



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:04 AM UTC

PDB ID : 8CT0 / pdb_00008ct0
Title : Crystal structure of FAD reductase CtcQ from Kitasatospora aureofaciens in complex with FAD and NAD
Authors : Hou, C.; Tsodikov, O.V.
Deposited on : 2022-05-13
Resolution : 2.45 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

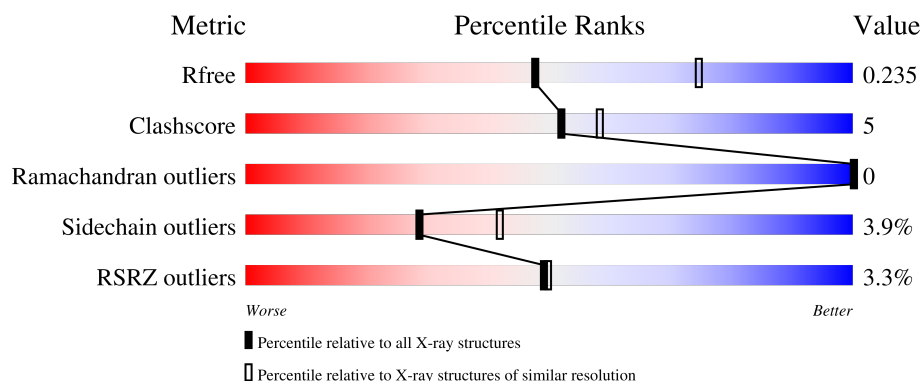
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	199	 6% 76% 8% 10%
1	B	199	 3% 77% 8% 12%
1	C	199	 4% 74% 13% 9%
1	D	199	 2% 77% 8% 13%
1	E	199	 3% 73% 9% 15%

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Mol	Chain	Length	Quality of chain
1	F	199	2% 77% 11% 12%
1	G	199	2% 83% • 14%
1	H	199	3% 74% 14% • 11%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11093 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 Flavin reductase (NADH).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	0	0
			1236	782	217	230	7			
1	B	171	Total	C	N	O	S	0	0	0
			1243	786	218	232	7			
1	C	172	Total	C	N	O	S	0	0	0
			1254	794	222	231	7			
1	D	172	Total	C	N	O	S	0	0	0
			1255	795	222	231	7			
1	E	168	Total	C	N	O	S	0	0	0
			1218	771	212	228	7			
1	F	175	Total	C	N	O	S	0	0	0
			1268	805	222	234	7			
1	G	172	Total	C	N	O	S	0	0	0
			1256	794	222	233	7			
1	H	178	Total	C	N	O	S	0	0	0
			1281	813	225	235	8			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	192	LEU	-	expression tag	UNP S4S3E3
A	193	GLU	-	expression tag	UNP S4S3E3
A	194	HIS	-	expression tag	UNP S4S3E3
A	195	HIS	-	expression tag	UNP S4S3E3
A	196	HIS	-	expression tag	UNP S4S3E3
A	197	HIS	-	expression tag	UNP S4S3E3
A	198	HIS	-	expression tag	UNP S4S3E3
A	199	HIS	-	expression tag	UNP S4S3E3
B	192	LEU	-	expression tag	UNP S4S3E3
B	193	GLU	-	expression tag	UNP S4S3E3
B	194	HIS	-	expression tag	UNP S4S3E3
B	195	HIS	-	expression tag	UNP S4S3E3
B	196	HIS	-	expression tag	UNP S4S3E3

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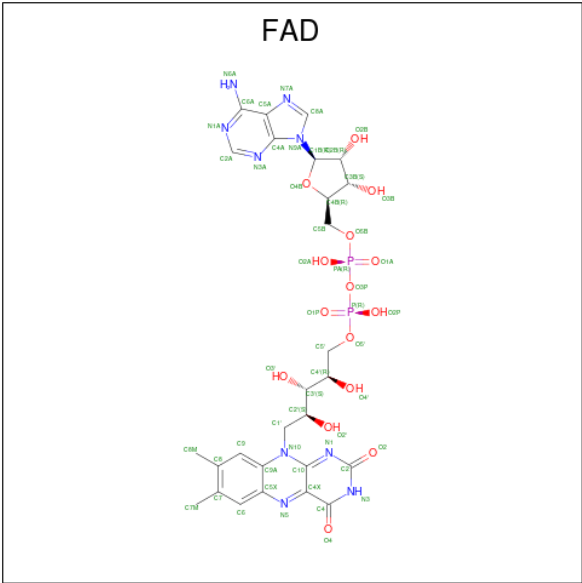
Chain	Residue	Modelled	Actual	Comment	Reference
B	197	HIS	-	expression tag	UNP S4S3E3
B	198	HIS	-	expression tag	UNP S4S3E3
B	199	HIS	-	expression tag	UNP S4S3E3
C	192	LEU	-	expression tag	UNP S4S3E3
C	193	GLU	-	expression tag	UNP S4S3E3
C	194	HIS	-	expression tag	UNP S4S3E3
C	195	HIS	-	expression tag	UNP S4S3E3
C	196	HIS	-	expression tag	UNP S4S3E3
C	197	HIS	-	expression tag	UNP S4S3E3
C	198	HIS	-	expression tag	UNP S4S3E3
C	199	HIS	-	expression tag	UNP S4S3E3
D	192	LEU	-	expression tag	UNP S4S3E3
D	193	GLU	-	expression tag	UNP S4S3E3
D	194	HIS	-	expression tag	UNP S4S3E3
D	195	HIS	-	expression tag	UNP S4S3E3
D	196	HIS	-	expression tag	UNP S4S3E3
D	197	HIS	-	expression tag	UNP S4S3E3
D	198	HIS	-	expression tag	UNP S4S3E3
D	199	HIS	-	expression tag	UNP S4S3E3
E	192	LEU	-	expression tag	UNP S4S3E3
E	193	GLU	-	expression tag	UNP S4S3E3
E	194	HIS	-	expression tag	UNP S4S3E3
E	195	HIS	-	expression tag	UNP S4S3E3
E	196	HIS	-	expression tag	UNP S4S3E3
E	197	HIS	-	expression tag	UNP S4S3E3
E	198	HIS	-	expression tag	UNP S4S3E3
E	199	HIS	-	expression tag	UNP S4S3E3
F	192	LEU	-	expression tag	UNP S4S3E3
F	193	GLU	-	expression tag	UNP S4S3E3
F	194	HIS	-	expression tag	UNP S4S3E3
F	195	HIS	-	expression tag	UNP S4S3E3
F	196	HIS	-	expression tag	UNP S4S3E3
F	197	HIS	-	expression tag	UNP S4S3E3
F	198	HIS	-	expression tag	UNP S4S3E3
F	199	HIS	-	expression tag	UNP S4S3E3
G	192	LEU	-	expression tag	UNP S4S3E3
G	193	GLU	-	expression tag	UNP S4S3E3
G	194	HIS	-	expression tag	UNP S4S3E3
G	195	HIS	-	expression tag	UNP S4S3E3
G	196	HIS	-	expression tag	UNP S4S3E3
G	197	HIS	-	expression tag	UNP S4S3E3
G	198	HIS	-	expression tag	UNP S4S3E3

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Chain	Residue	Modelled	Actual	Comment	Reference
G	199	HIS	-	expression tag	UNP S4S3E3
H	192	LEU	-	expression tag	UNP S4S3E3
H	193	GLU	-	expression tag	UNP S4S3E3
H	194	HIS	-	expression tag	UNP S4S3E3
H	195	HIS	-	expression tag	UNP S4S3E3
H	196	HIS	-	expression tag	UNP S4S3E3
H	197	HIS	-	expression tag	UNP S4S3E3
H	198	HIS	-	expression tag	UNP S4S3E3
H	199	HIS	-	expression tag	UNP S4S3E3

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



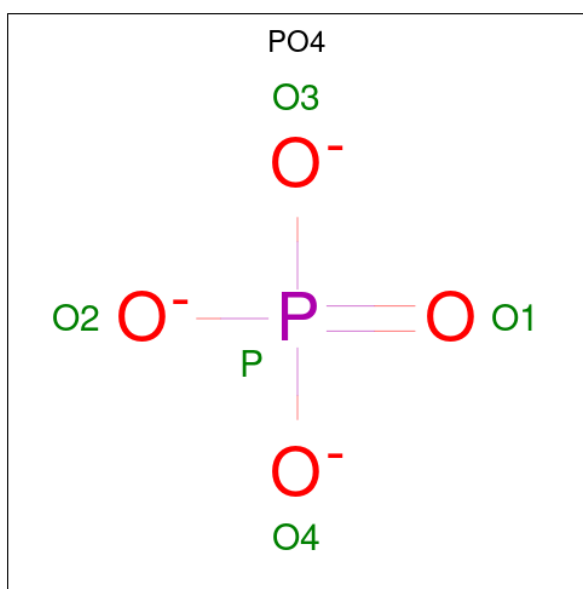
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			44	22	5	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	F	1	Total	C	N	O	P	0	0
			36	18	4	12	2		
2	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	H	1	Total	C	N	O	P	0	0
			36	18	4	12	2		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P) (labeled as "Ligand of Interest" by depositor).



