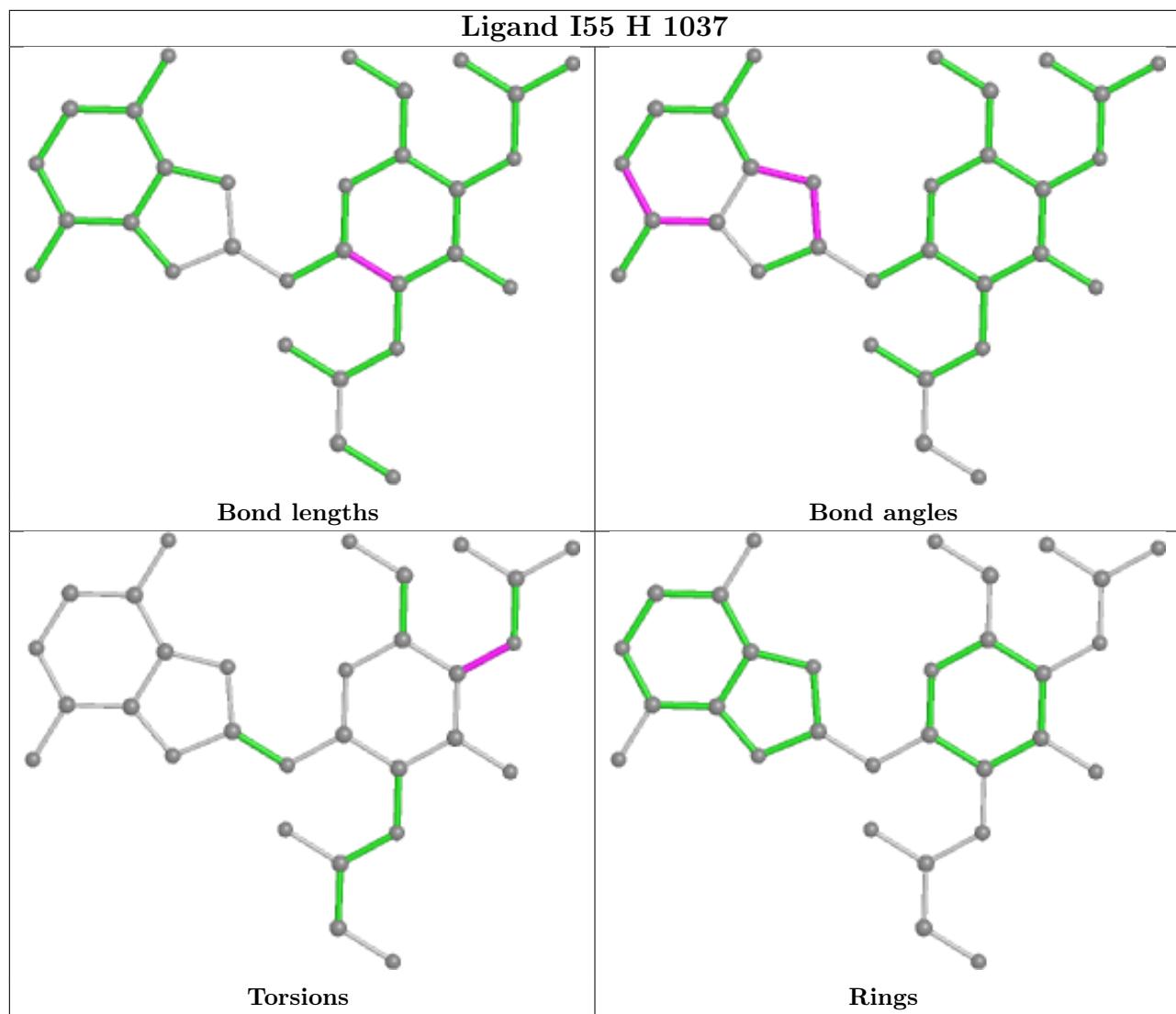


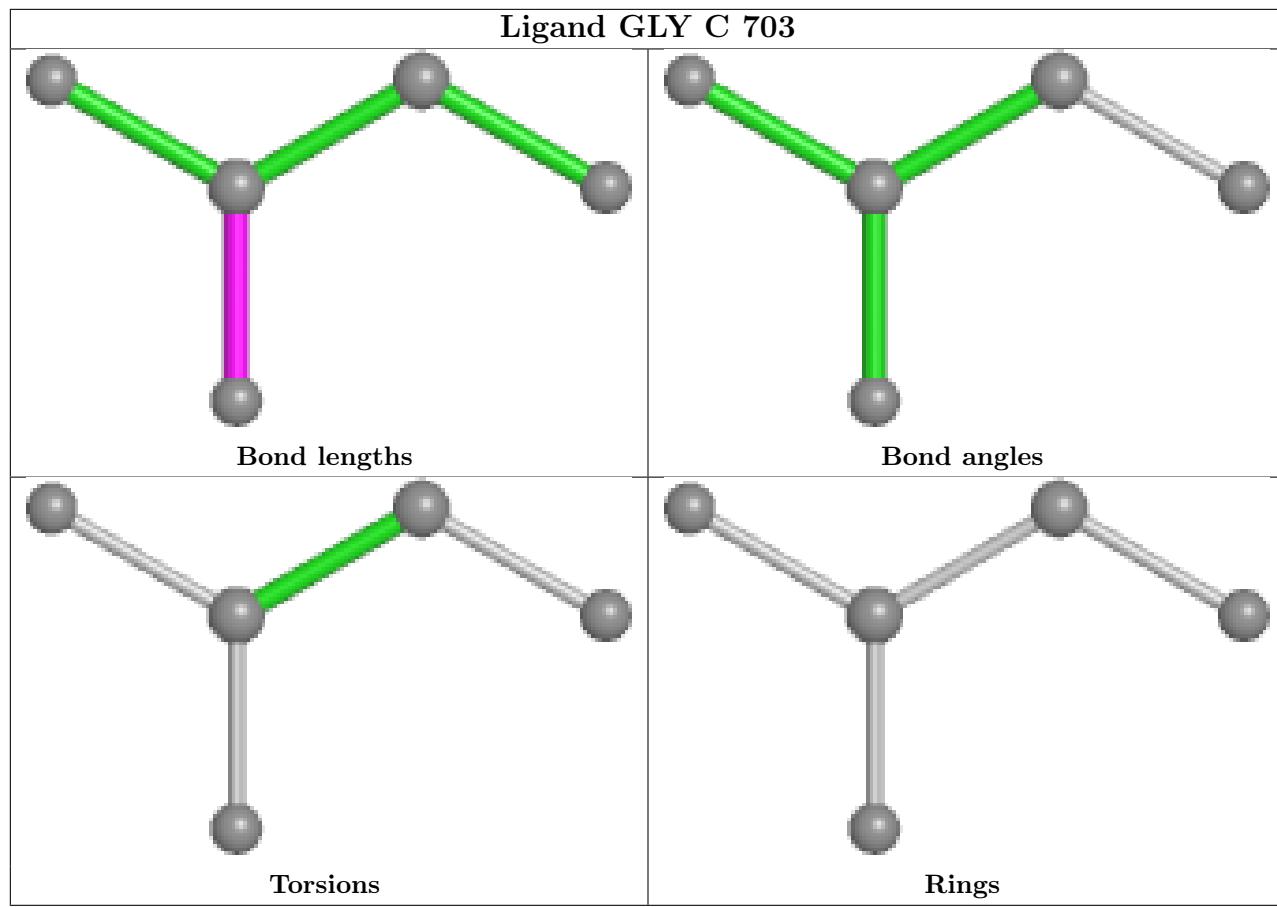


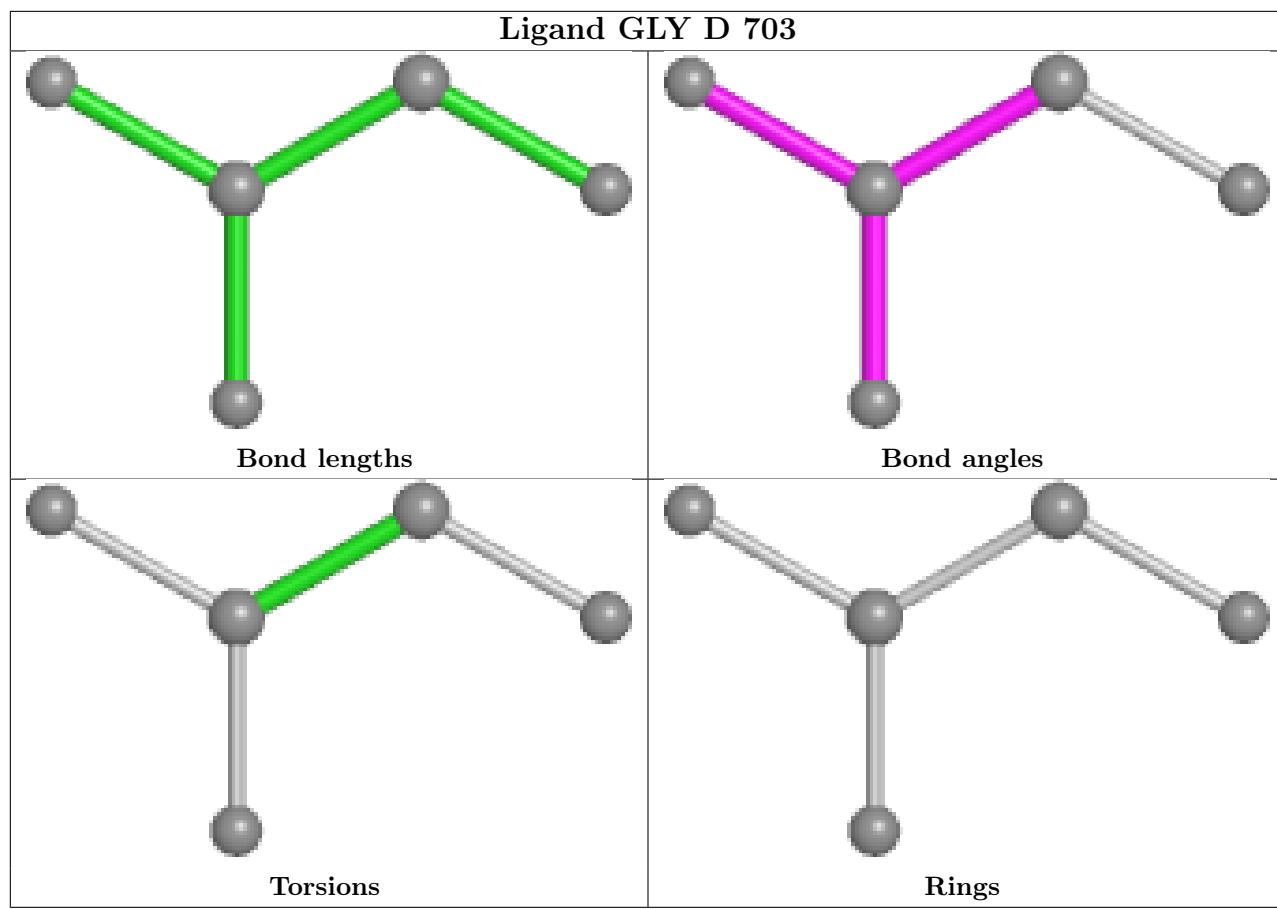


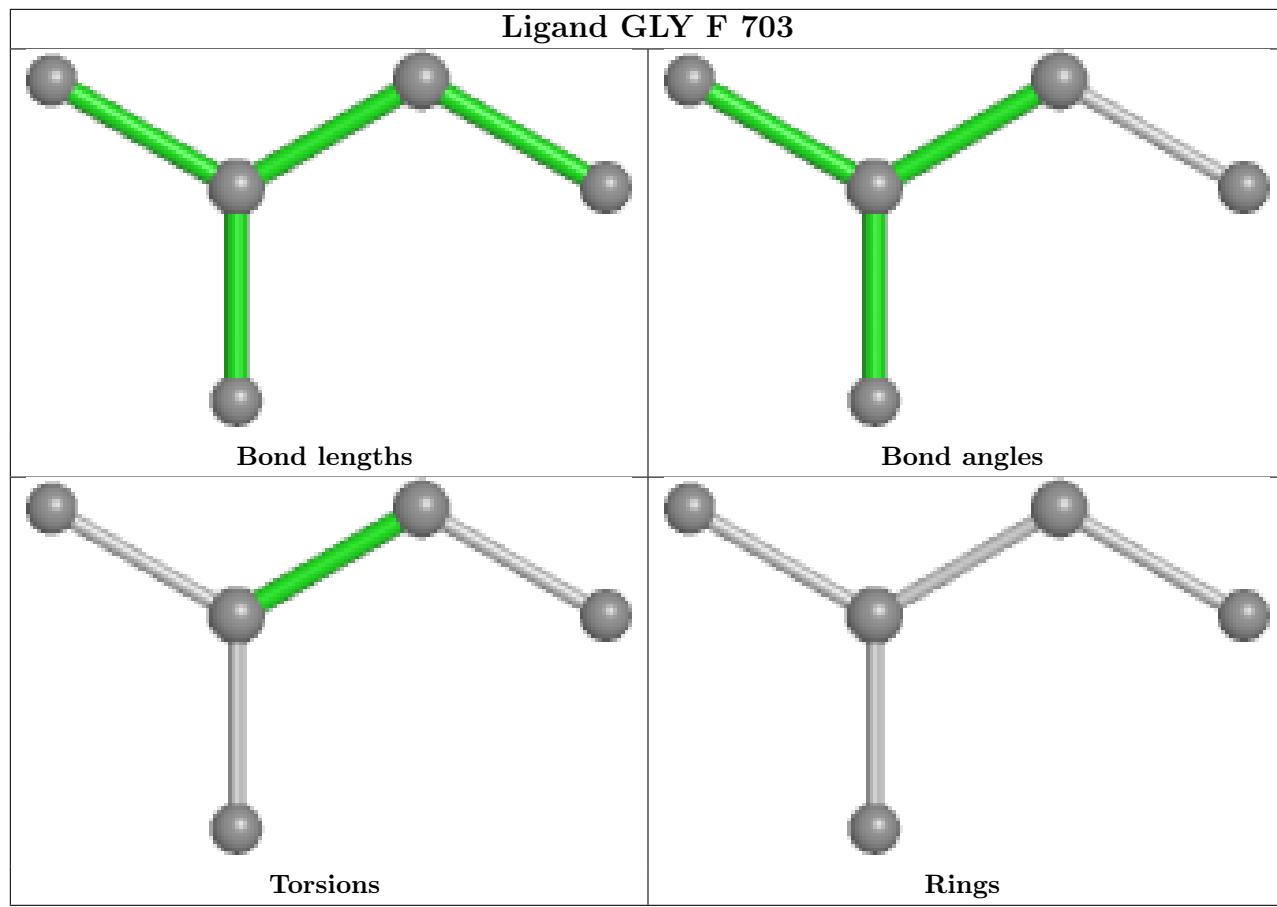


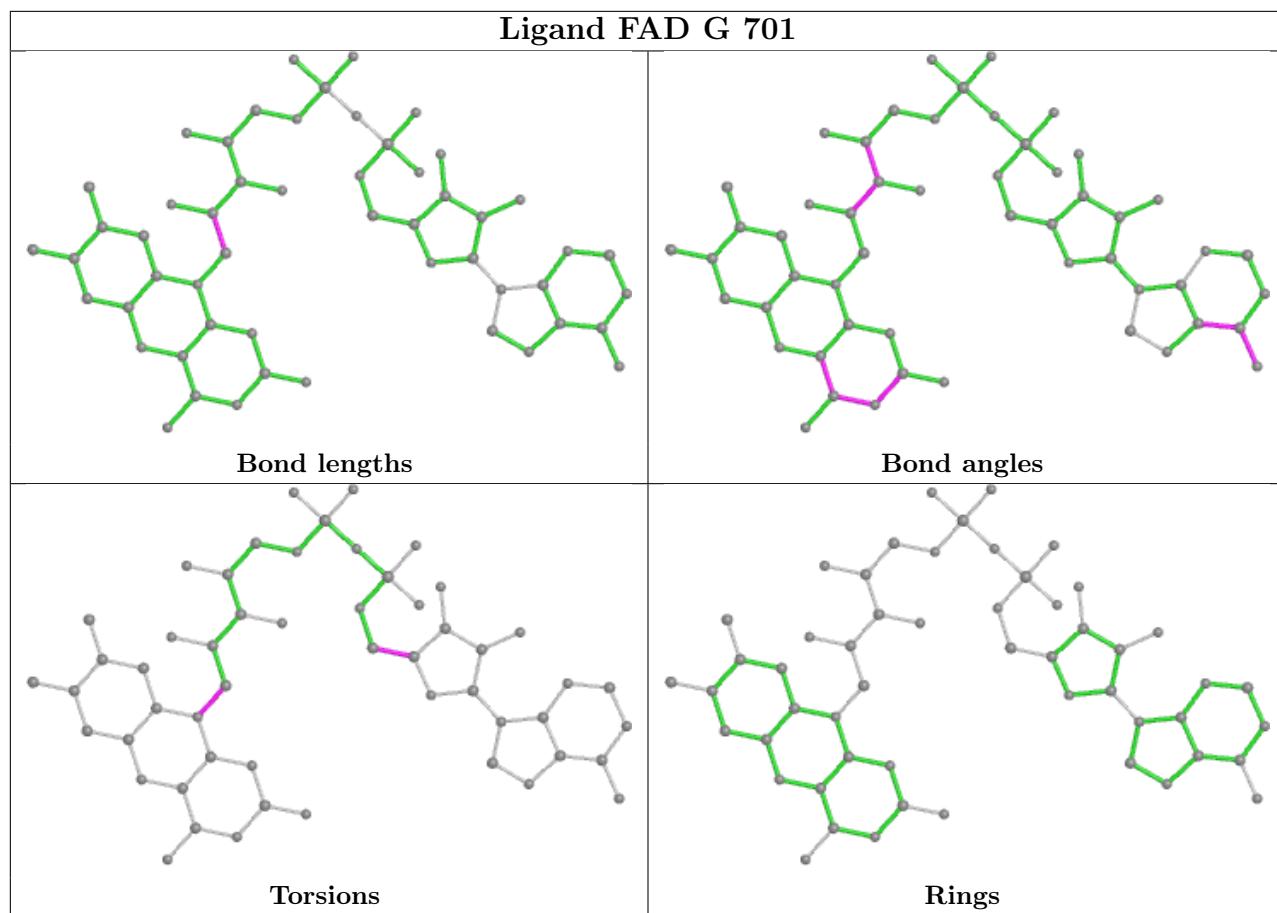


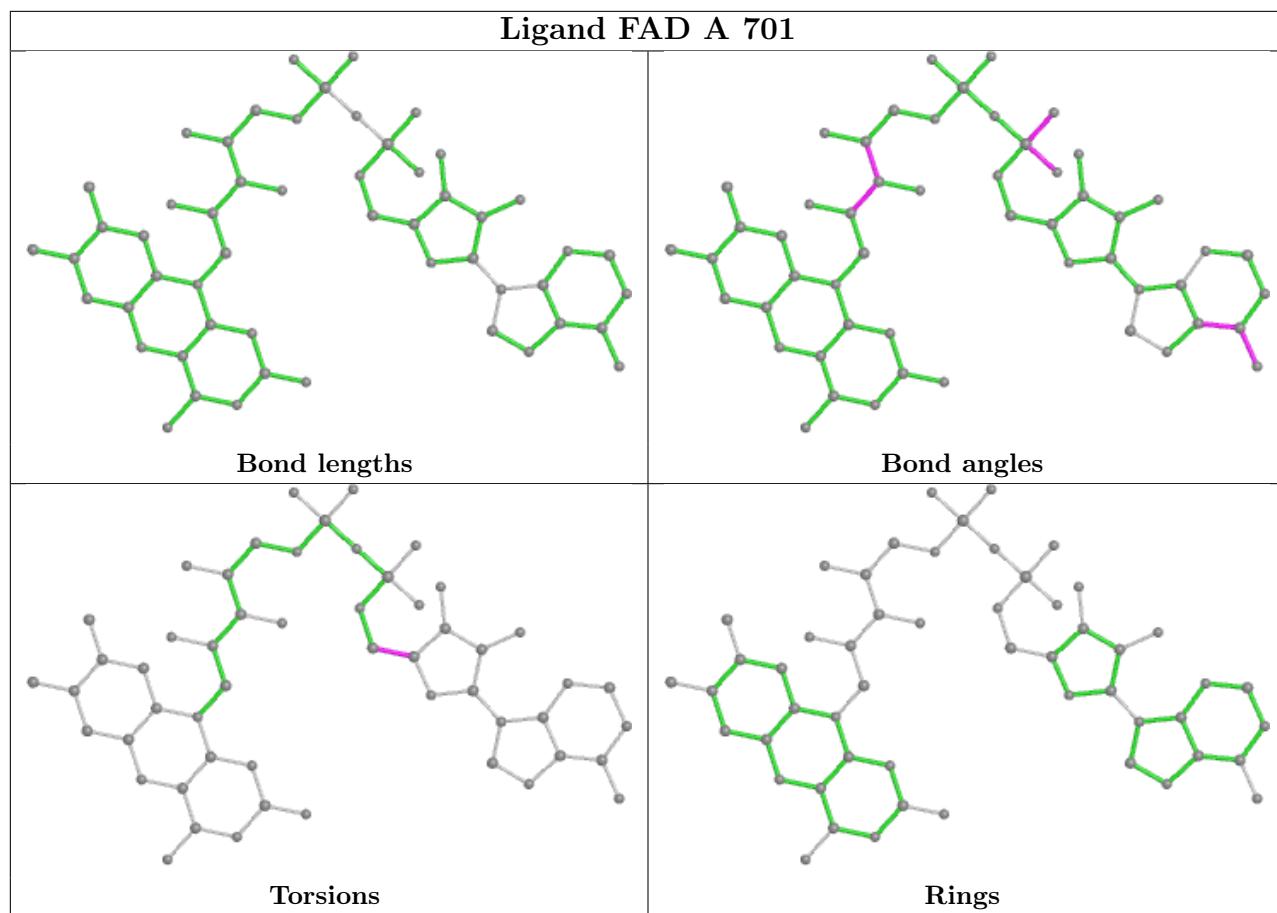


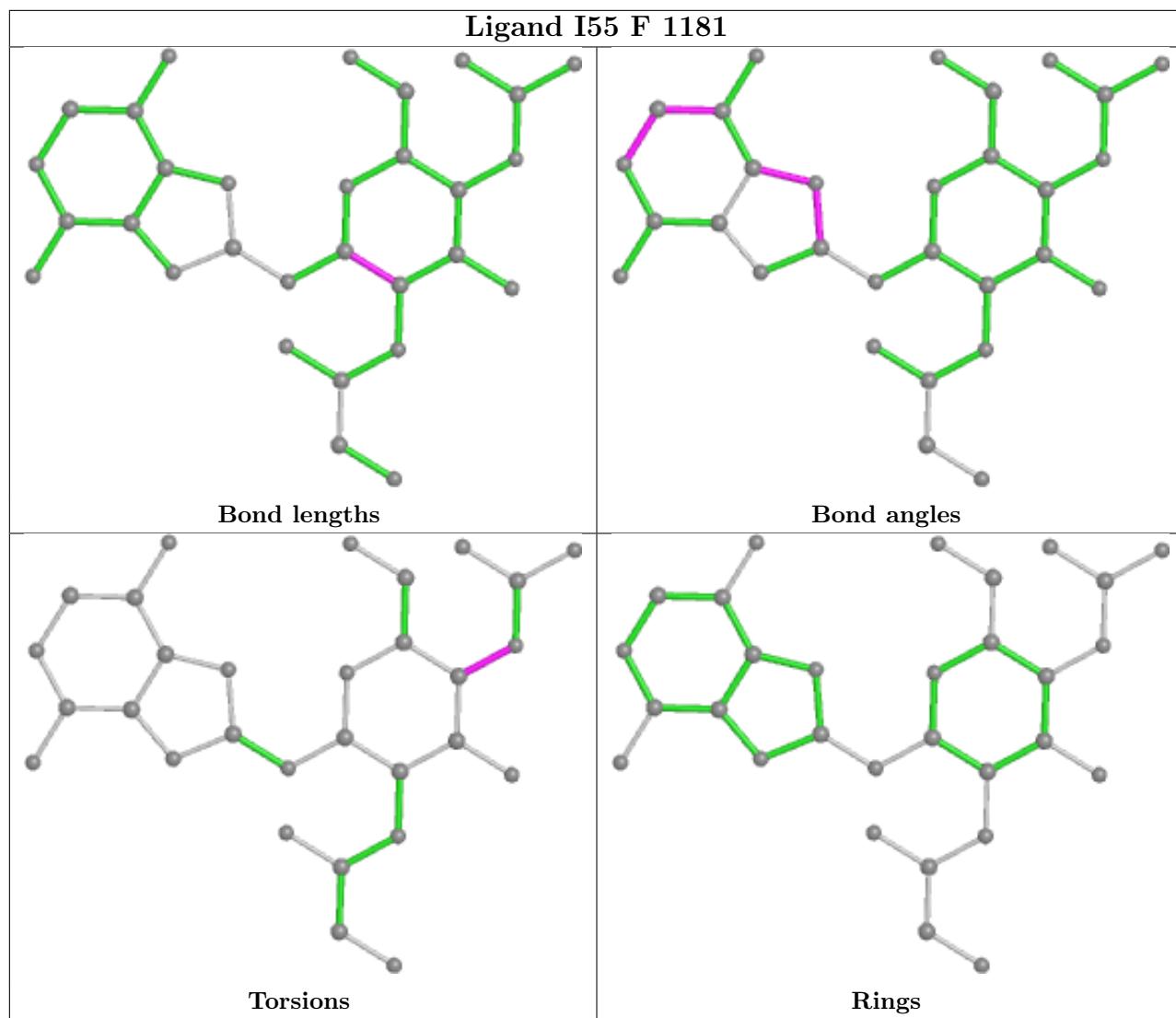


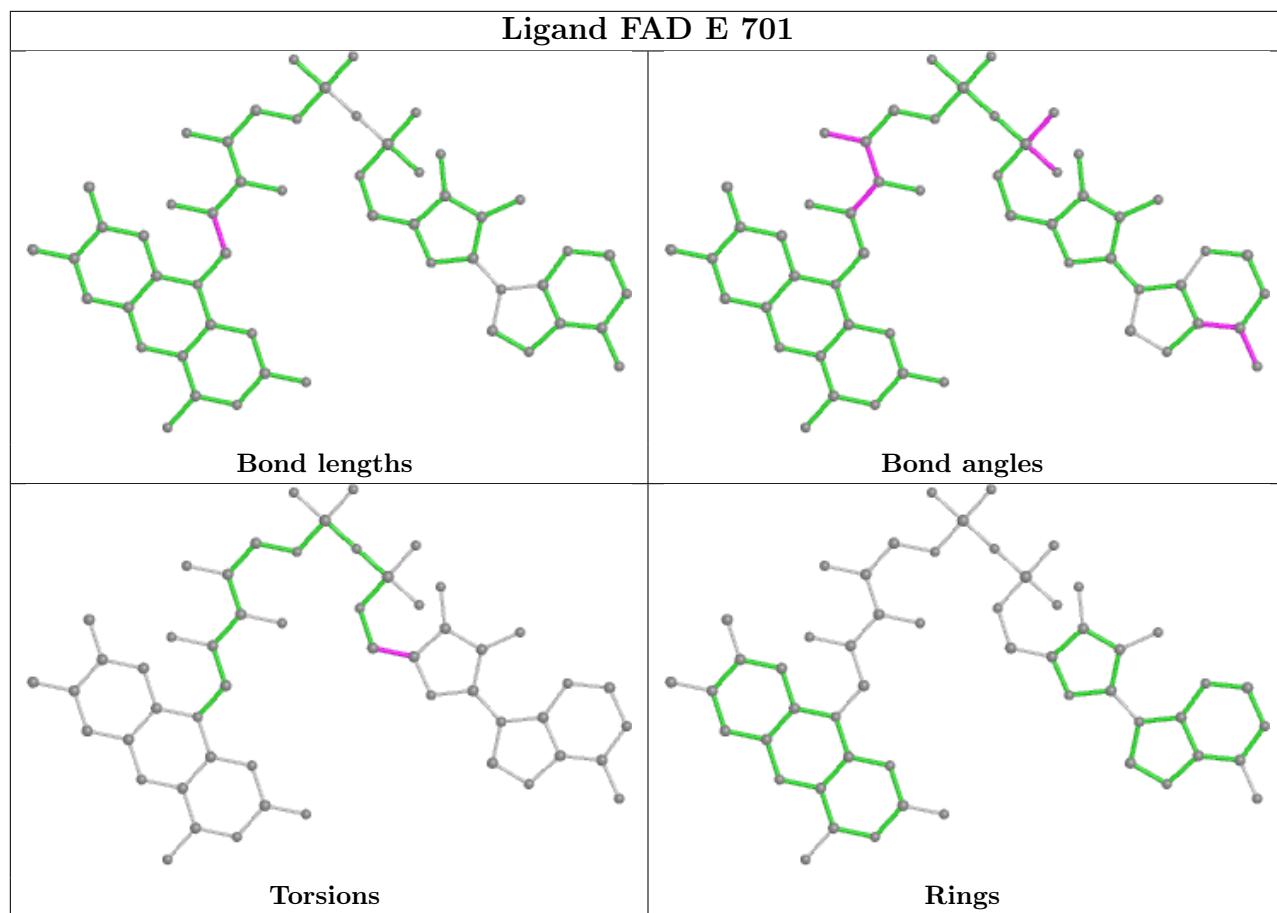


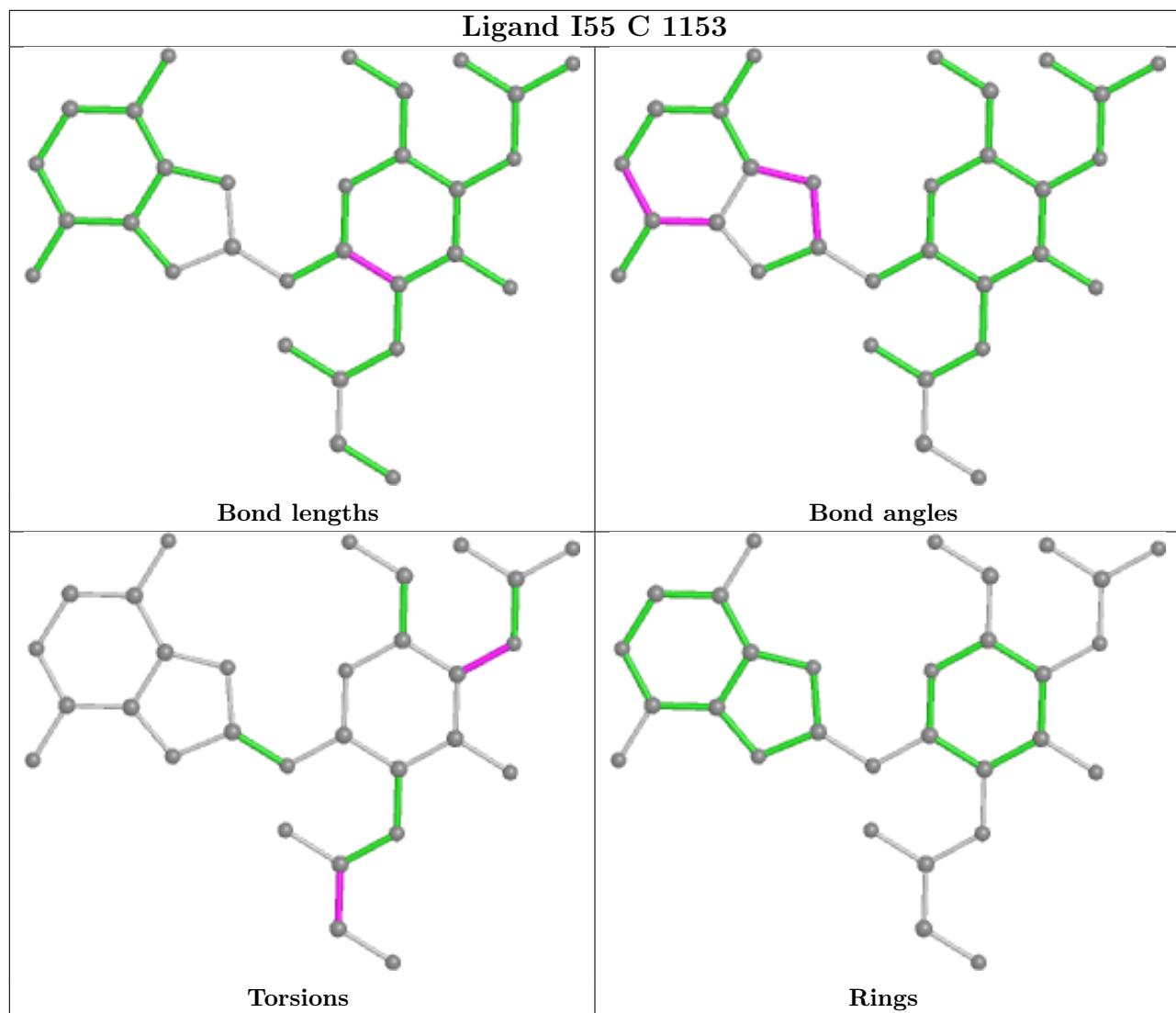


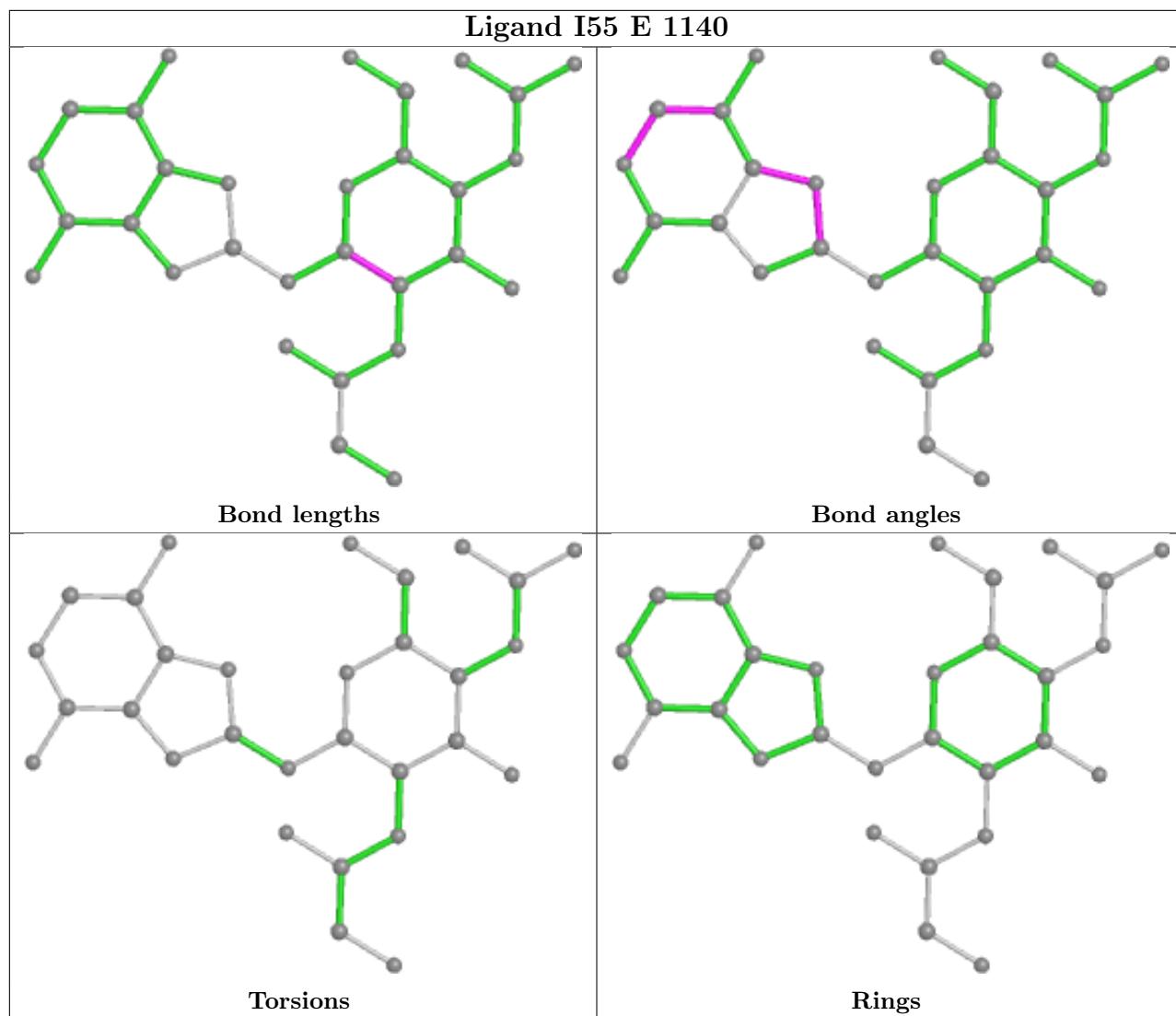


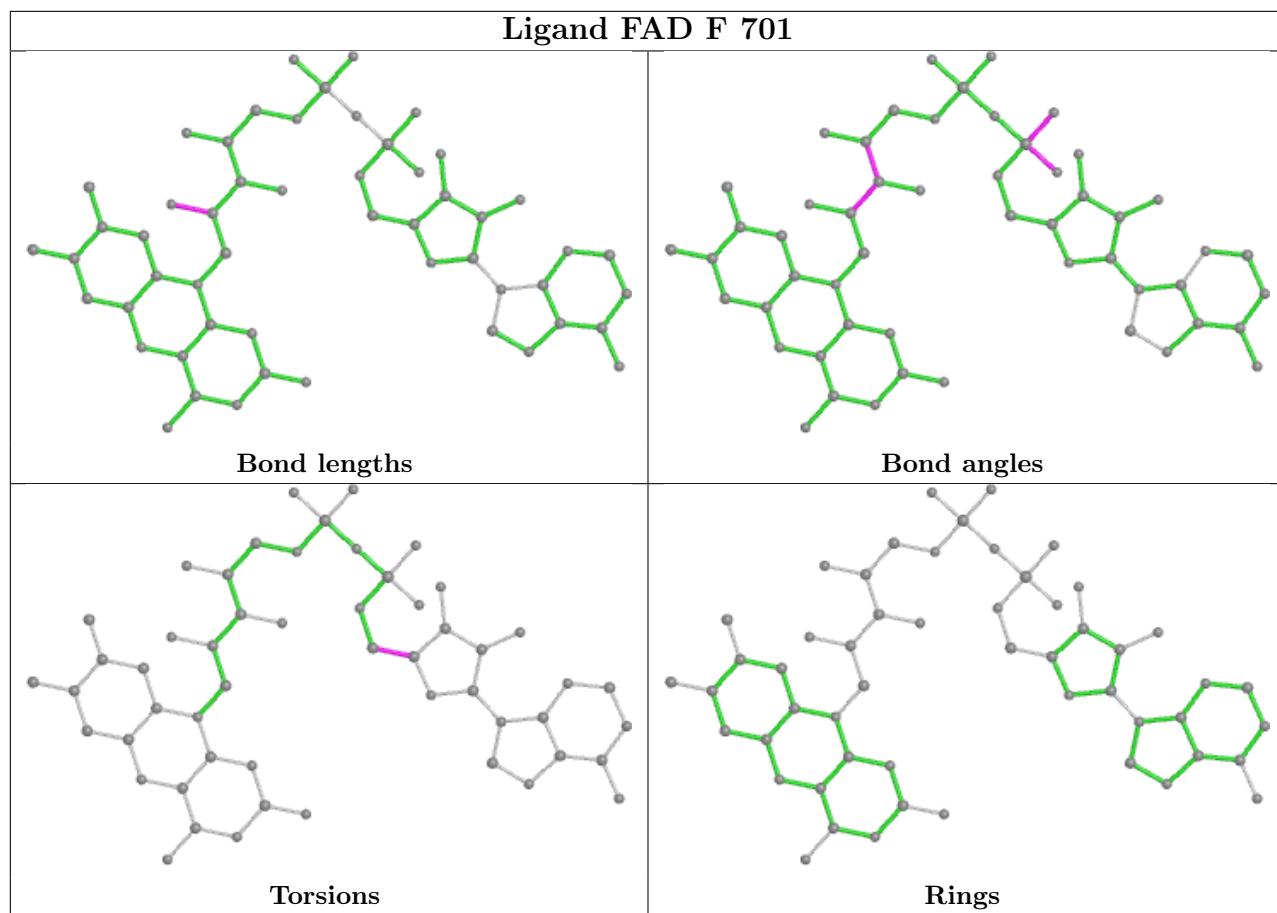


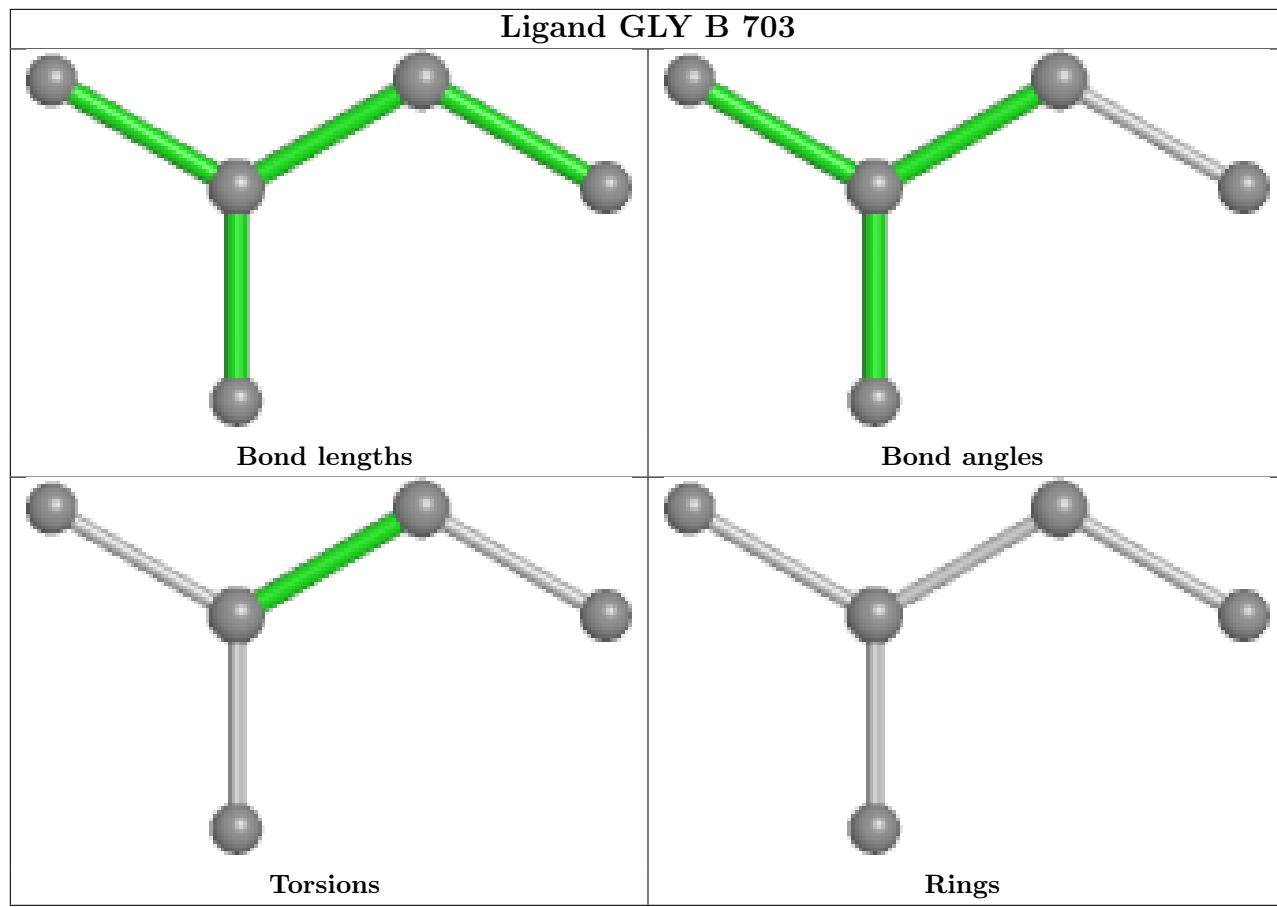


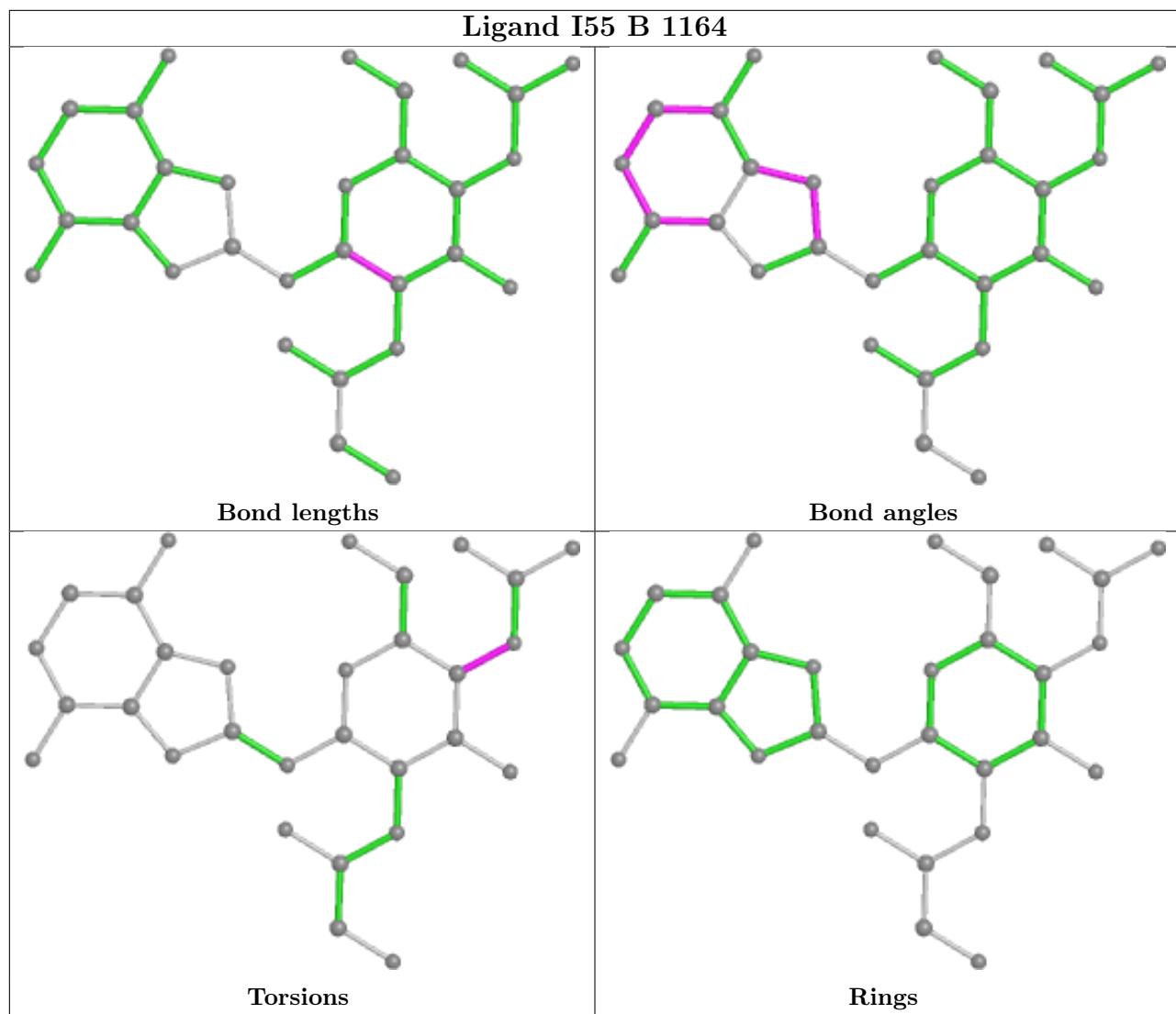


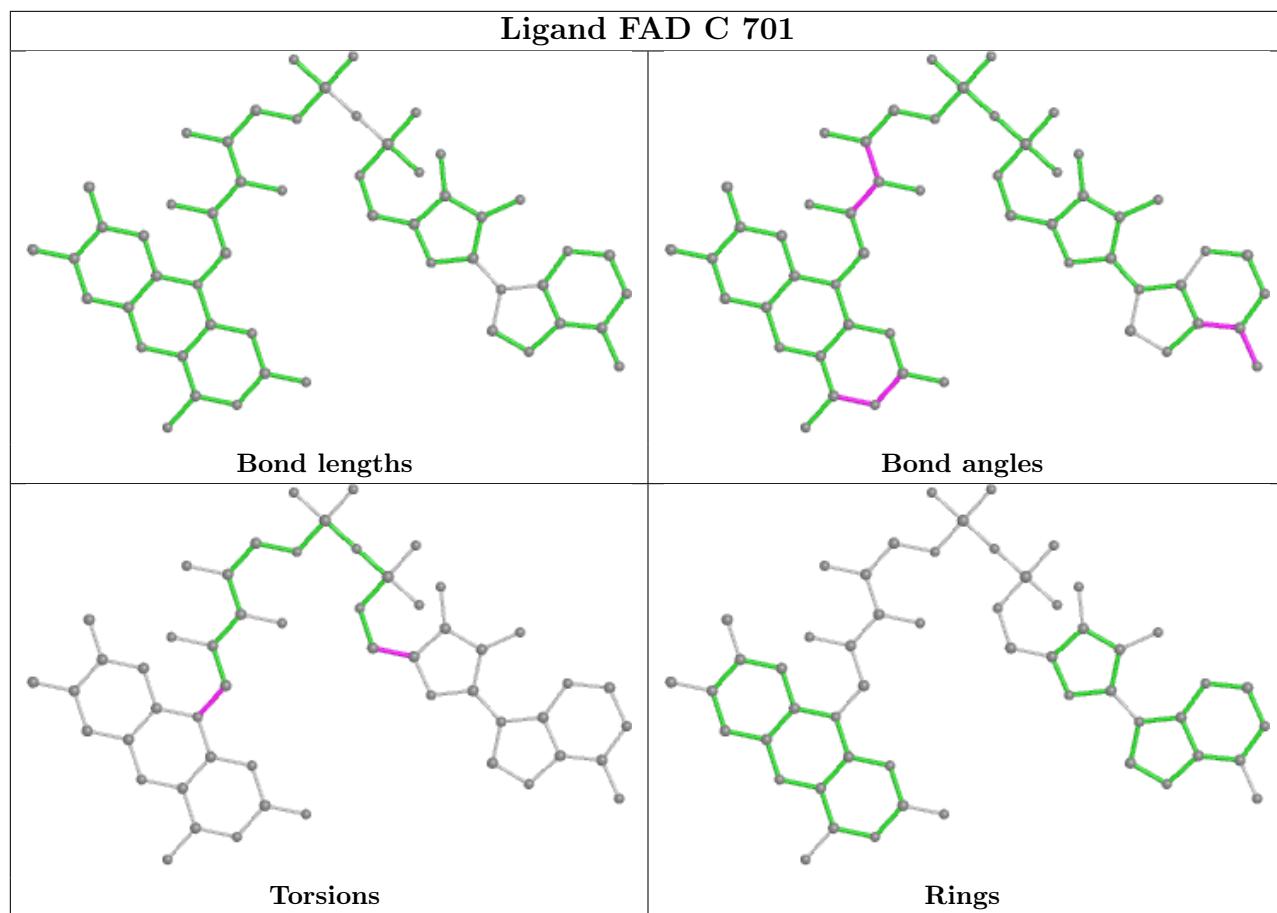


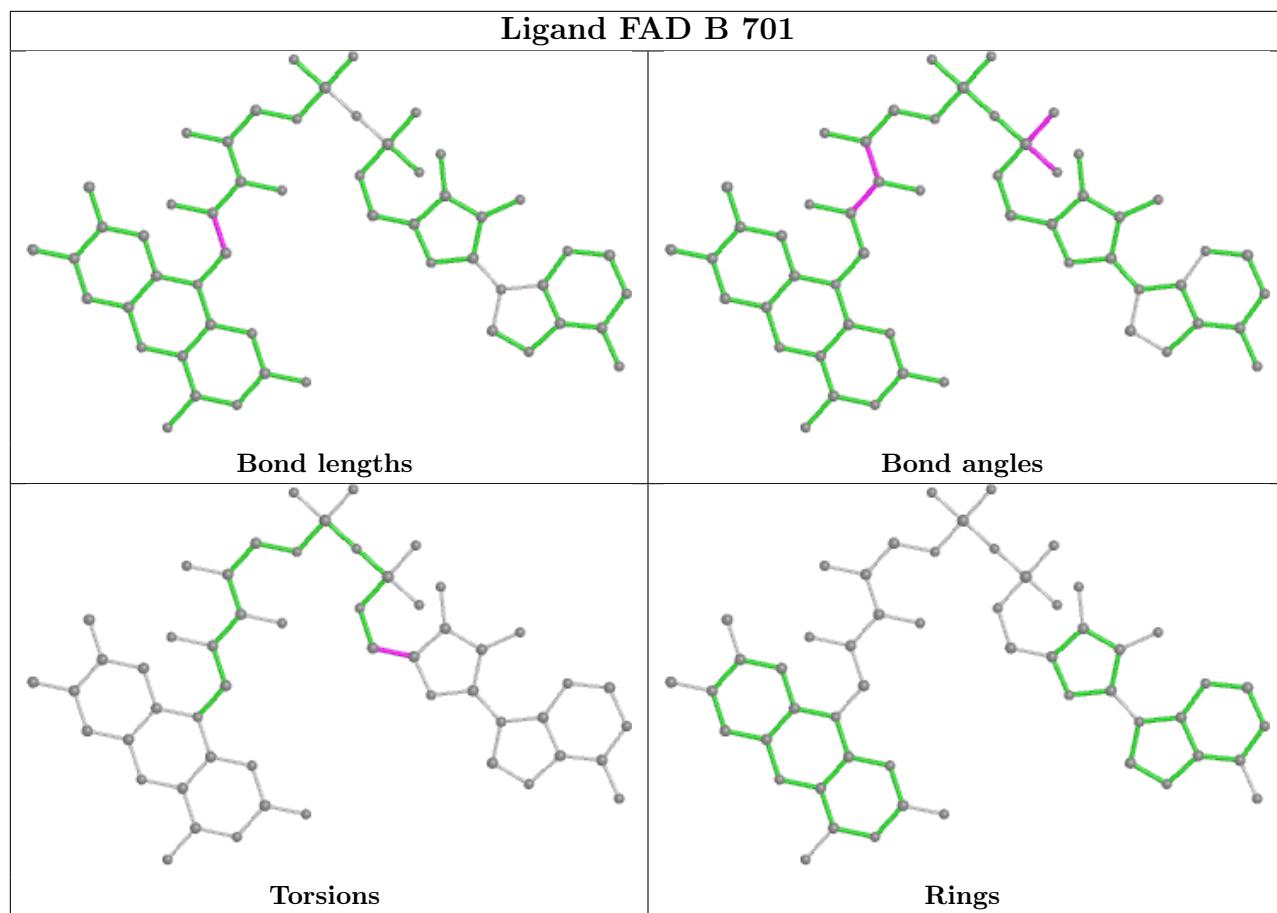


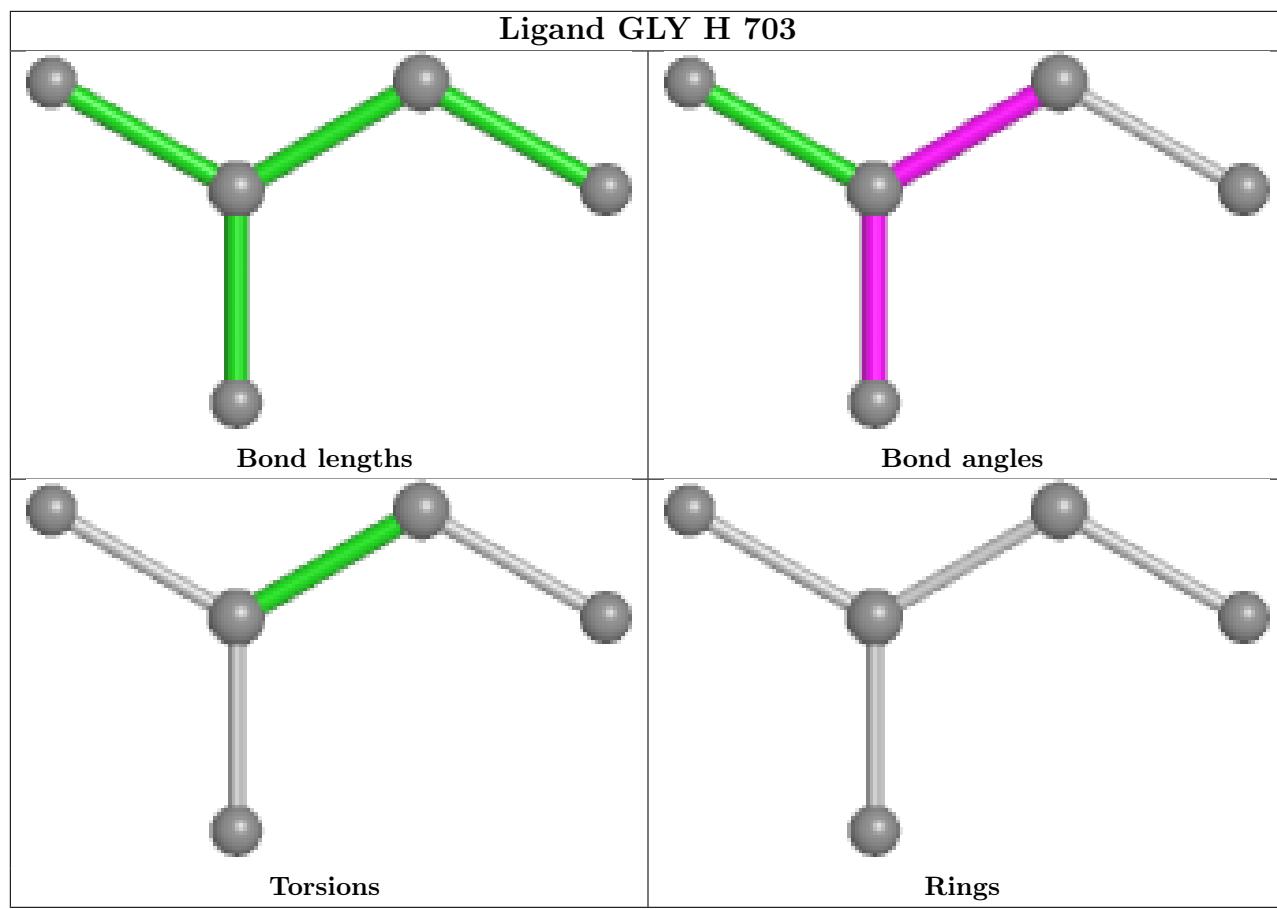












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

## 6 Fit of model and data i

### 6.1 Protein, DNA and RNA chains i

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	482/512 (94%)	0.14	5 (1%)	82	85	15, 28, 52, 94
1	B	482/512 (94%)	0.08	5 (1%)	82	85	12, 25, 48, 70
1	C	482/512 (94%)	0.07	1 (0%)	95	95	11, 26, 55, 75