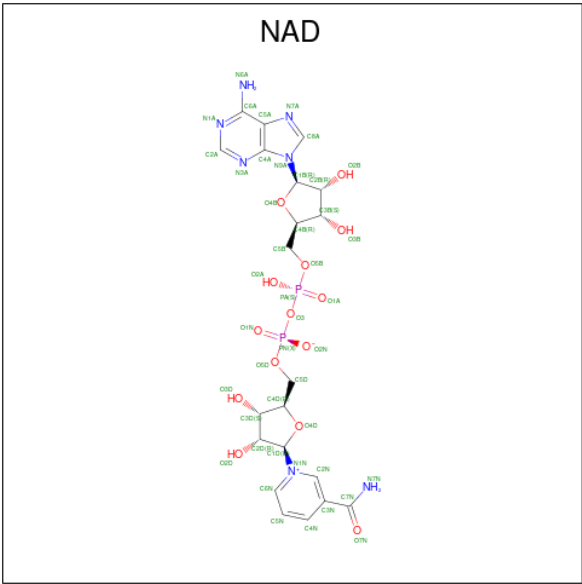
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	G	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		

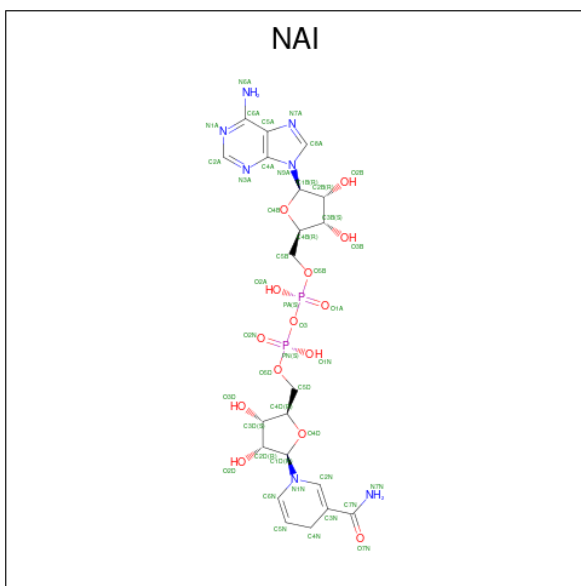
- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0
			44	21	7	14	2	0

- Molecule 5 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID:

NAI) (formula: $\text{C}_{21}\text{H}_{29}\text{N}_7\text{O}_{14}\text{P}_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	H	1	Total 44	C 21	N 7	O 14	P 2	0	0

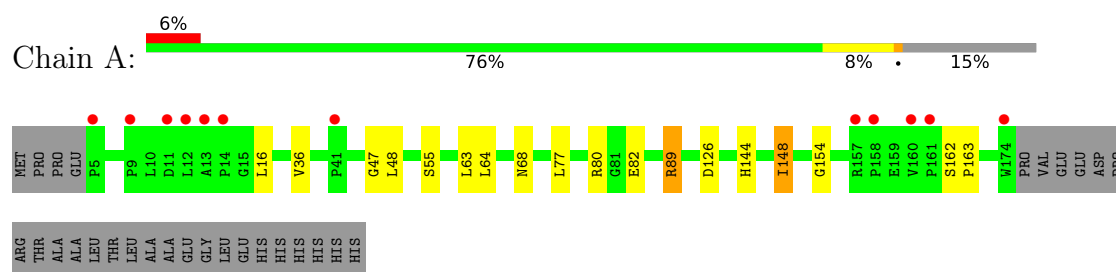
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	46	Total O 46 46	0	0
6	B	34	Total O 34 34	0	0
6	C	29	Total O 29 29	0	0
6	D	17	Total O 17 17	0	0
6	E	26	Total O 26 26	0	0
6	F	24	Total O 24 24	0	0
6	G	45	Total O 45 45	0	0
6	H	14	Total O 14 14	0	0

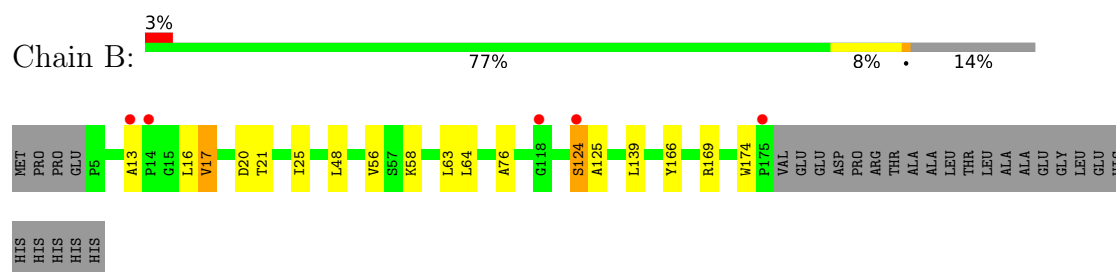
3 Residue-property plots [i](#)

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.

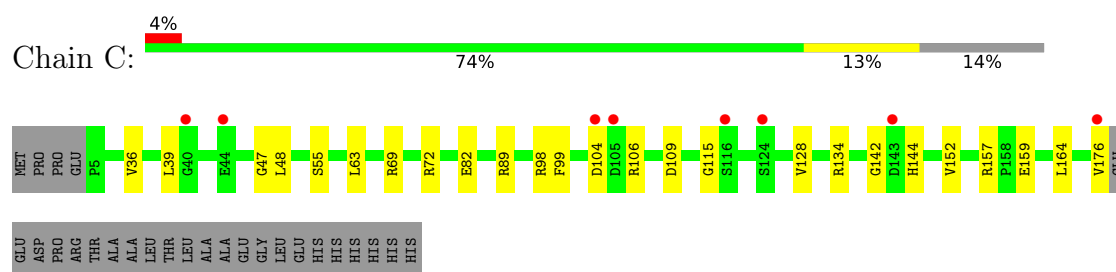
- Molecule 1: Flavin reductase (NADH)



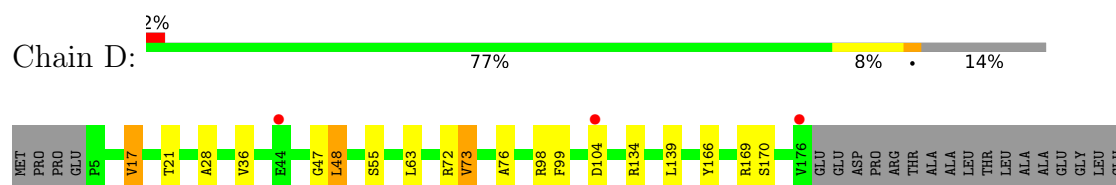
- Molecule 1: Flavin reductase (NADH)



- Molecule 1: Flavin reductase (NADH)



- Molecule 1: Flavin reductase (NADH)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.74Å 123.60Å 102.70Å 90.00° 99.10° 90.00°	Depositor
Resolution (Å)	34.97 – 2.45 34.97 – 2.45	Depositor EDS
% Data completeness (in resolution range)	95.4 (34.97-2.45) 95.4 (34.97-2.45)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.194 , 0.256 (Not available) , 0.235	Depositor DCC
R_{free} test set	2512 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	20.8	Xtriage
Anisotropy	0.771	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11093	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: FAD, PO4, NAI, NAD

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	1.00	0/1265	1.37	3/1731 (0.2%)
1	B	1.01	0/1272	1.35	2/1740 (0.1%)
1	C	1.00	0/1284	1.34	2/1757 (0.1%)
1	D	1.03	0/1285	1.35	2/1759 (0.1%)
1	E	1.01	0/1245	1.35	2/1702 (0.1%)
1	F	1.00	0/1300	1.37	0/1782
1	G	1.01	0/1286	1.31	0/1761
1	H	1.01	0/1313	1.33	0/1798
All	All	1.01	0/10250	1.34	11/14030 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	ARG	CA-C-N	5.45	126.13	120.03
1	A	89	ARG	C-N-CA	5.45	126.13	120.03
1	D	76	ALA	CA-C-N	5.36	127.41	120.44
1	D	76	ALA	C-N-CA	5.36	127.41	120.44
1	A	154	GLY	CA-C-O	-5.22	118.10	122.33
1	B	76	ALA	CA-C-N	5.15	127.49	120.54
1	B	76	ALA	C-N-CA	5.15	127.49	120.54
1	E	18	ASP	CA-C-N	5.12	125.78	119.99
1	E	18	ASP	C-N-CA	5.12	125.78	119.99
1	C	115	GLY	CA-C-N	5.01	127.24	120.38
1	C	115	GLY	C-N-CA	5.01	127.24	120.38

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	1236	0	1237	13	0
1	B	1243	0	1240	18	0
1	C	1254	0	1262	10	0
1	D	1255	0	1263	12	0
1	E	1218	0	1212	13	0
1	F	1268	0	1269	13	0
1	G	1256	0	1257	3	0
1	H	1281	0	1281	26	0
2	A	106	0	62	1	0
2	B	106	0	62	6	0
2	C	44	0	27	0	0
2	D	106	0	62	3	0
2	E	106	0	62	6	0
2	F	89	0	50	1	0
2	G	106	0	62	1	0
2	H	36	0	19	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	10	0	0	0	0
3	D	10	0	0	0	0
3	E	5	0	0	0	0
3	F	10	0	0	0	0
3	G	5	0	0	0	0
3	H	10	0	0	0	0
4	C	44	0	26	1	0
5	H	44	0	27	5	0
6	A	46	0	0	1	0
6	B	34	0	0	1	0
6	C	29	0	0	0	0
6	D	17	0	0	0	0
6	E	26	0	0	0	0
6	F	24	0	0	2	0
6	G	45	0	0	1	0
6	H	14	0	0	1	0
All	All	11093	0	10480	109	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 5.

All (109) 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)
2:B:201:FAD:O2'	2:B:201:FAD:H2A	1.50	1.10
1:D:55:SER:HB3	2:E:201:FAD:H8A	1.45	0.96
2:B:201:FAD:O2'	2:B:201:FAD:C2A	2.29	0.81
2:E:201:FAD:H2A	2:E:201:FAD:O2'	1.81	0.80
1:B:13:ALA:C	1:B:13:ALA:N	2.44	0.76
1:A:55:SER:OG	2:F:201:FAD:H8A	1.87	0.74
5:H:202:NAI:H51A	5:H:202:NAI:O2N	1.90	0.71
1:D:17:VAL:HG13	1:D:21:THR:HB	1.79	0.64
1:D:55:SER:CB	2:E:201:FAD:H8A	2.24	0.64
1:B:13:ALA:O	1:B:16:LEU:HD13	2.00	0.62
5:H:202:NAI:H8A	5:H:202:NAI:H52N	1.80	0.62
2:E:201:FAD:H2A	2:E:201:FAD:C2'	2.30	0.62
2:B:201:FAD:H8A	1:H:55:SER:HB3	1.84	0.60
1:C:69:ARG:NH1	1:C:142:GLY:O	2.35	0.60
1:E:162:SER:HA	1:E:174:TRP:HB3	1.82	0.60
2:E:201:FAD:O2'	2:E:201:FAD:C2A	2.49	0.60
1:D:166:TYR:OH	1:D:169:ARG:HA	2.03	0.59
1:D:139:LEU:HD21	1:E:8:LEU:HD11	1.85	0.58
1:E:39:LEU:O	1:E:80:ARG:HG3	2.04	0.58
2:B:201:FAD:H8A	1:H:55:SER:CB	2.35	0.57
1:C:157:ARG:NH1	1:C:159:GLU:OE2	2.37	0.57
1:B:58:LYS:HE3	1:H:23:LEU:HD11	1.86	0.57
2:B:201:FAD:C2A	2:B:201:FAD:HO2'	2.16	0.56
1:F:166:TYR:OH	1:F:169:ARG:HA	2.07	0.55
1:D:63:LEU:HD12	1:D:63:LEU:C	2.32	0.55
1:B:139:LEU:HD22	1:H:139:LEU:HD13	1.89	0.54
1:H:128:VAL:HG12	1:H:160:VAL:CG2	2.37	0.54
1:B:16:LEU:HD23	1:H:61:PRO:HD2	1.90	0.54
1:B:48:LEU:C	1:B:48:LEU:HD12	2.34	0.53
1:E:89:ARG:HA	1:E:163:PRO:HA	1.91	0.53
1:G:63:LEU:HD12	1:G:63:LEU:C	2.34	0.53
1:C:98:ARG:NH1	1:C:106:ARG:O	2.41	0.52
5:H:202:NAI:H8A	5:H:202:NAI:C5D	2.38	0.52
1:B:13:ALA:O	1:B:16:LEU:CD1	2.58	0.51
1:A:89:ARG:HA	1:A:163:PRO:HA	1.91	0.51
1:C:144:HIS:NE2	4:C:202:NAD:H4N	2.26	0.51
1:E:63:LEU:C	1:E:63:LEU:HD12	2.35	0.51
1:B:139:LEU:HD21	1:H:8:LEU:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:VAL:HG13	1:B:21:THR:HB	1.93	0.51
1:D:134:ARG:HG3	1:E:13:ALA:HB2	1.91	0.51
5:H:202:NAI:H51A	5:H:202:NAI:PN	2.52	0.50
1:B:125:ALA:C	6:B:306:HOH:O	2.55	0.49
1:E:104:ASP:HB3	2:E:202:FAD:H8A	1.94	0.49
1:H:46:TYR:HB3	1:H:73:VAL:HG22	1.95	0.48
1:H:163:PRO:HG2	1:H:165:MET:HE2	1.95	0.48
1:B:48:LEU:HD12	1:B:48:LEU:O	2.13	0.48
1:C:63:LEU:HD12	1:C:63:LEU:C	2.38	0.48
1:A:80:ARG:HG2	1:A:82:GLU:HG2	1.95	0.47
1:H:89:ARG:O	1:H:164:LEU:HB2	2.14	0.47
2:D:202:FAD:H2'	2:D:202:FAD:N1	2.29	0.47
1:A:63:LEU:C	1:A:63:LEU:HD12	2.39	0.47
1:H:165:MET:HE1	1:H:174:TRP:HE3	1.80	0.47
1:A:16:LEU:HD21	1:F:150:ALA:HB1	1.96	0.47
1:F:64:LEU:HD12	1:F:64:LEU:C	2.40	0.47
1:A:64:LEU:C	1:A:64:LEU:HD12	2.40	0.47
1:H:169:ARG:HA	5:H:202:NAI:O2A	2.14	0.46
1:C:82:GLU:OE1	1:C:134:ARG:NH1	2.49	0.46
1:C:48:LEU:C	1:C:48:LEU:HD12	2.41	0.46
1:H:157:ARG:NE	1:H:159:GLU:OE1	2.44	0.46
1:B:56:VAL:O	1:H:144:HIS:CG	2.69	0.46
1:C:89:ARG:O	1:C:164:LEU:HB2	2.16	0.46
1:D:104:ASP:HB3	2:D:201:FAD:H1B	1.98	0.46
1:E:82:GLU:OE2	1:E:118:GLY:HA3	2.16	0.46
2:G:201:FAD:H2B	6:G:341:HOH:O	2.16	0.46
1:H:64:LEU:C	1:H:64:LEU:HD12	2.40	0.46
1:A:77:LEU:C	1:A:77:LEU:HD23	2.40	0.45
1:B:64:LEU:C	1:B:64:LEU:HD12	2.41	0.45
1:E:36:VAL:O	1:E:47:GLY:HA2	2.16	0.45
1:C:36:VAL:O	1:C:47:GLY:HA2	2.17	0.45
1:A:144:HIS:CG	1:F:56:VAL:O	2.69	0.45
1:B:25:ILE:CD1	1:H:155:GLY:HA2	2.47	0.45
1:F:72:ARG:HD2	6:F:314:HOH:O	2.17	0.45
1:H:39:LEU:HD13	1:H:121:PRO:HD3	1.99	0.44
1:F:93:GLU:HB2	6:F:315:HOH:O	2.16	0.44
1:D:28:ALA:HB1	1:E:128:VAL:HG22	1.99	0.44
1:F:36:VAL:O	1:F:47:GLY:HA2	2.18	0.44
1:G:64:LEU:HD12	1:G:64:LEU:C	2.43	0.44
1:D:98:ARG:HG3	1:D:99:PHE:CD2	2.53	0.44
1:G:77:LEU:C	1:G:77:LEU:HD12	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:LEU:HB3	1:D:73:VAL:HG11	2.01	0.43
1:E:64:LEU:C	1:E:64:LEU:HD12	2.43	0.43
1:F:77:LEU:C	1:F:77:LEU:HD23	2.43	0.43
1:A:89:ARG:HG2	1:A:126:ASP:HA	2.00	0.43
1:F:86:ASN:HB3	1:F:127:VAL:HG11	2.01	0.42
1:H:36:VAL:O	1:H:47:GLY:HA2	2.18	0.42
1:D:36:VAL:O	1:D:47:GLY:HA2	2.19	0.42
1:A:148:ILE:HD12	1:F:8:LEU:HD23	2.01	0.42
1:H:80:ARG:HG3	1:H:82:GLU:HG2	2.02	0.42
1:F:63:LEU:C	1:F:63:LEU:HD12	2.45	0.42
1:H:80:ARG:HG3	1:H:82:GLU:CG	2.49	0.42
1:A:16:LEU:CD2	1:F:150:ALA:HB1	2.50	0.42
1:B:174:TRP:CE3	1:H:175:PRO:HG3	2.55	0.42
1:E:166:TYR:OH	1:E:169:ARG:HA	2.19	0.42
2:H:201:FAD:H9	2:H:201:FAD:H1'1	1.89	0.42
1:A:36:VAL:O	1:A:47:GLY:HA2	2.20	0.42
1:A:68:ASN:HB2	6:A:314:HOH:O	2.19	0.42
2:B:201:FAD:O2B	1:H:55:SER:OG	2.27	0.42
1:B:63:LEU:HD12	1:B:63:LEU:C	2.45	0.41
1:B:166:TYR:OH	1:B:169:ARG:HA	2.20	0.41
1:E:8:LEU:HD23	1:E:8:LEU:HA	1.94	0.41
1:H:64:LEU:HA	1:H:147:VAL:O	2.20	0.41
2:A:201:FAD:H9	2:A:201:FAD:H1'1	1.91	0.41
1:H:75:LYS:HA	1:H:75:LYS:HD2	1.94	0.41
1:H:89:ARG:HA	1:H:128:VAL:HG13	2.03	0.41
1:B:124:SER:O	1:B:125:ALA:HB3	2.20	0.41
1:C:48:LEU:HA	1:C:99:PHE:O	2.20	0.41
2:D:202:FAD:H9	2:D:202:FAD:H1'2	1.83	0.41
1:F:167:TRP:CZ2	1:F:168:ARG:HD2	2.56	0.41
1:H:72:ARG:HD3	6:H:303:HOH:O	2.20	0.41