1	D	479/512 (93%)	0.60	50 (10%)	6	8	17, 42, 86, 108
1	E	482/512 (94%)	0.08	5 (1%)	82	85	15, 28, 52, 98
1	F	482/512 (94%)	0.06	3 (0%)	89	91	12, 25, 48, 72
1	G	482/512 (94%)	0.09	6 (1%)	79	82	11, 26, 56, 75
1	H	479/512 (93%)	0.76	66 (13%)	2	4	17, 42, 87, 109
All	All	3850/4096 (93%)	0.23	141 (3%)	41	48	11, 29, 68, 109
							3 (0%)

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	220	LEU	6.6
1	H	36	VAL	5.7
1	D	224	HIS	5.7
1	H	34	PRO	5.6
1	D	361	TRP	5.5
1	H	393	GLY	5.5
1	H	202	ILE	5.3
1	D	384	LEU	5.2
1	D	202	ILE	5.0
1	H	206	HIS	4.9
1	H	392	ASP	4.9
1	D	206	HIS	4.9
1	H	491	HIS	4.7
1	E	10	GLN	4.7
1	D	211	GLY	4.5
1	D	394	LEU	4.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	D	225	VAL	4.5
1	H	13	VAL	4.4
1	H	192	GLY	4.3
1	H	211	GLY	4.1
1	H	394	LEU	4.1
1	D	34	PRO	4.1
1	D	217	GLY	4.1
1	H	38	VAL	4.0
1	E	11	THR	4.0
1	D	37	ARG	3.9
1	H	361	TRP	3.9
1	H	384	LEU	3.9
1	D	14	ILE	3.9
1	H	217	GLY	3.8
1	H	208	ARG	3.7
1	H	33	ARG	3.7
1	D	36	VAL	3.6
1	G	242	GLY	3.6
1	D	240	LEU	3.5