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	168/199 (84%)	161 (96%)	7 (4%)	0	100	100
1	B	168/199 (84%)	157 (94%)	11 (6%)	0	100	100
1	C	170/199 (85%)	166 (98%)	4 (2%)	0	100	100
1	D	170/199 (85%)	166 (98%)	4 (2%)	0	100	100
1	E	164/199 (82%)	158 (96%)	6 (4%)	0	100	100
1	F	173/199 (87%)	165 (95%)	8 (5%)	0	100	100
1	G	170/199 (85%)	164 (96%)	6 (4%)	0	100	100
1	H	176/199 (88%)	168 (96%)	8 (4%)	0	100	100
All	All	1359/1592 (85%)	1305 (96%)	54 (4%)	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	130/155 (84%)	127 (98%)	3 (2%)	44	59
1	B	131/155 (84%)	128 (98%)	3 (2%)	44	59
1	C	132/155 (85%)	124 (94%)	8 (6%)	17	24
1	D	132/155 (85%)	127 (96%)	5 (4%)	29	43
1	E	127/155 (82%)	119 (94%)	8 (6%)	16	23
1	F	133/155 (86%)	127 (96%)	6 (4%)	24	37
1	G	132/155 (85%)	128 (97%)	4 (3%)	36	51
1	H	133/155 (86%)	129 (97%)	4 (3%)	36	51
All	All	1050/1240 (85%)	1009 (96%)	41 (4%)	28	42

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LEU
1	A	148	ILE
1	A	162	SER
1	B	17	VAL
1	B	20	ASP
1	B	124	SER
1	C	39	LEU
1	C	55	SER
1	C	72	ARG
1	C	104	ASP
1	C	109	ASP
1	C	128	VAL
1	C	152	VAL
1	C	176	VAL
1	D	17	VAL
1	D	48	LEU
1	D	72	ARG
1	D	73	VAL
1	D	170	SER
1	E	23	LEU
1	E	34	THR
1	E	39	LEU
1	E	80	ARG
1	E	82	GLU
1	E	89	ARG
1	E	124	SER
1	E	128	VAL
1	F	39	LEU
1	F	42	ASP
1	F	48	LEU
1	F	55	SER
1	F	70	ASP
1	F	176	VAL
1	G	39	LEU
1	G	48	LEU
1	G	55	SER
1	G	126	ASP
1	H	39	LEU
1	H	55	SER
1	H	160	VAL
1	H	162	SER

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

28 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	201	-	58,58,58	0.59	0	85,89,89	0.95	5 (5%)
2	FAD	G	202	-	58,58,58	0.63	0	85,89,89	0.62	1 (1%)
2	FAD	C	201	-	46,47,58	0.59	0	66,72,89	0.68	0
3	PO4	E	203	-	4,4,4	0.77	0	6,6,6	0.48	0
5	NAI	H	202	-	47,48,48	0.56	0	64,73,73	0.62	1 (1%)
3	PO4	C	203	-	4,4,4	0.89	0	6,6,6	0.48	0
3	PO4	F	204	-	4,4,4	0.64	0	6,6,6	0.47	0
3	PO4	D	204	-	4,4,4	0.76	0	6,6,6	0.46	0
2	FAD	B	202	-	58,58,58	0.64	1 (1%)	85,89,89	0.62	1 (1%)
2	FAD	H	201	-	38,38,58	0.64	0	54,58,89	0.67	0
3	PO4	B	203	-	4,4,4	0.74	0	6,6,6	0.45	0
2	FAD	A	202	-	58,58,58	0.57	0	85,89,89	0.74	3 (3%)
2	FAD	F	202	-	38,38,58	0.64	0	54,58,89	0.70	1 (1%)
3	PO4	H	203	-	4,4,4	0.73	0	6,6,6	0.48	0
4	NAD	C	202	-	46,48,48	0.57	0	64,73,73	0.67	2 (3%)
2	FAD	E	202	-	58,58,58	0.60	0	85,89,89	0.64	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	F	203	-	4,4,4	0.66	0	6,6,6	0.47	0
3	PO4	G	203	-	4,4,4	0.87	0	6,6,6	0.43	0
2	FAD	B	201	-	58,58,58	0.66	1 (1%)	85,89,89	0.74	2 (2%)
2	FAD	F	201	-	58,58,58	0.58	0	85,89,89	0.77	2 (2%)
3	PO4	H	204	-	4,4,4	0.71	0	6,6,6	0.44	0
2	FAD	A	201	-	58,58,58	0.52	0	85,89,89	0.61	1 (1%)
3	PO4	A	203	-	4,4,4	0.71	0	6,6,6	0.44	0
3	PO4	C	204	-	4,4,4	0.74	0	6,6,6	0.48	0
2	FAD	G	201	-	58,58,58	0.54	0	85,89,89	0.69	0
3	PO4	D	203	-	4,4,4	0.74	0	6,6,6	0.46	0
2	FAD	E	201	-	58,58,58	0.61	0	85,89,89	0.79	3 (3%)
2	FAD	D	202	-	58,58,58	0.53	0	85,89,89	0.65	1 (1%)

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	F	201	-	-	14/34/50/50	0/6/6/6
2	FAD	D	201	-	-	11/34/50/50	0/6/6/6
4	NAD	C	202	-	-	11/30/62/62	0/5/5/5
2	FAD	A	201	-	-	4/34/50/50	0/6/6/6
2	FAD	G	202	-	-	11/34/50/50	0/6/6/6
2	FAD	E	202	-	-	1/34/50/50	0/6/6/6
2	FAD	B	202	-	-	5/34/50/50	0/6/6/6
2	FAD	C	201	-	-	9/30/46/50	0/4/4/6
2	FAD	H	201	-	-	6/27/27/50	0/3/3/6
2	FAD	A	202	-	-	5/34/50/50	0/6/6/6
2	FAD	F	202	-	-	4/27/27/50	0/3/3/6
5	NAI	H	202	-	-	14/29/72/72	0/5/5/5
2	FAD	G	201	-	-	10/34/50/50	0/6/6/6
2	FAD	E	201	-	-	3/34/50/50	0/6/6/6
2	FAD	D	202	-	-	13/34/50/50	0/6/6/6
2	FAD	B	201	-	-	11/34/50/50	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	FAD	P-O3P	2.17	1.61	1.59
2	B	202	FAD	PA-O3P	2.11	1.61	1.59