1	H	224	HIS	3.5
1	H	199	ALA	3.5
1	H	220	LEU	3.5
1	H	243	LEU	3.5
1	A	10	GLN	3.5
1	D	13	VAL	3.4
1	F	392	ASP	3.4
1	H	219	PHE	3.3
1	D	212	VAL	3.2
1	D	243	LEU	3.2
1	D	219	PHE	3.1
1	D	33	ARG	3.0
1	D	204	ALA	3.0
1	D	223	GLY	3.0
1	A	11	THR	3.0
1	H	191	GLY	3.0
1	D	38	VAL	3.0
1	H	209	VAL	3.0
1	D	352	ILE	2.9
1	D	359	GLY	2.9
1	H	189	GLN	2.9
1	H	385	MET	2.9
1	H	25	VAL	2.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	H	39	THR	2.8
1	D	189	GLN	2.8
1	H	387	GLY	2.8
1	B	491	HIS	2.7
1	H	379	ARG	2.7
1	H	227	VAL	2.7
1	D	193	ARG	2.7
1	E	491	HIS	2.7
1	D	236	LEU	2.7
1	D	205	SER	2.7
1	H	457	THR	2.6
1	E	395	ARG	2.6
1	H	193	ARG	2.6
1	H	238	ALA	2.6
1	H	203	ARG	2.6
1	G	10	GLN	2.6
1	D	356	SER	2.6
1	H	389	THR	2.6
1	D	491	HIS	2.5
1	H	358	GLU	2.5
1	D	358	GLU	2.5
1	H	218	ASP	2.5
1	H	352	ILE	2.5
1	H	356	SER	2.5
1	H	190	ALA	2.5
1	H	484	ALA	2.5
1	H	386	ASP	2.5
1	D	355	THR	2.5
1	H	41	LEU	2.4
1	D	226	VAL	2.4
1	H	483	TYR	2.4
1	H	225	VAL	2.4
1	H	482	TYR	2.4
1	D	208	ARG	2.4
1	D	216	ASP	2.3
1	D	391	VAL	2.3
1	D	30	ALA	2.3
1	H	32	THR	2.3
1	E	206	HIS	2.3
1	A	395	ARG	2.3
1	H	213	VAL	2.3
1	D	379	ARG	2.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	H	35	ASP	2.2
1	A	193	ARG	2.2
1	H	194	LEU	2.2
1	H	391	VAL	2.2
1	B	473	ARG	2.2
1	G	208	ARG	2.2
1	B	36	VAL	2.2
1	D	239	ALA	2.2
1	B	392	ASP	2.2
1	H	16	VAL	2.2
1	H	37	ARG	2.2
1	D	222	ALA	2.2
1	D	40	LEU	2.2
1	H	382	VAL	2.2
1	H	236	LEU	2.1
1	H	376	LEU	2.1
1	H	235	ARG	2.1
1	B	206	HIS	2.1
1	H	226	VAL	2.1
1	H	237	VAL	2.1
1	F	35	ASP	2.1
1	G	398	ARG	2.1
1	H	204	ALA	2.1
1	D	215	ASP	2.1
1	H	240	LEU	2.1
1	D	90	GLU	2.1
1	C	479	LEU	2.1
1	D	21	LEU	2.1
1	D	23	LEU	2.0
1	D	404	ILE	2.0
1	A	392	ASP	2.0
1	F	398	ARG	2.0
1	H	14	ILE	2.0
1	D	190	ALA	2.0
1	D	227	VAL	2.0
1	H	27	VAL	2.0
1	D	393	GLY	2.0
1	G	101	ALA	2.0
1	G	243	LEU	2.0
1	H	21	LEU	2.0
1	H	239	ALA	2.0

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

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

## 6.3 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

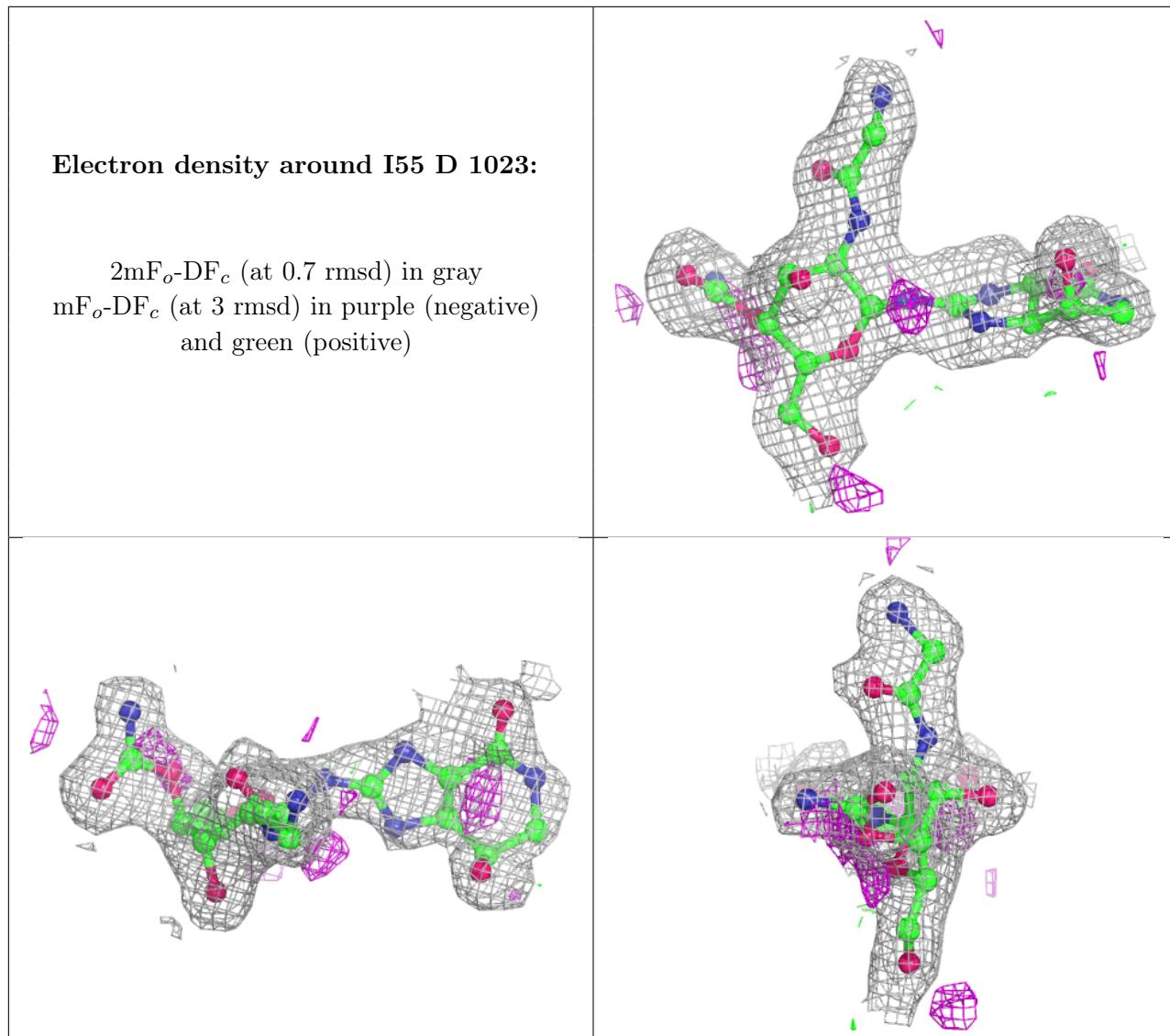
## 6.4 Ligands [\(i\)](#)