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	201	FAD	C1'-C2'-C3'	3.34	118.72	109.66
4	C	202	NAD	C4D-O4D-C1D	-3.09	107.09	109.92
2	D	201	FAD	C1'-C2'-C3'	2.85	117.39	109.66
2	E	201	FAD	C1'-C2'-C3'	2.73	117.07	109.66
2	A	202	FAD	O5'-C5'-C4'	2.65	116.44	109.36
2	D	201	FAD	C2'-C1'-N10	2.52	122.13	110.20
5	H	202	NAI	C3D-C2D-C1D	2.52	106.22	101.46
4	C	202	NAD	C6N-N1N-C2N	-2.33	119.90	121.88
2	E	201	FAD	C4-N3-C2	-2.21	121.71	125.64
2	D	201	FAD	O3'-C3'-C4'	2.20	113.92	108.93
2	A	202	FAD	C4-N3-C2	-2.17	121.79	125.64
2	A	202	FAD	C1'-C2'-C3'	2.16	115.50	109.66
2	B	201	FAD	C1'-C2'-C3'	2.15	115.49	109.66
2	D	202	FAD	C4-N3-C2	-2.13	121.87	125.64
2	D	201	FAD	C4-N3-C2	-2.10	121.92	125.64
2	A	201	FAD	C4-N3-C2	-2.09	121.92	125.64
2	B	202	FAD	C4-N3-C2	-2.08	121.95	125.64
2	B	201	FAD	C4-N3-C2	-2.07	121.97	125.64
2	F	202	FAD	C4-N3-C2	-2.05	122.00	125.64
2	F	201	FAD	C4-N3-C2	-2.03	122.03	125.64
2	D	201	FAD	O4'-C4'-C5'	-2.03	105.51	109.99
2	G	202	FAD	C4-N3-C2	-2.02	122.05	125.64
2	E	202	FAD	C4-N3-C2	-2.02	122.06	125.64
2	E	201	FAD	O5'-C5'-C4'	2.01	114.72	109.36

There are no chirality outliers.

All (132) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	FAD	C5B-O5B-PA-O1A
2	A	201	FAD	C5B-O5B-PA-O3P
2	A	202	FAD	C3'-C4'-C5'-O5'
2	A	202	FAD	O4'-C4'-C5'-O5'
2	B	201	FAD	C3'-C4'-C5'-O5'
2	B	201	FAD	O4'-C4'-C5'-O5'
2	B	201	FAD	C5'-O5'-P-O2P

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Mol	Chain	Res	Type	Atoms
2	B	202	FAD	C5B-O5B-PA-O1A
2	C	201	FAD	C5B-O5B-PA-O1A
2	C	201	FAD	C5B-O5B-PA-O2A
2	D	201	FAD	N10-C1'-C2'-O2'
2	D	201	FAD	C2'-C3'-C4'-O4'
2	D	201	FAD	C2'-C3'-C4'-C5'
2	D	201	FAD	C3'-C4'-C5'-O5'
2	D	202	FAD	O3'-C3'-C4'-C5'
2	D	202	FAD	C3'-C4'-C5'-O5'
2	D	202	FAD	O4'-C4'-C5'-O5'
2	D	202	FAD	C5'-O5'-P-O2P
2	D	202	FAD	C5'-O5'-P-O3P
2	E	201	FAD	PA-O3P-P-O5'
2	F	201	FAD	C5B-O5B-PA-O2A
2	F	201	FAD	C2'-C3'-C4'-O4'
2	F	201	FAD	O3'-C3'-C4'-O4'
2	F	201	FAD	O3'-C3'-C4'-C5'
2	G	201	FAD	C5B-O5B-PA-O1A
2	G	201	FAD	C3'-C4'-C5'-O5'
2	G	201	FAD	O4'-C4'-C5'-O5'
2	G	201	FAD	C5'-O5'-P-O2P
2	G	201	FAD	C5'-O5'-P-O3P
2	G	202	FAD	C3'-C4'-C5'-O5'
2	G	202	FAD	O4'-C4'-C5'-O5'
2	G	202	FAD	C5'-O5'-P-O1P
2	G	202	FAD	C5'-O5'-P-O2P
2	G	202	FAD	C5'-O5'-P-O3P
4	C	202	NAD	C5B-O5B-PA-O1A
4	C	202	NAD	C5B-O5B-PA-O3
4	C	202	NAD	PN-O3-PA-O5B
4	C	202	NAD	C5D-O5D-PN-O3
5	H	202	NAI	C5B-O5B-PA-O1A
5	H	202	NAI	C5B-O5B-PA-O2A
5	H	202	NAI	C5B-O5B-PA-O3
5	H	202	NAI	C5D-O5D-PN-O3
5	H	202	NAI	C5D-O5D-PN-O2N
5	H	202	NAI	O4D-C1D-N1N-C6N
2	D	201	FAD	O3'-C3'-C4'-O4'
2	D	201	FAD	O3'-C3'-C4'-C5'
2	D	202	FAD	C2'-C3'-C4'-C5'
2	F	201	FAD	C2'-C3'-C4'-C5'
2	D	202	FAD	O3'-C3'-C4'-O4'

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Mol	Chain	Res	Type	Atoms
2	D	202	FAD	C2'-C3'-C4'-O4'
2	D	202	FAD	O4B-C4B-C5B-O5B
2	D	202	FAD	C3B-C4B-C5B-O5B
2	F	201	FAD	O4B-C4B-C5B-O5B
2	F	201	FAD	C3B-C4B-C5B-O5B
4	C	202	NAD	O4D-C4D-C5D-O5D
4	C	202	NAD	C3D-C4D-C5D-O5D
5	H	202	NAI	O4B-C4B-C5B-O5B
5	H	202	NAI	C3B-C4B-C5B-O5B
5	H	202	NAI	O4D-C4D-C5D-O5D
2	E	201	FAD	O4B-C1B-N9A-C4A
2	F	201	FAD	O4B-C1B-N9A-C4A
2	D	201	FAD	O4'-C4'-C5'-O5'
5	H	202	NAI	C3D-C4D-C5D-O5D
2	A	202	FAD	C2'-C3'-C4'-C5'
2	F	202	FAD	C3'-C4'-C5'-O5'
2	G	202	FAD	C2'-C3'-C4'-O4'
2	G	202	FAD	C2'-C3'-C4'-C5'
2	F	202	FAD	C5B-O5B-PA-O1A
2	G	202	FAD	O3'-C3'-C4'-O4'
2	F	202	FAD	O4'-C4'-C5'-O5'
2	C	201	FAD	C2'-C3'-C4'-O4'
2	A	202	FAD	PA-O3P-P-O5'
2	D	202	FAD	PA-O3P-P-O5'
4	C	202	NAD	PA-O3-PN-O5D
5	H	202	NAI	PA-O3-PN-O5D
2	H	201	FAD	C5B-O5B-PA-O1A
2	H	201	FAD	C2'-C3'-C4'-O4'
2	F	201	FAD	O4B-C1B-N9A-C8A
5	H	202	NAI	C2D-C1D-N1N-C2N
2	F	201	FAD	C3'-C4'-C5'-O5'
2	H	201	FAD	PA-O3P-P-O1P
2	G	202	FAD	O3'-C3'-C4'-C5'
2	D	201	FAD	N10-C1'-C2'-C3'
2	C	201	FAD	C2'-C3'-C4'-C5'
2	A	201	FAD	C5B-O5B-PA-O2A
2	B	201	FAD	C5'-O5'-P-O1P
2	B	201	FAD	C5'-O5'-P-O3P
2	B	202	FAD	C5B-O5B-PA-O2A
2	B	202	FAD	C5B-O5B-PA-O3P
2	C	201	FAD	C5B-O5B-PA-O3P
2	D	201	FAD	C5B-O5B-PA-O1A