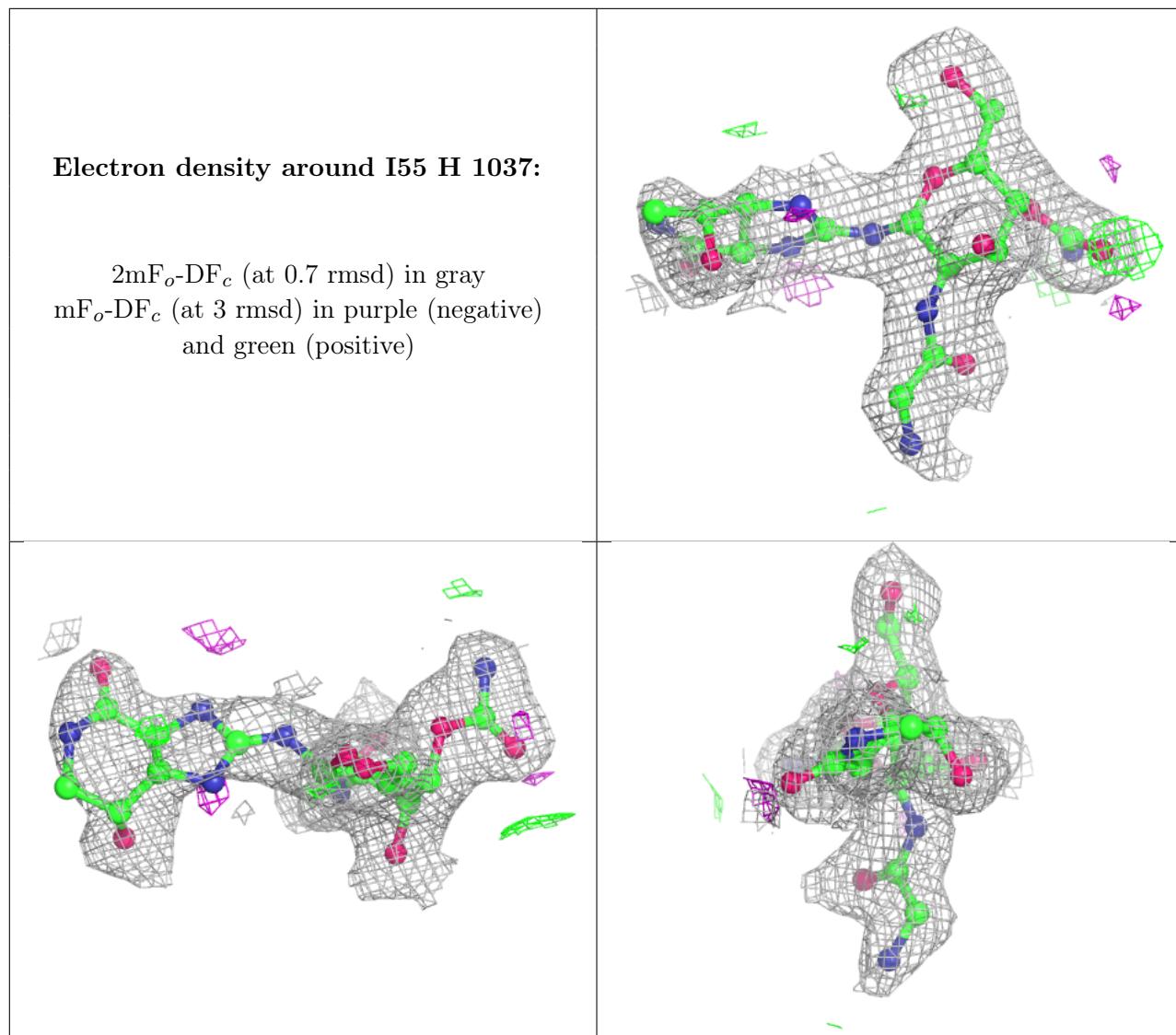
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

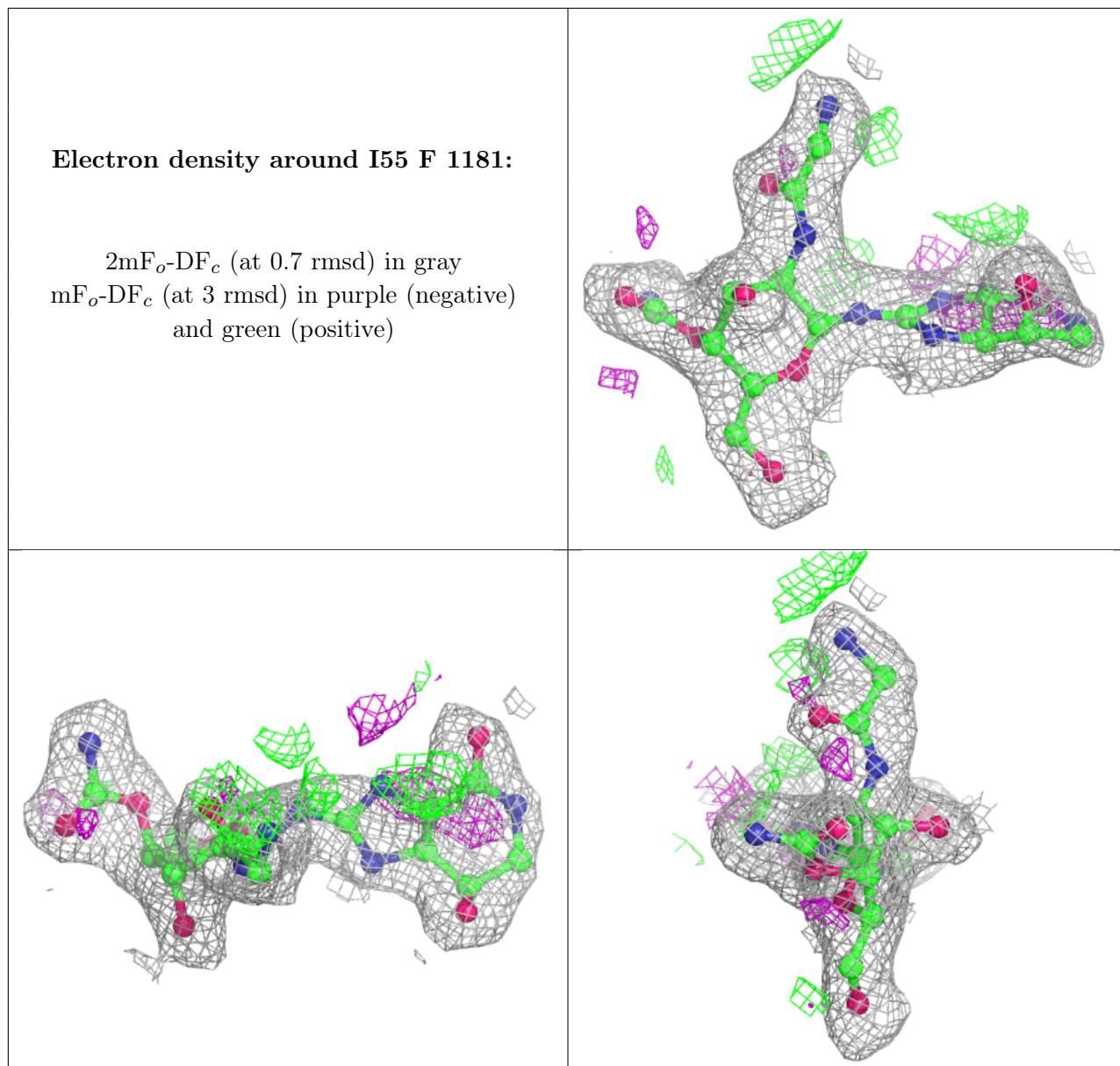
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	I55	D	1023	30/30	0.90	0.16	25,37,62,63	0
4	I55	H	1037	30/30	0.90	0.17	25,37,62,62	0
4	I55	F	1181	30/30	0.91	0.15	21,33,48,49	0
4	I55	G	1156	30/30	0.91	0.16	20,31,46,48	0
4	I55	C	1153	30/30	0.91	0.14	20,30,45,46	0
4	I55	B	1164	30/30	0.92	0.13	20,31,50,50	0
3	GLY	A	703	5/5	0.92	0.11	24,24,28,28	0
3	GLY	H	703	5/5	0.92	0.13	35,37,41,42	0
4	I55	A	1147	30/30	0.93	0.15	19,29,45,47	0
2	FAD	H	701	53/53	0.93	0.13	31,40,66,67	0
4	I55	E	1140	30/30	0.93	0.13	20,29,45,48	0
3	GLY	D	703	5/5	0.94	0.12	36,39,42,42	0
2	FAD	D	701	53/53	0.94	0.12	32,39,64,65	0
3	GLY	C	703	5/5	0.95	0.13	25,26,27,29	0
2	FAD	C	701	53/53	0.96	0.11	19,21,32,33	0
3	GLY	E	703	5/5	0.96	0.12	23,23,28,28	0
3	GLY	F	703	5/5	0.96	0.15	22,24,24,24	0
2	FAD	A	701	53/53	0.96	0.11	17,20,24,24	0
3	GLY	B	703	5/5	0.96	0.12	20,22,24,25	0
2	FAD	G	701	53/53	0.96	0.11	17,21,32,33	0
2	FAD	B	701	53/53	0.97	0.11	11,15,17,18	0
2	FAD	E	701	53/53	0.97	0.10	17,20,23,25	0
3	GLY	G	703	5/5	0.97	0.11	25,25,28,29	0
2	FAD	F	701	53/53	0.97	0.10	12,15,18,19	0

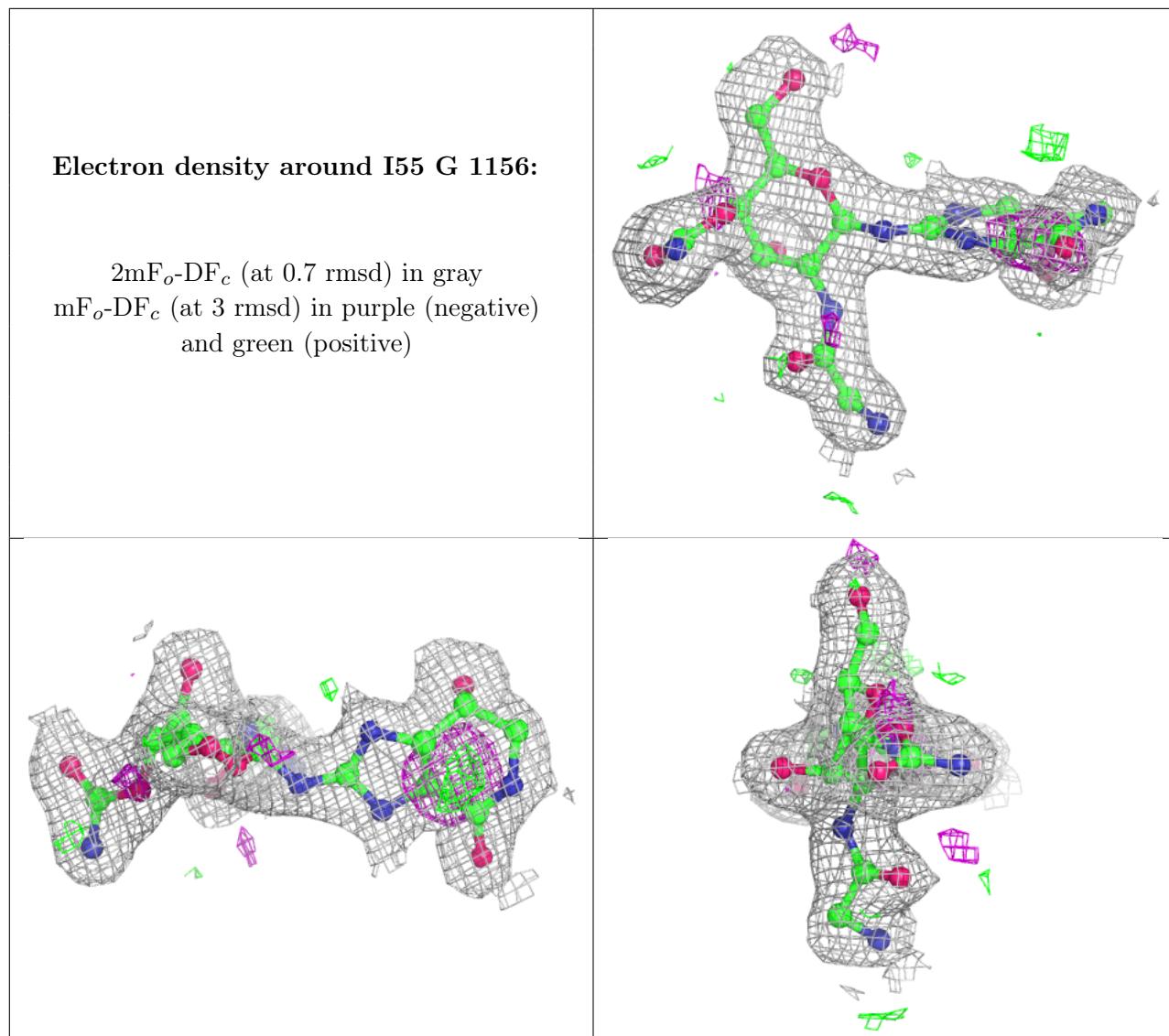
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different

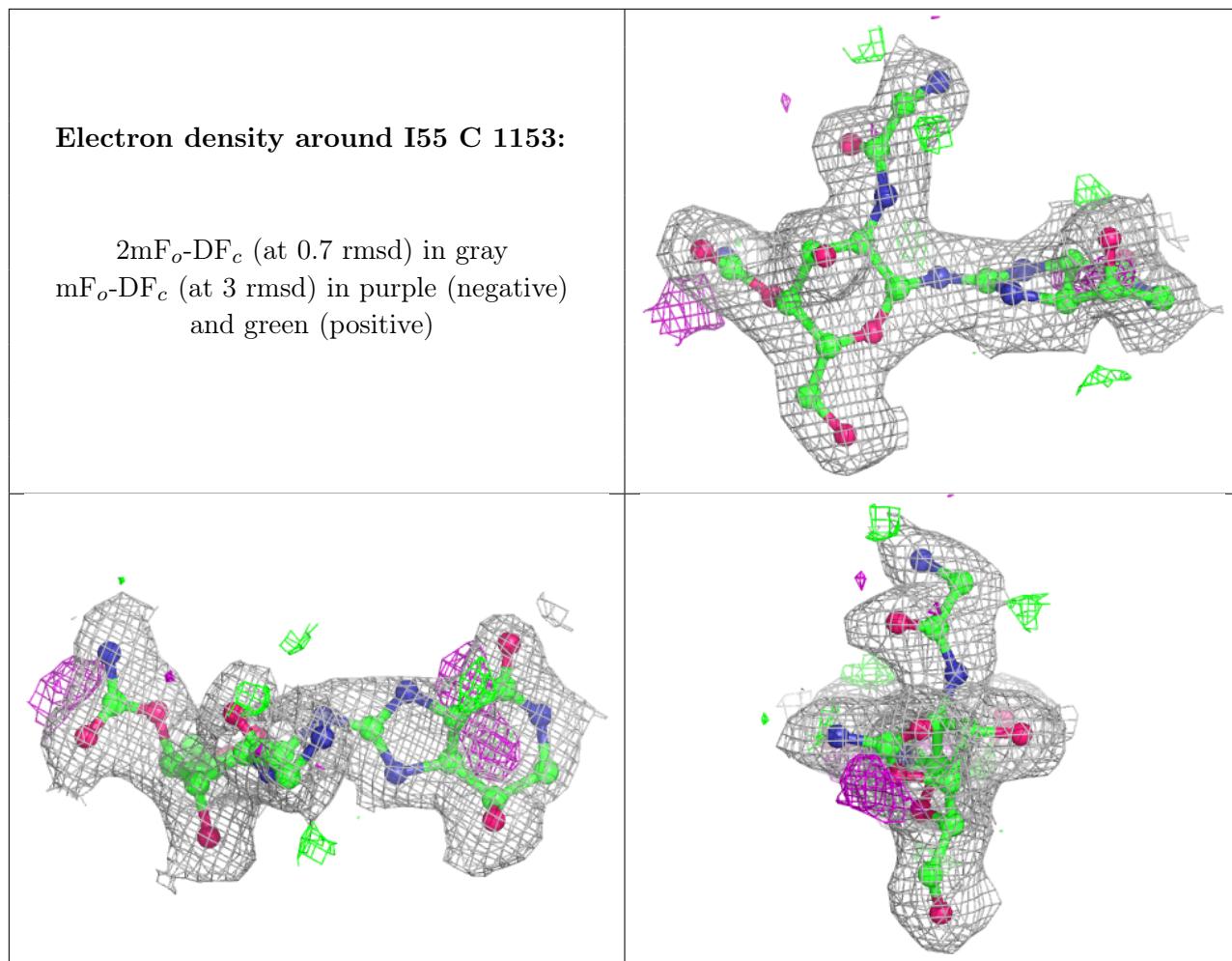
orientation to approximate a three-dimensional view.

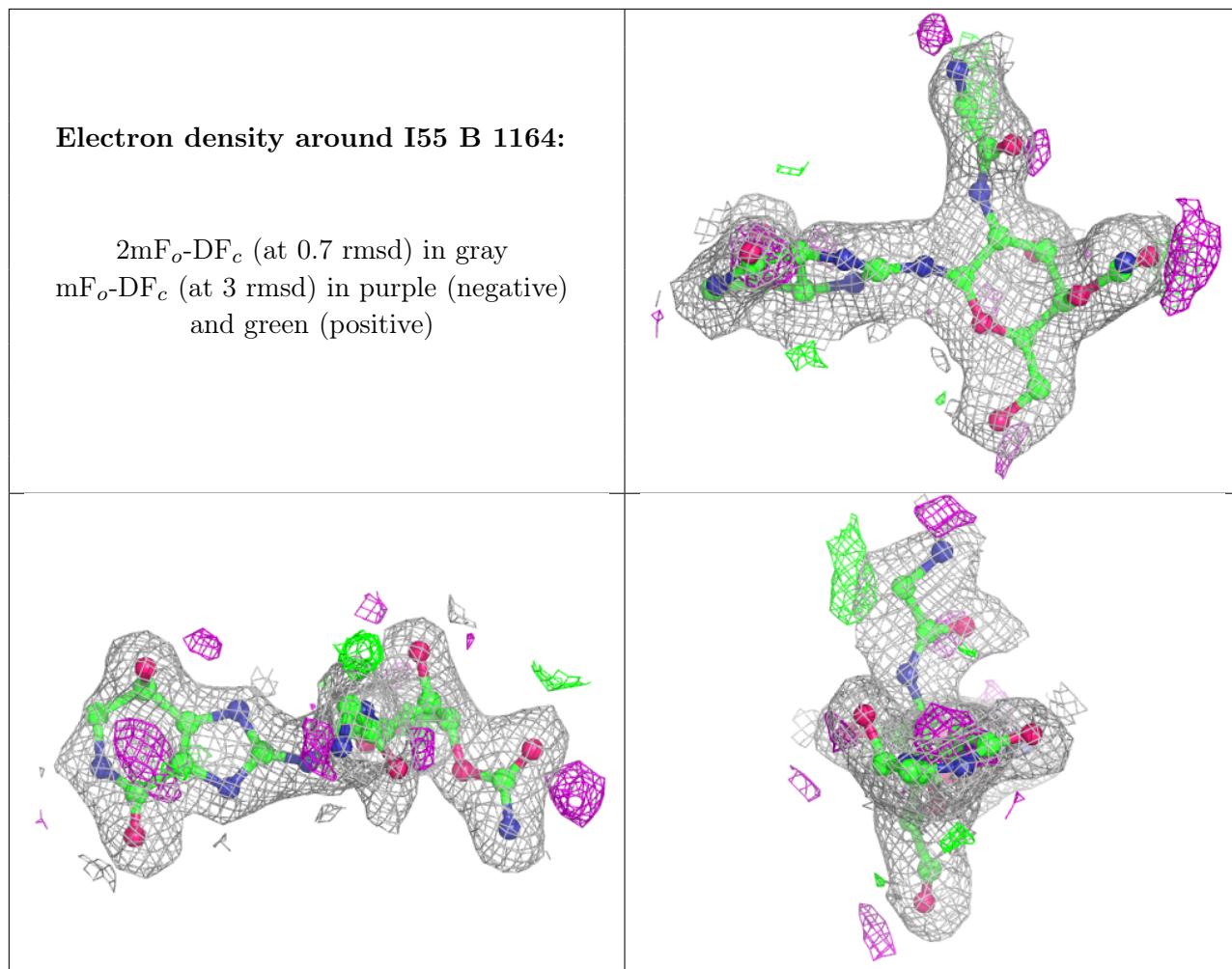


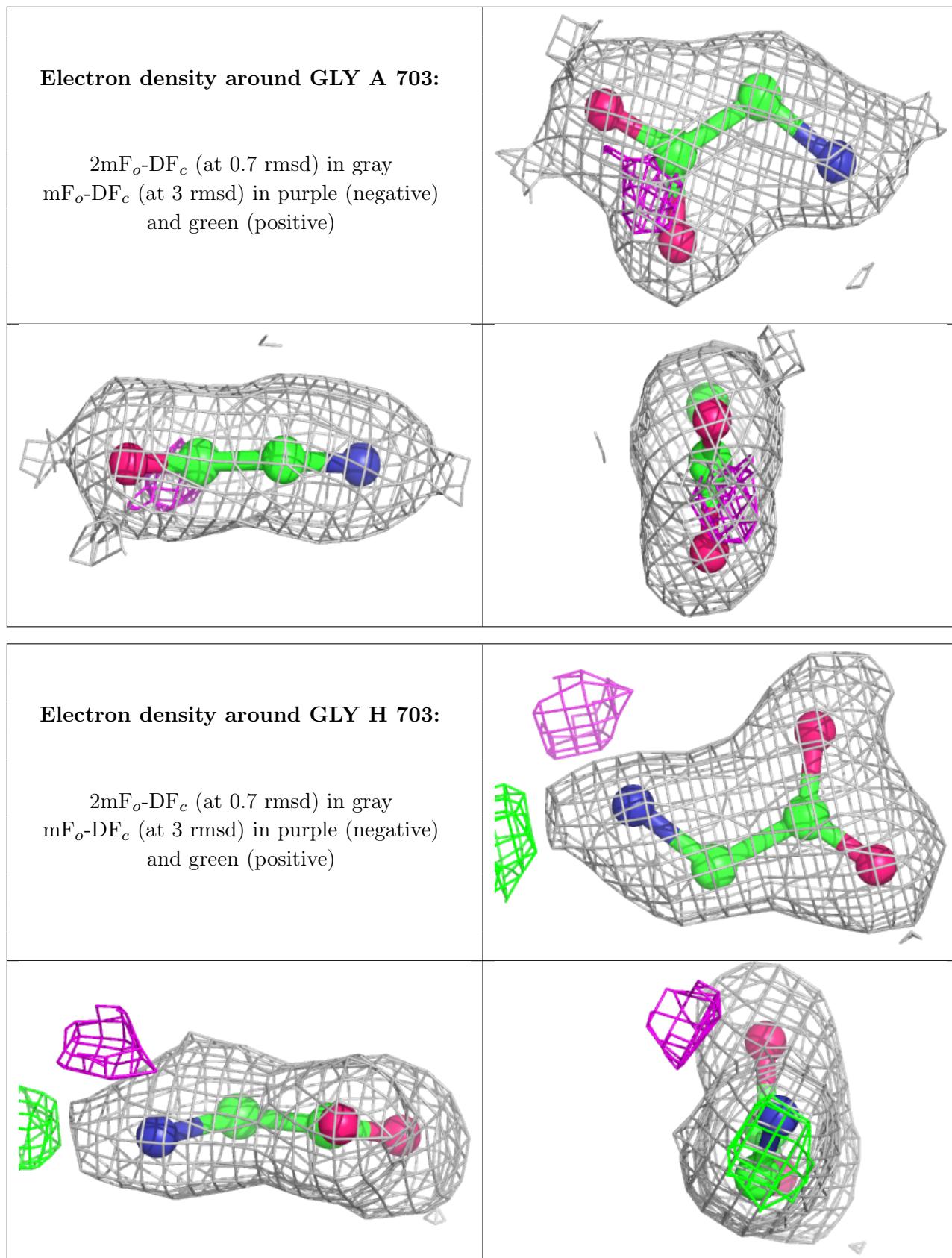


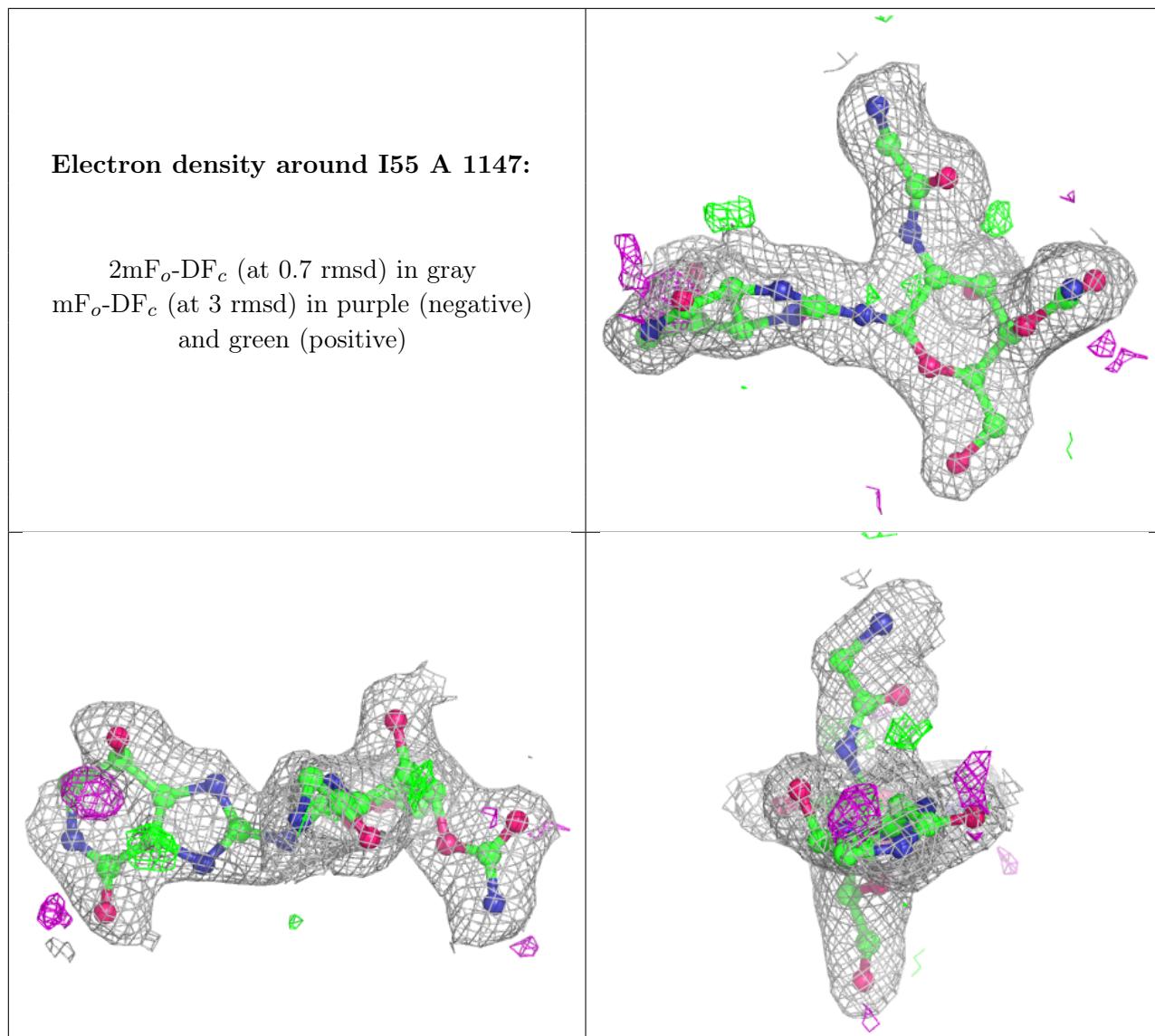


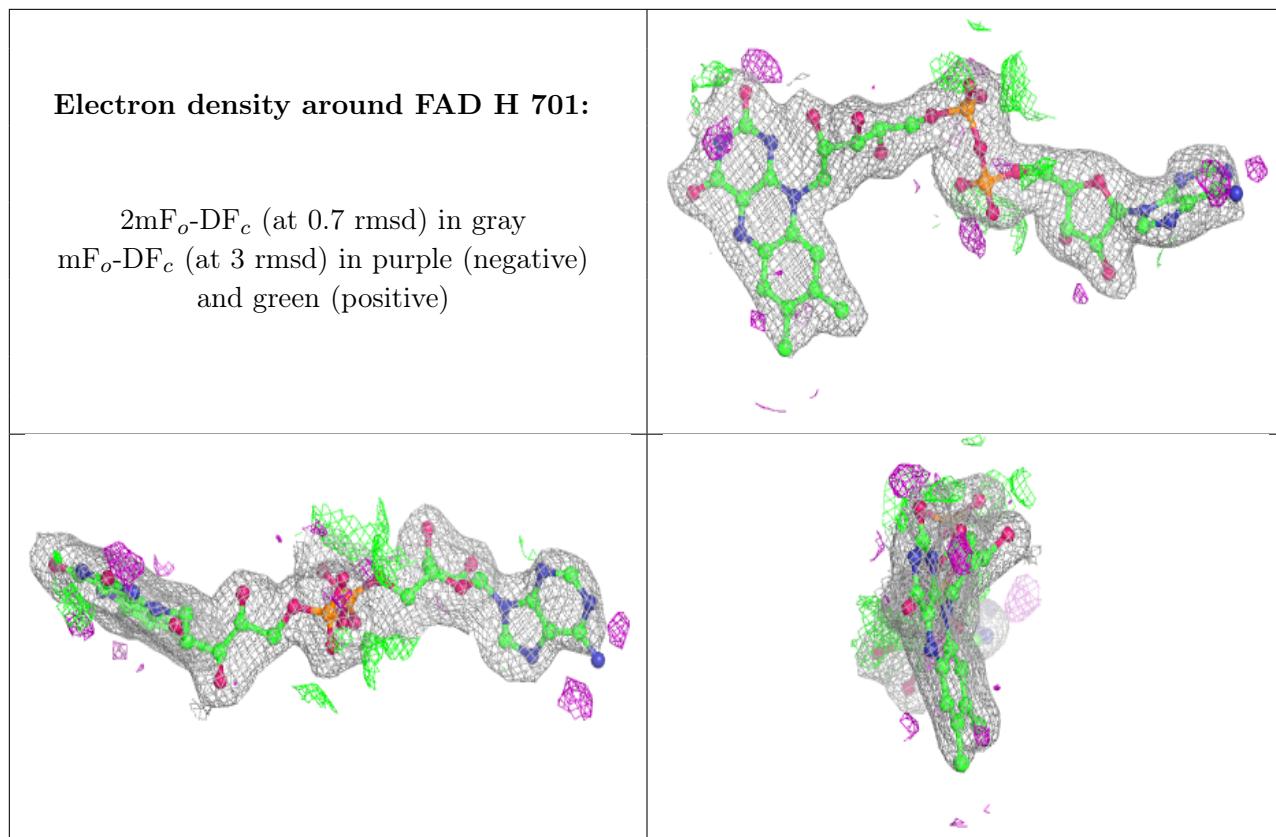


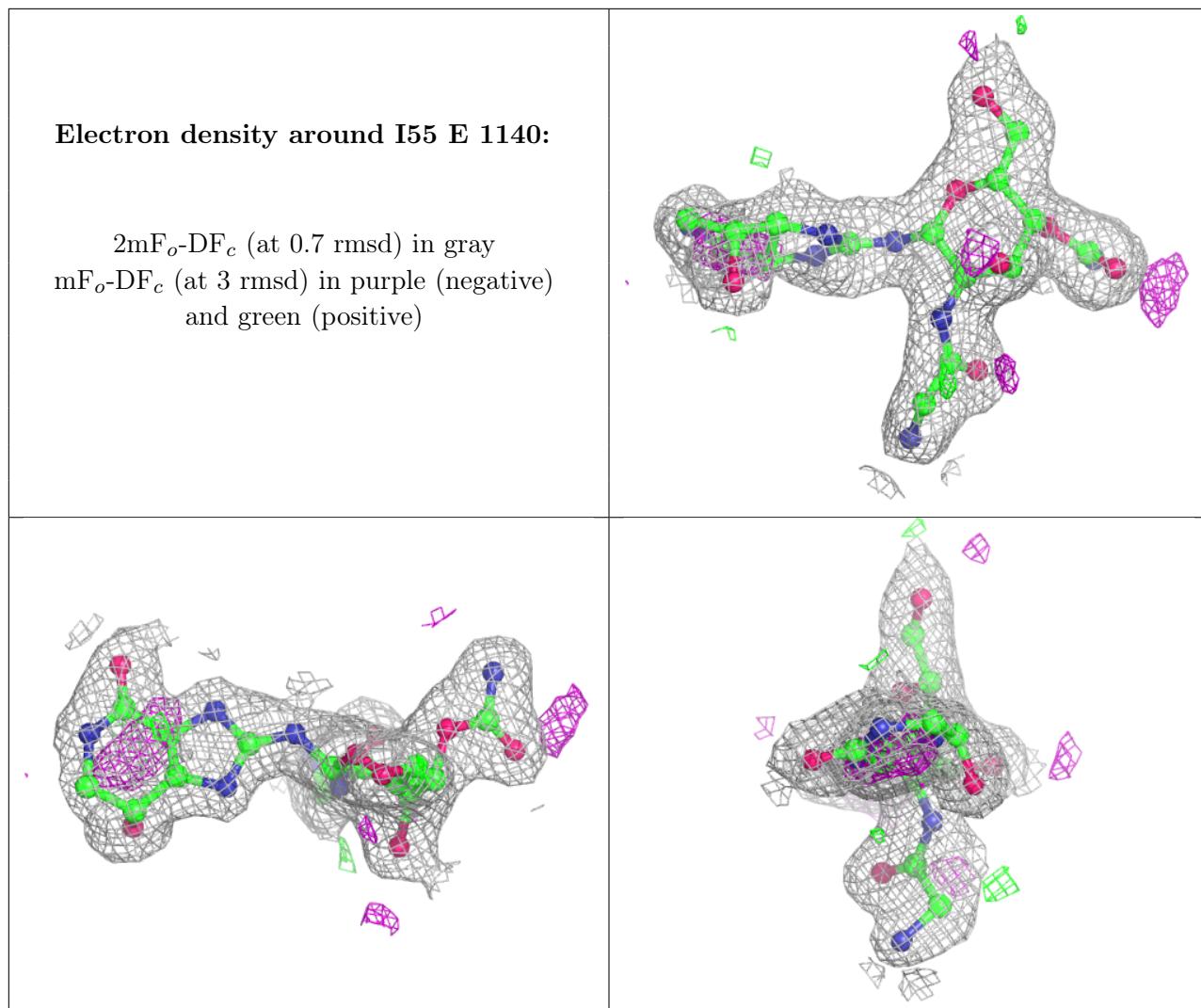


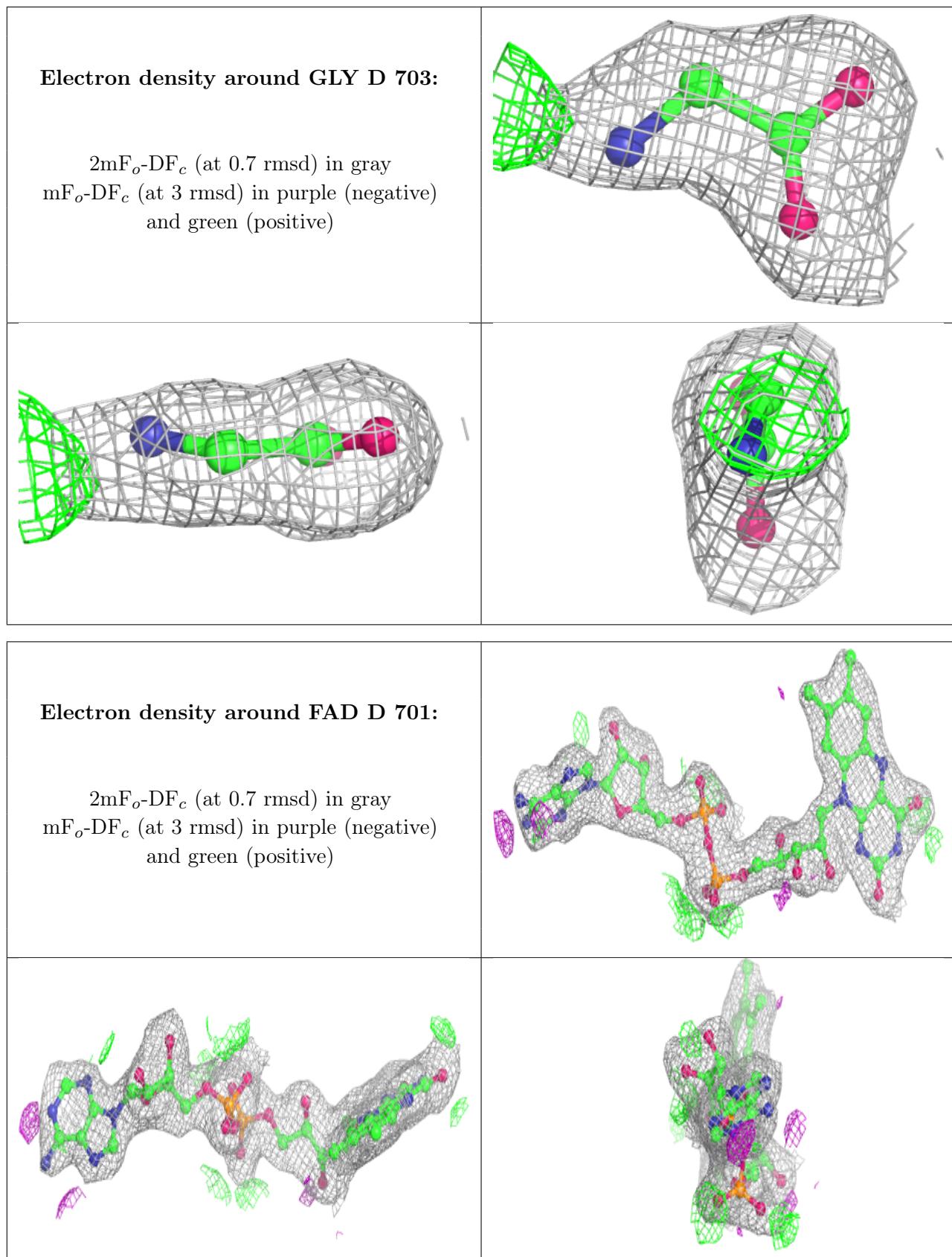