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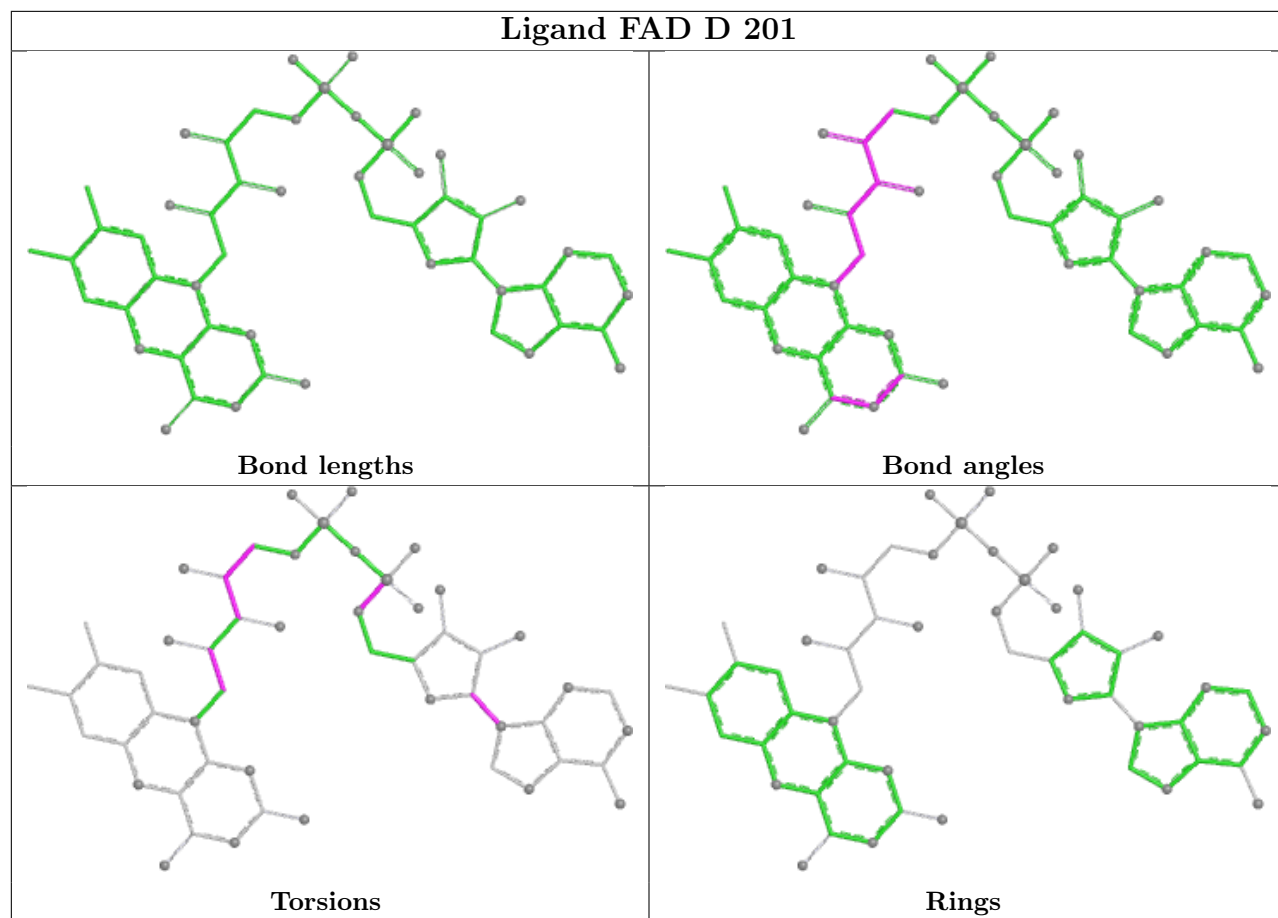
Mol	Chain	Res	Type	Atoms
2	D	202	FAD	C2'-C1'-N10-C10
2	E	202	FAD	C5B-O5B-PA-O1A
2	F	201	FAD	C5B-O5B-PA-O1A
2	F	201	FAD	C5B-O5B-PA-O3P
2	G	201	FAD	C5B-O5B-PA-O2A
2	G	201	FAD	C5B-O5B-PA-O3P
4	C	202	NAD	C5B-O5B-PA-O2A
4	C	202	NAD	C5D-O5D-PN-O1N
5	H	202	NAI	C5D-O5D-PN-O1N
2	E	201	FAD	O4B-C1B-N9A-C8A
2	H	201	FAD	C2'-C3'-C4'-C5'
2	B	201	FAD	O4B-C1B-N9A-C4A
5	H	202	NAI	C2D-C1D-N1N-C6N
2	C	201	FAD	P-O3P-PA-O2A
2	D	202	FAD	C4'-C5'-O5'-P
2	D	201	FAD	O4B-C1B-N9A-C8A
2	D	201	FAD	O4B-C1B-N9A-C4A
2	G	201	FAD	C2'-C3'-C4'-C5'
2	B	201	FAD	O4B-C1B-N9A-C8A
4	C	202	NAD	C4D-C5D-O5D-PN
2	C	201	FAD	P-O3P-PA-O1A
2	G	201	FAD	P-O3P-PA-O1A
2	G	201	FAD	P-O3P-PA-O2A
2	C	201	FAD	O3'-C3'-C4'-O4'
2	H	201	FAD	O3'-C3'-C4'-O4'
2	A	202	FAD	O3'-C3'-C4'-C5'
2	F	201	FAD	O4'-C4'-C5'-O5'
2	B	202	FAD	C2'-C3'-C4'-O4'
2	F	202	FAD	C2'-C3'-C4'-O4'
2	B	201	FAD	PA-O3P-P-O1P
2	G	202	FAD	P-O3P-PA-O1A
2	G	202	FAD	P-O3P-PA-O2A
2	H	201	FAD	PA-O3P-P-O2P
4	C	202	NAD	PN-O3-PA-O1A
2	C	201	FAD	O4B-C4B-C5B-O5B
2	B	202	FAD	O3'-C3'-C4'-O4'
2	A	201	FAD	C2'-C3'-C4'-O4'
2	B	201	FAD	C3B-C4B-C5B-O5B
2	B	201	FAD	O2'-C2'-C3'-C4'
2	B	201	FAD	PA-O3P-P-O2P
2	F	201	FAD	PA-O3P-P-O2P

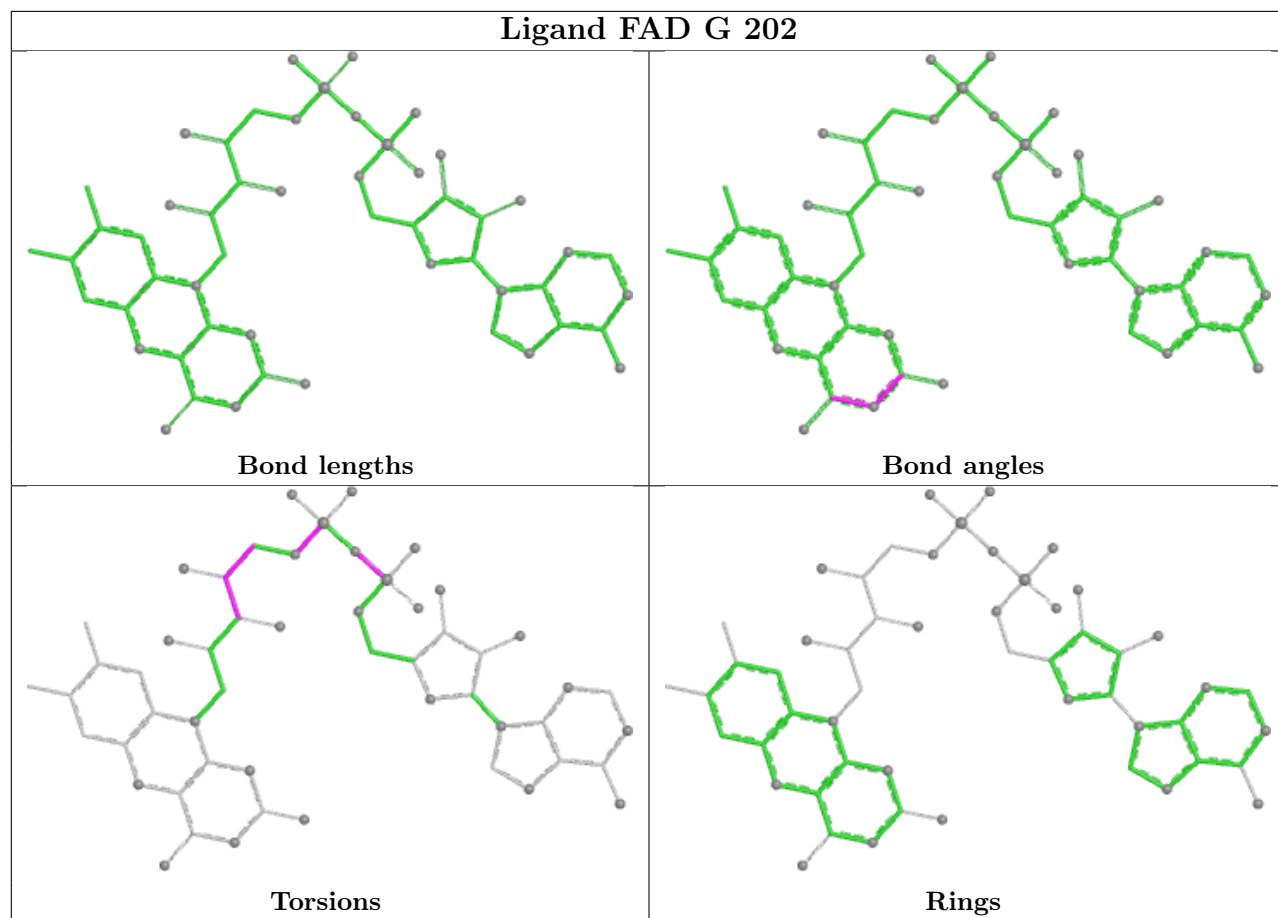
There are no ring outliers.