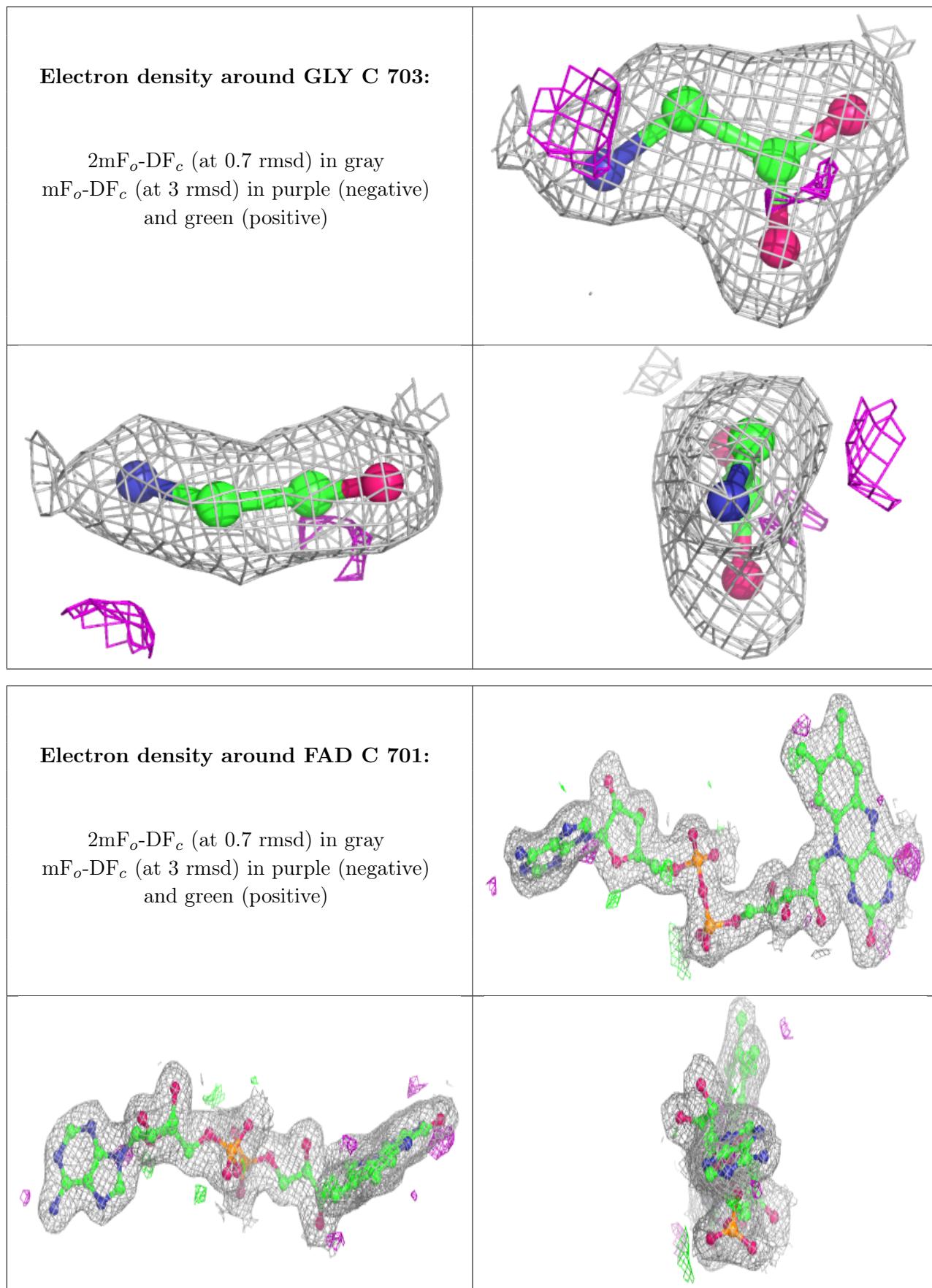


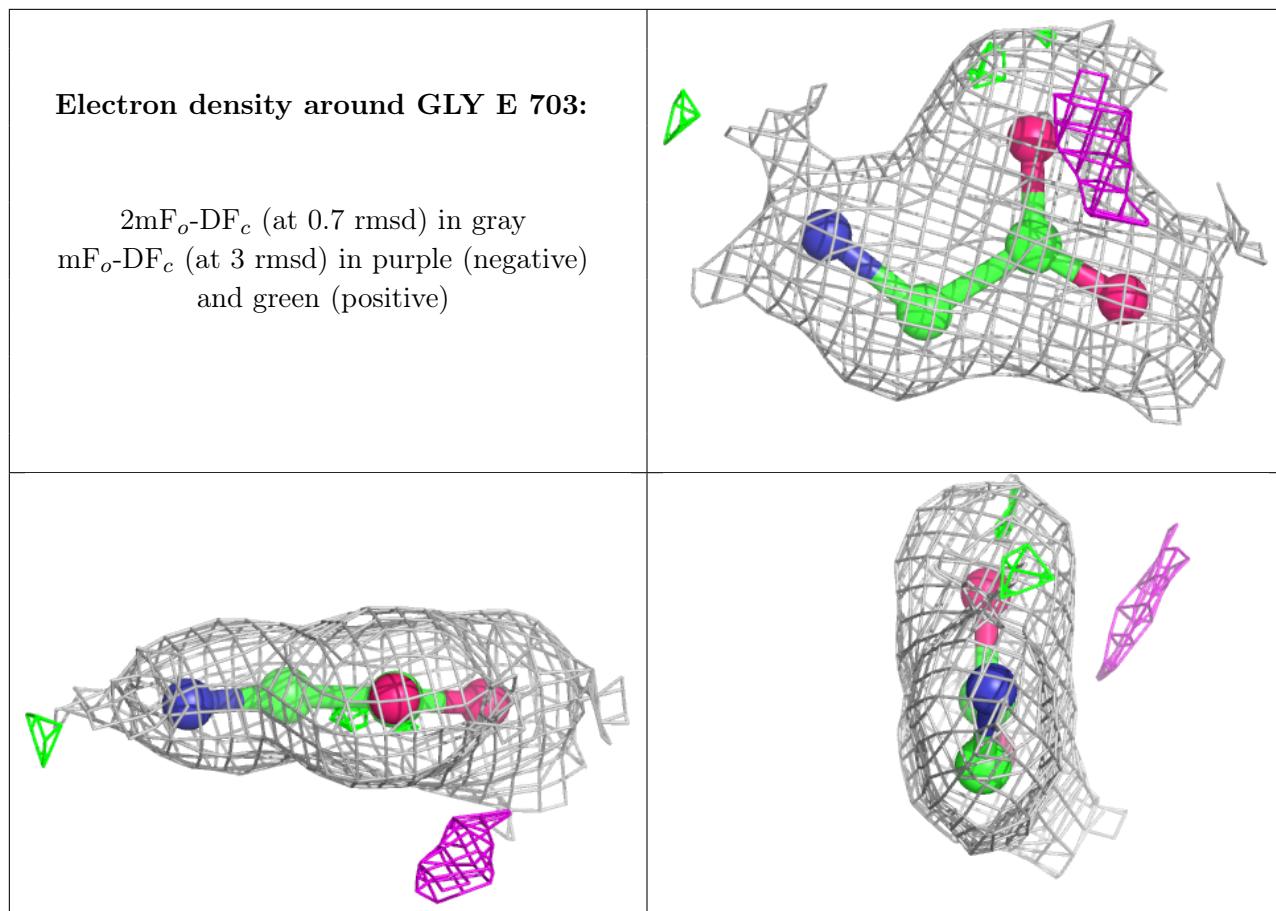


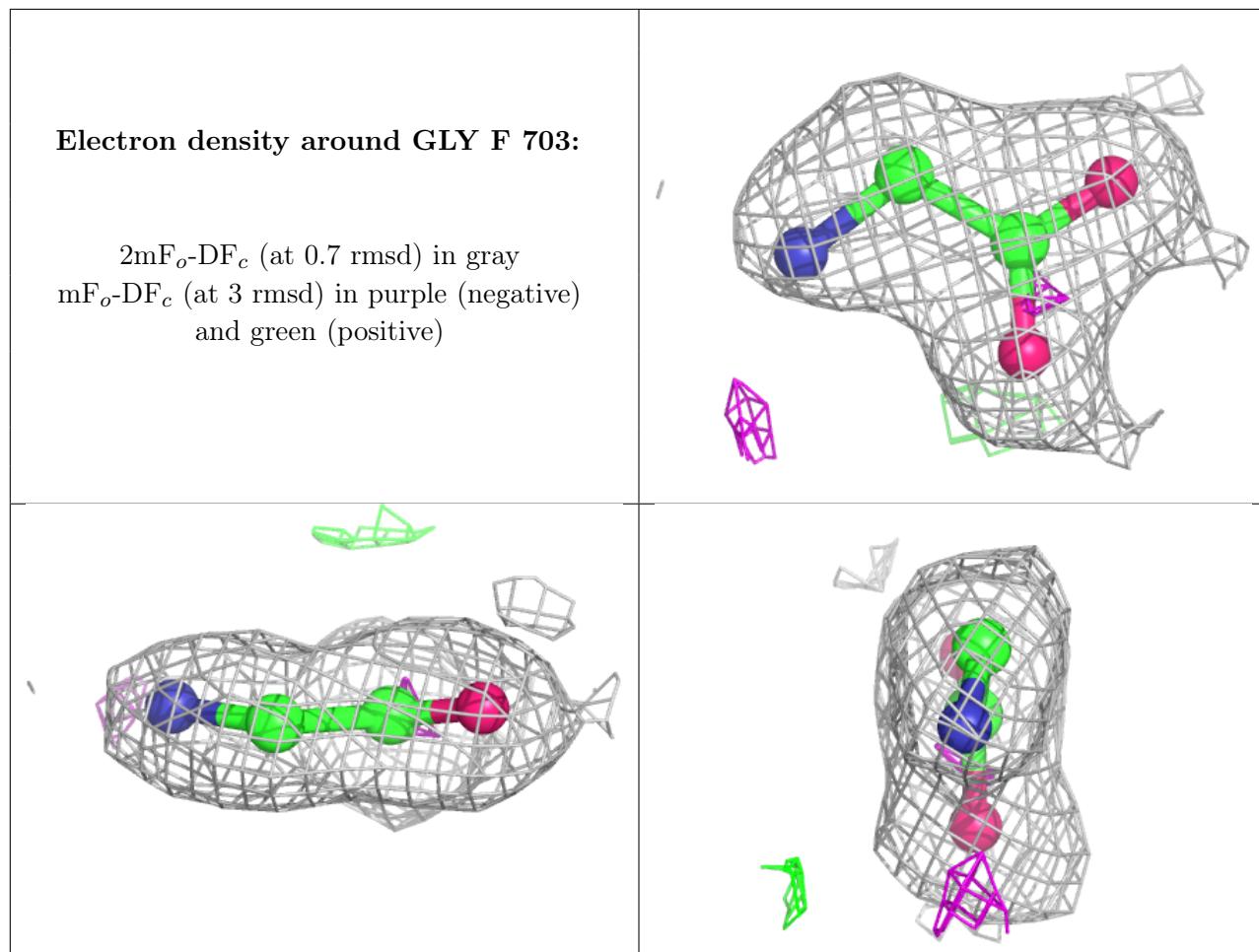


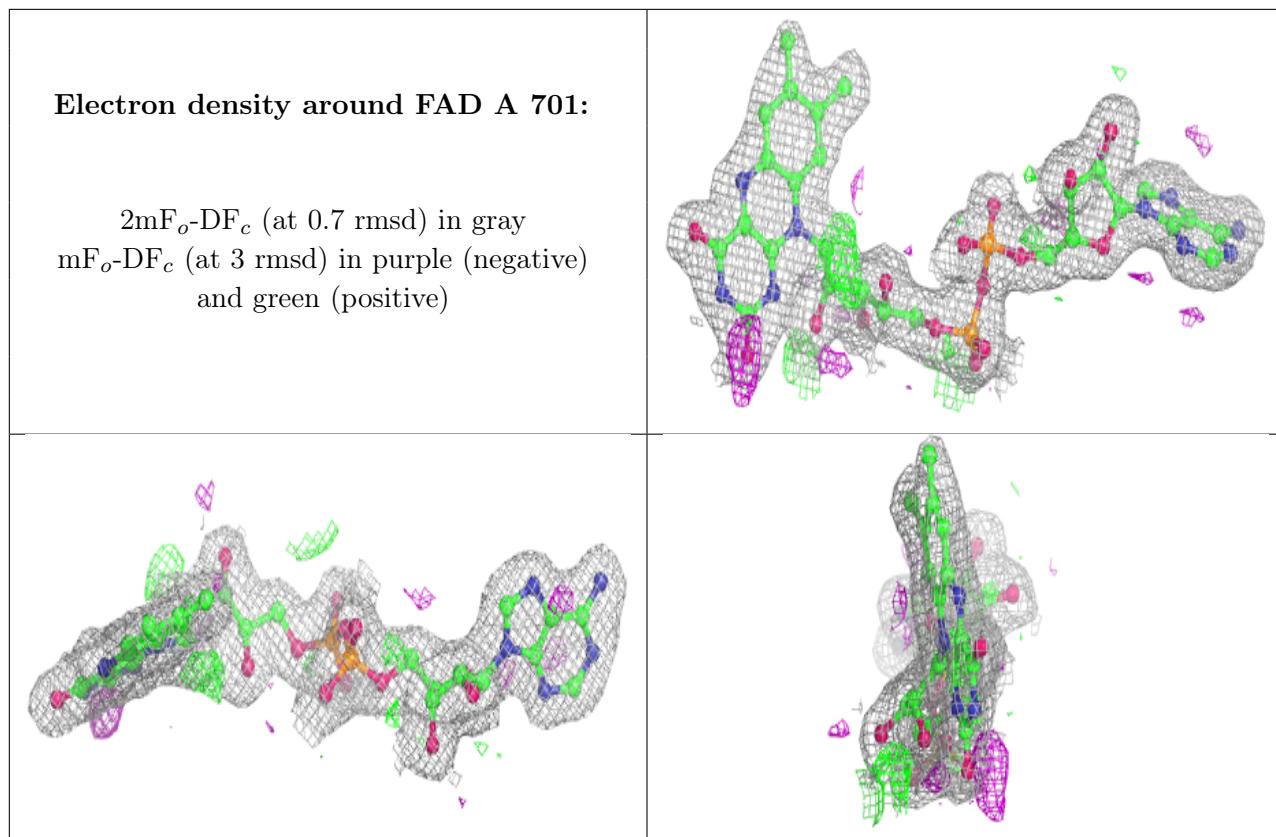


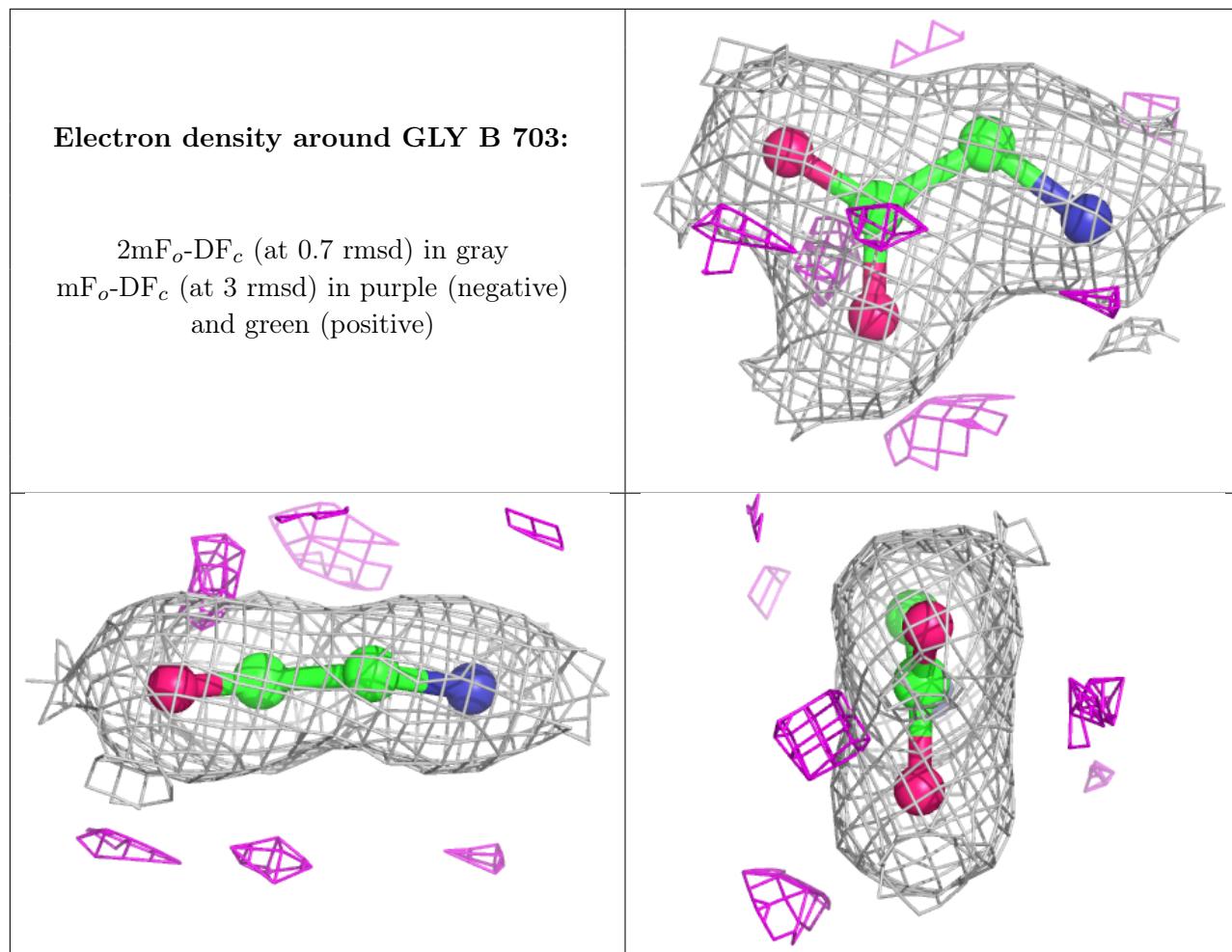