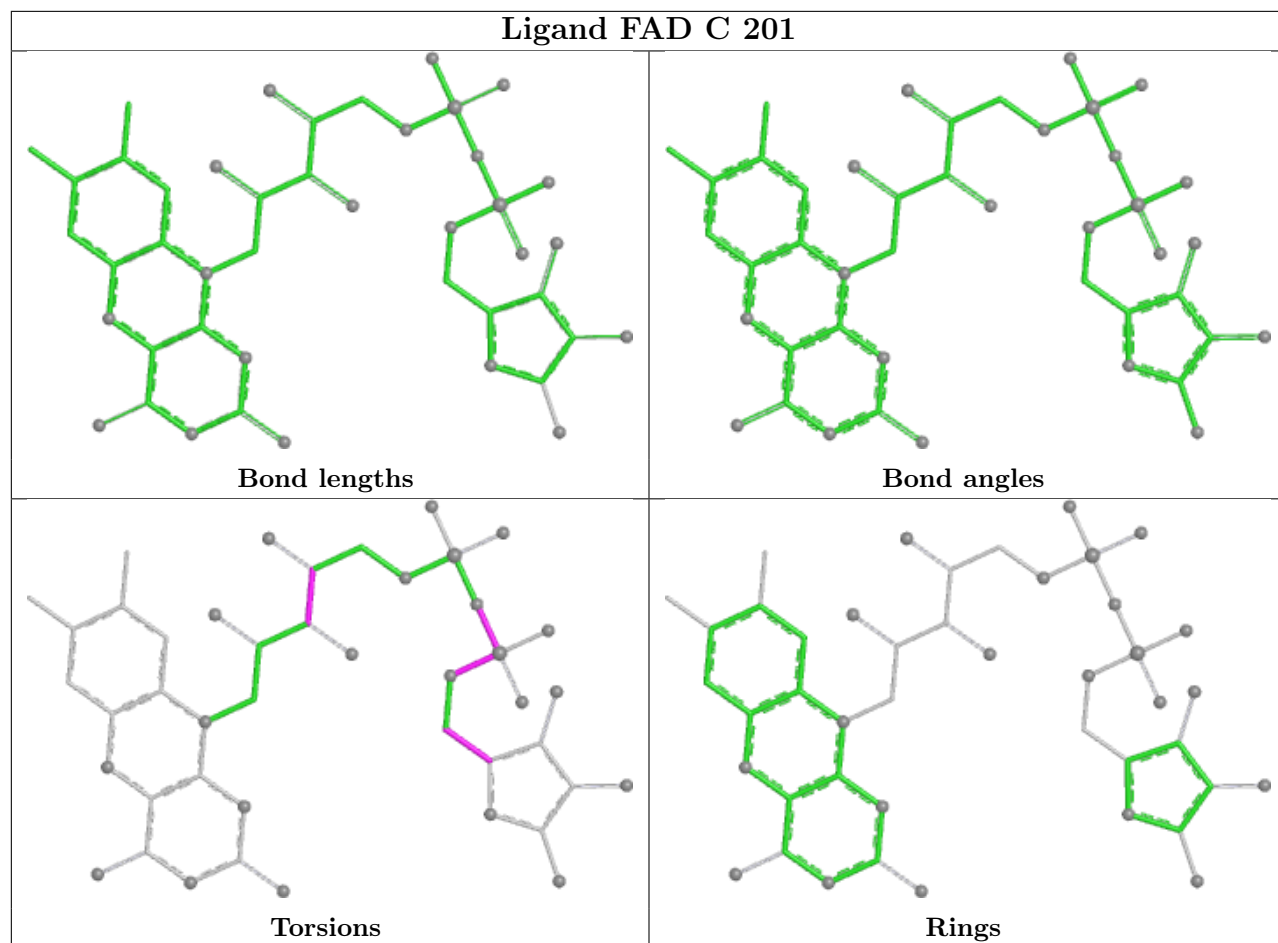
11 monomers are involved in 25 short contacts:

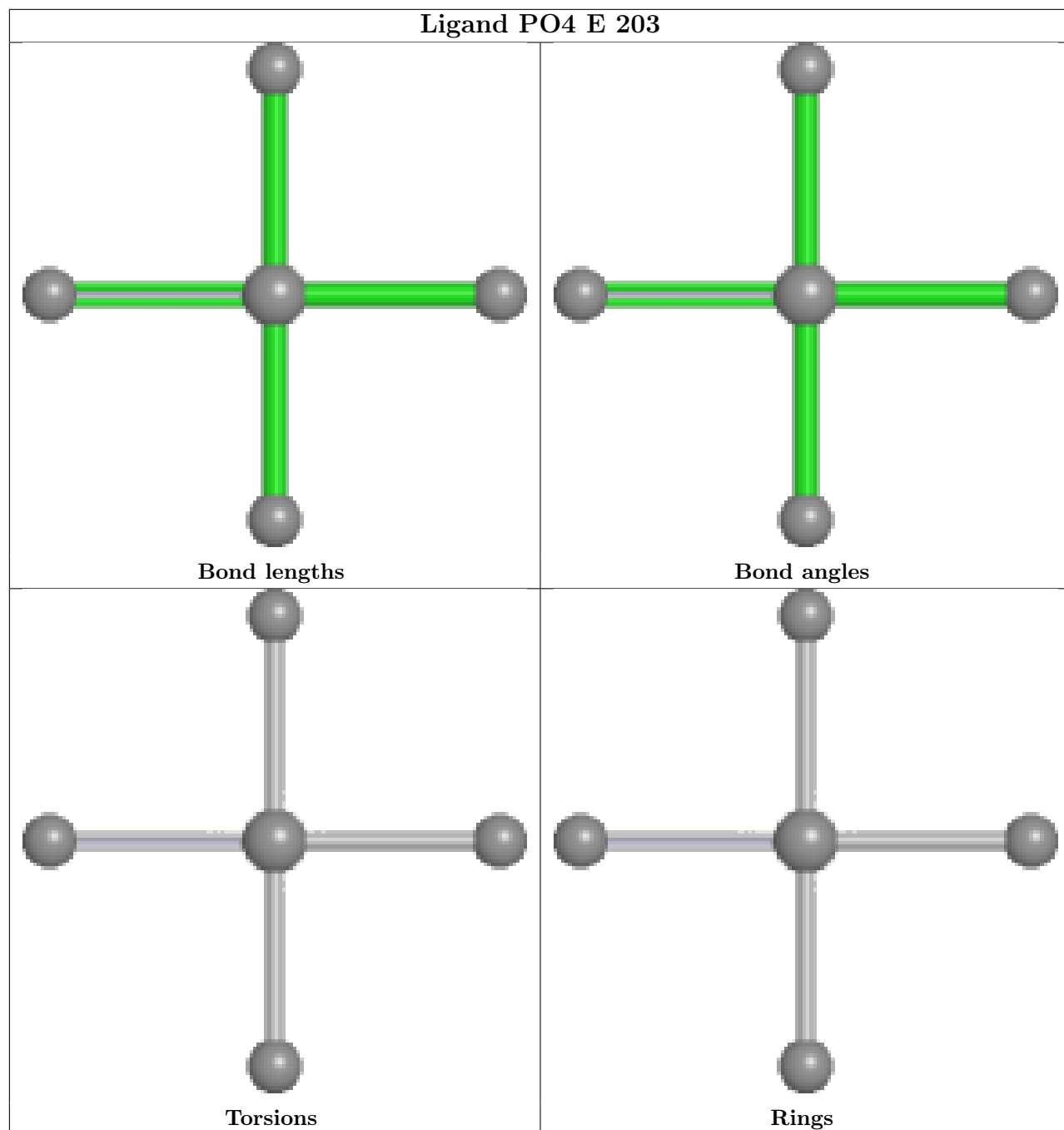
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	201	FAD	1	0
5	H	202	NAI	5	0
2	H	201	FAD	1	0
4	C	202	NAD	1	0
2	E	202	FAD	1	0
2	B	201	FAD	6	0
2	F	201	FAD	1	0
2	A	201	FAD	1	0
2	G	201	FAD	1	0
2	E	201	FAD	5	0
2	D	202	FAD	2	0