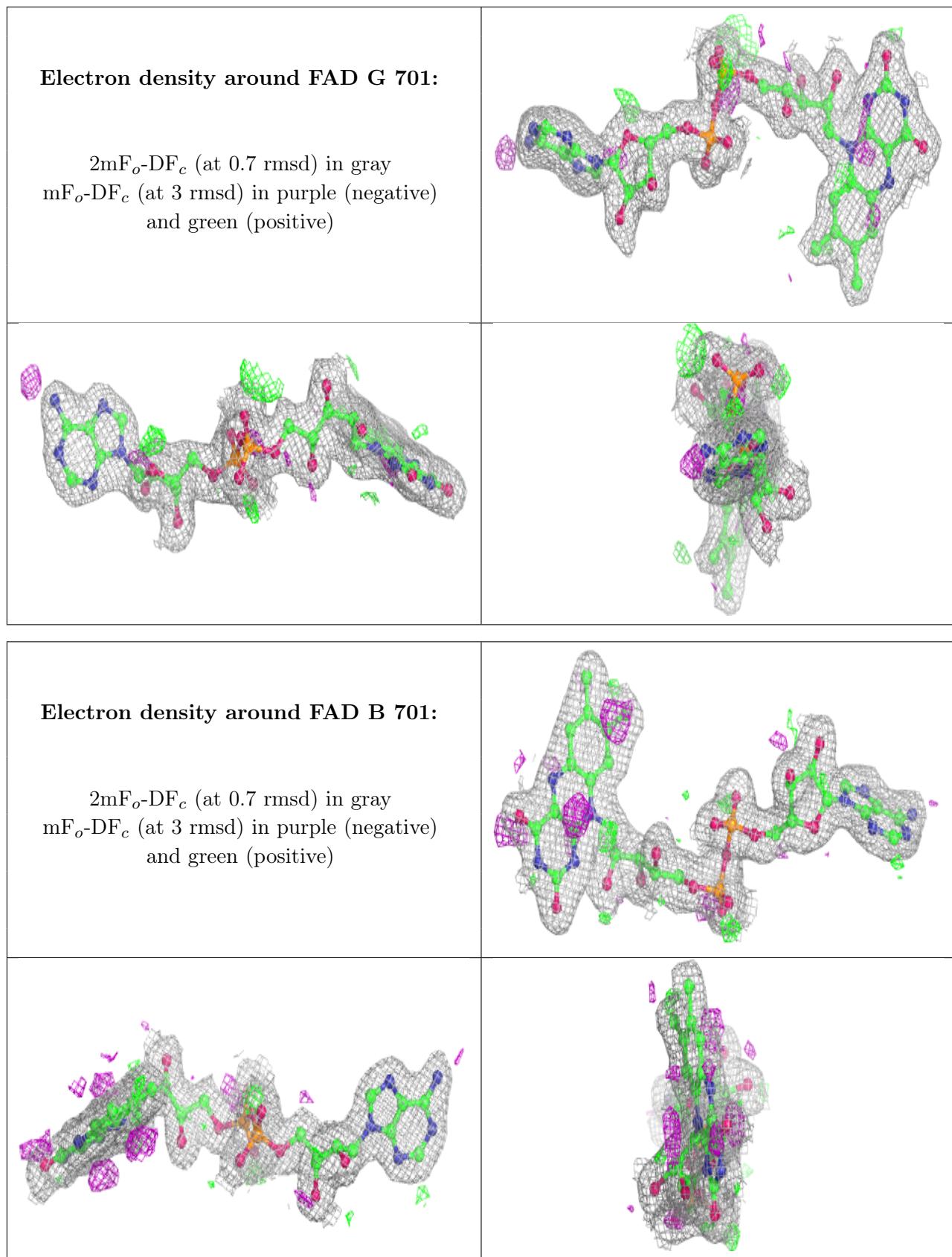


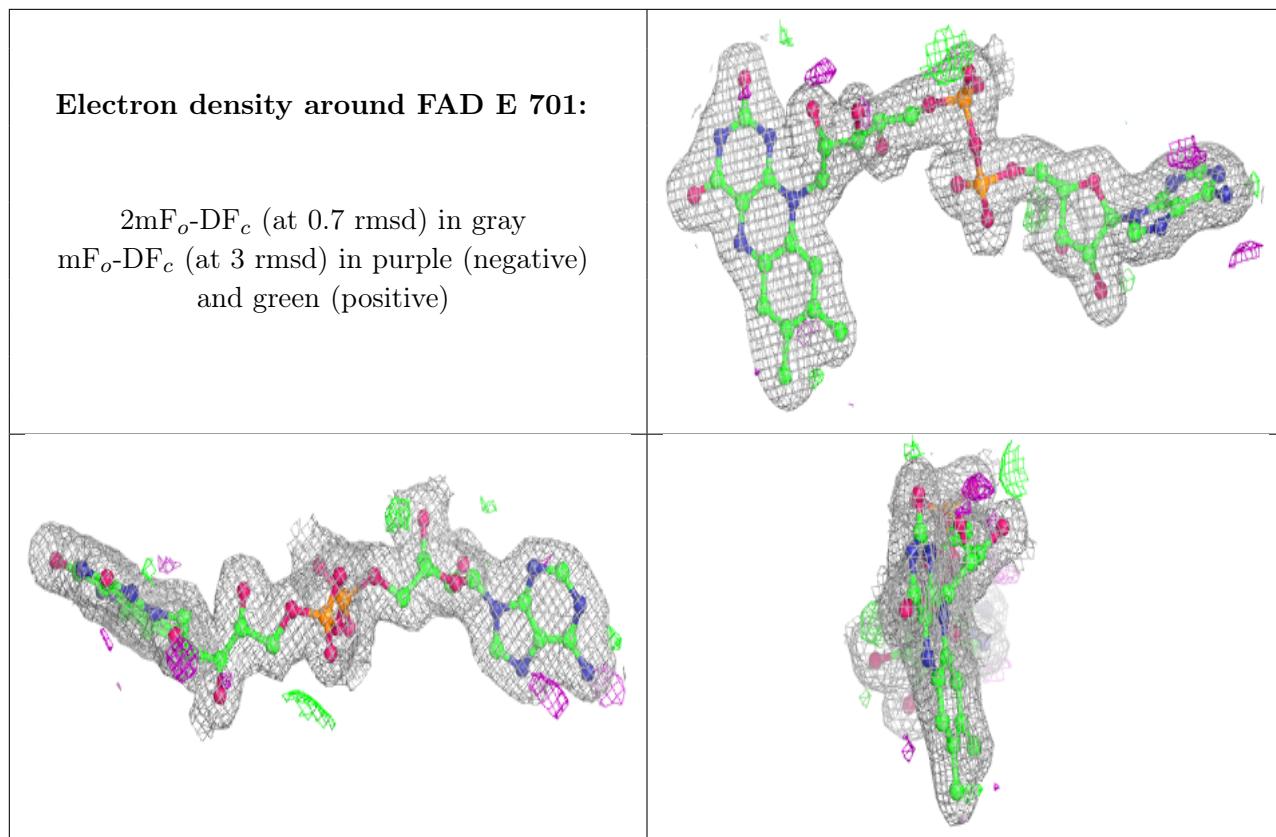


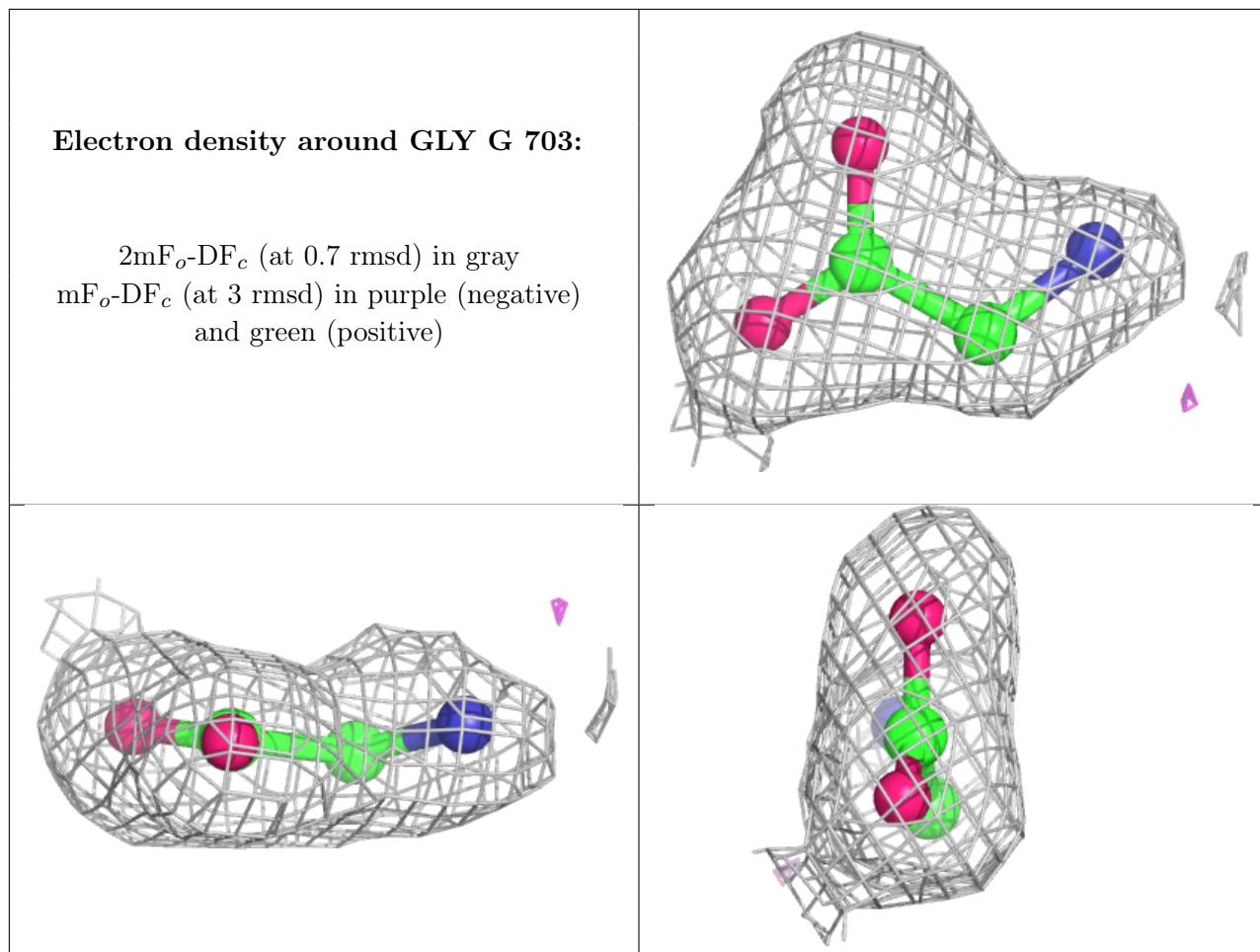


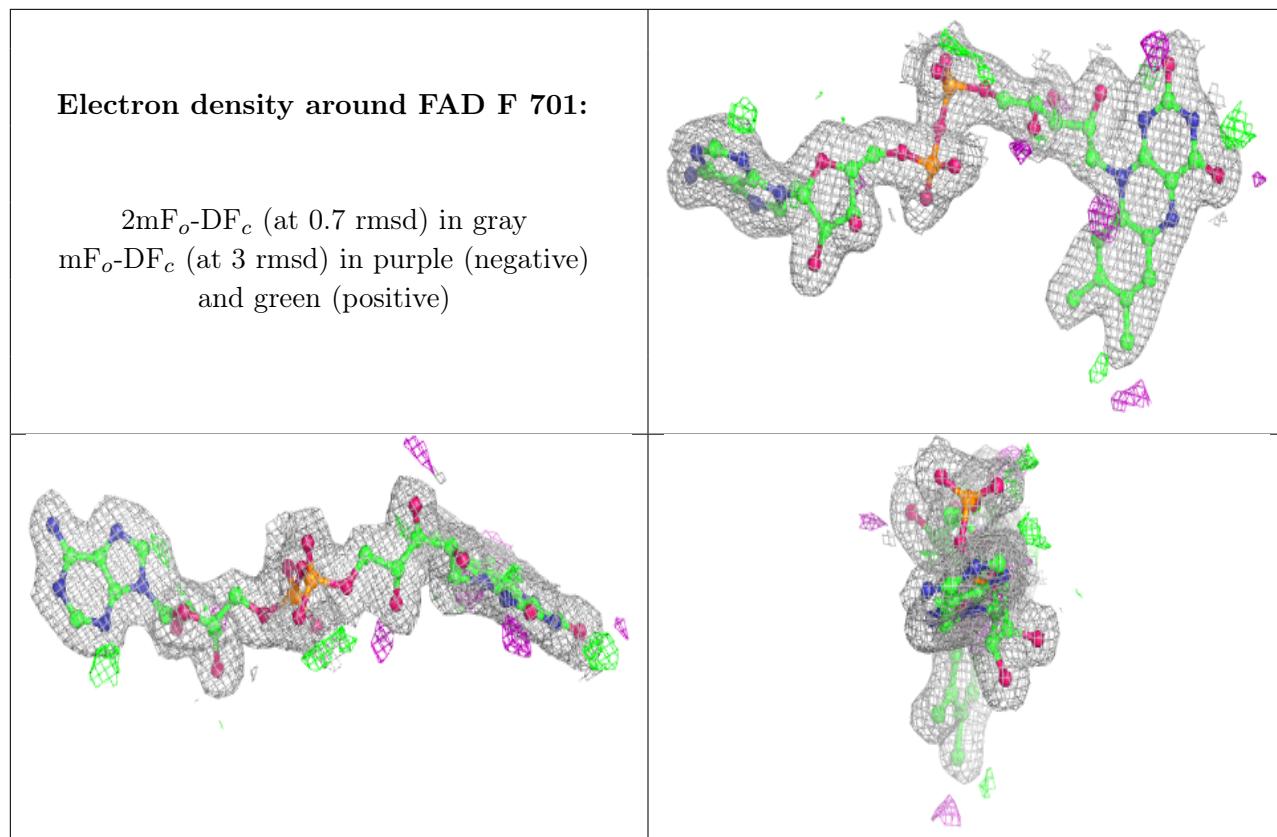












## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.