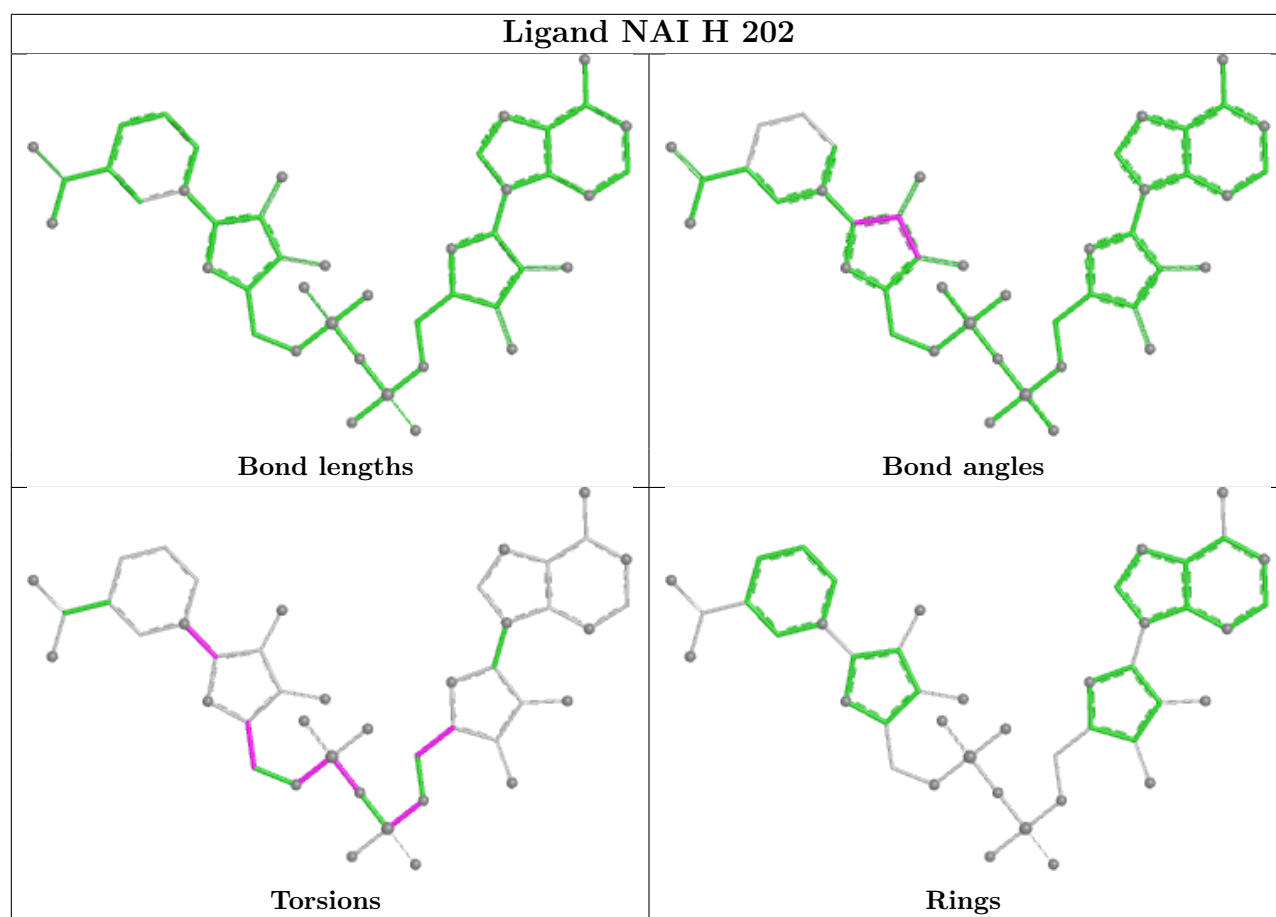
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

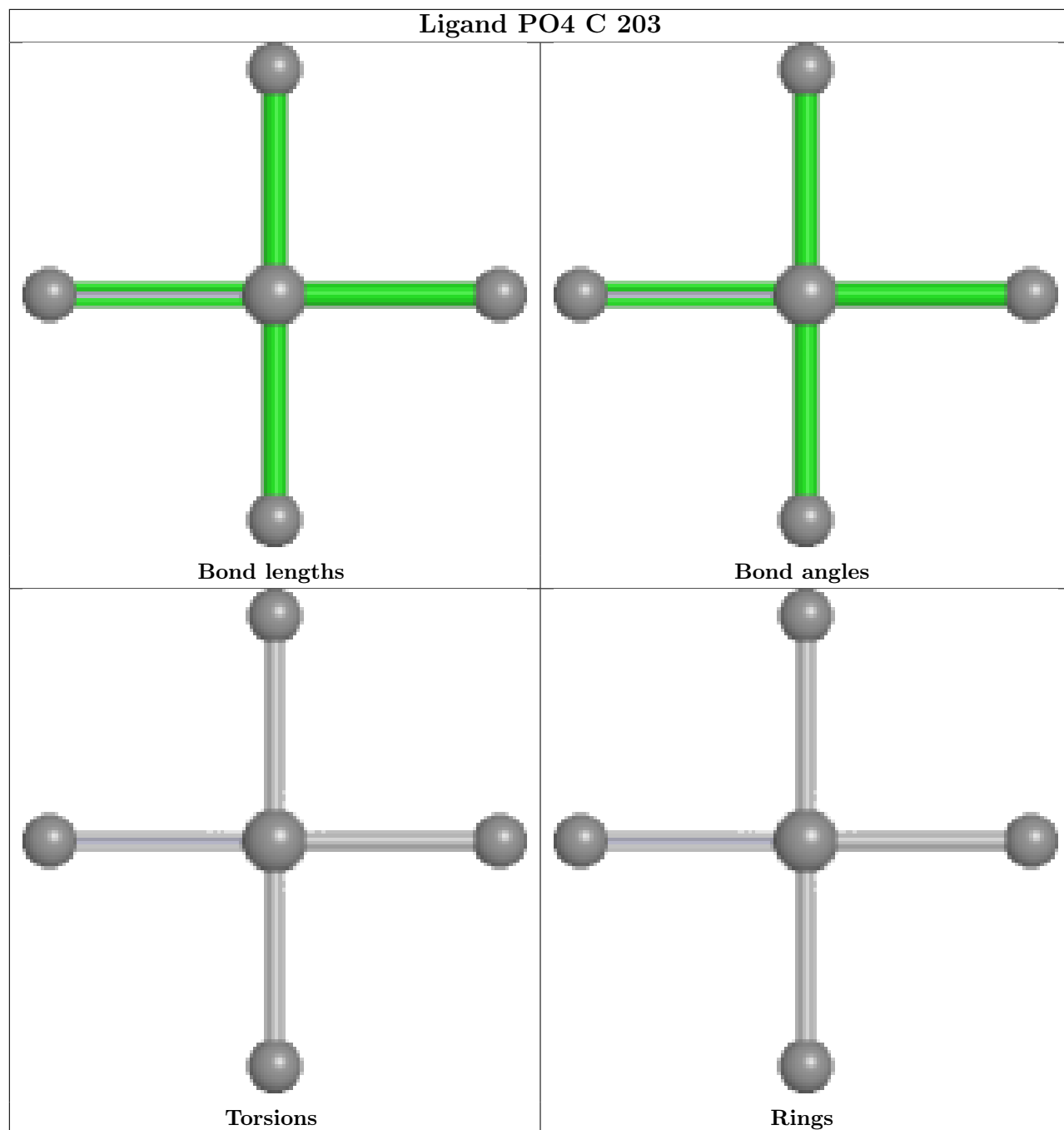


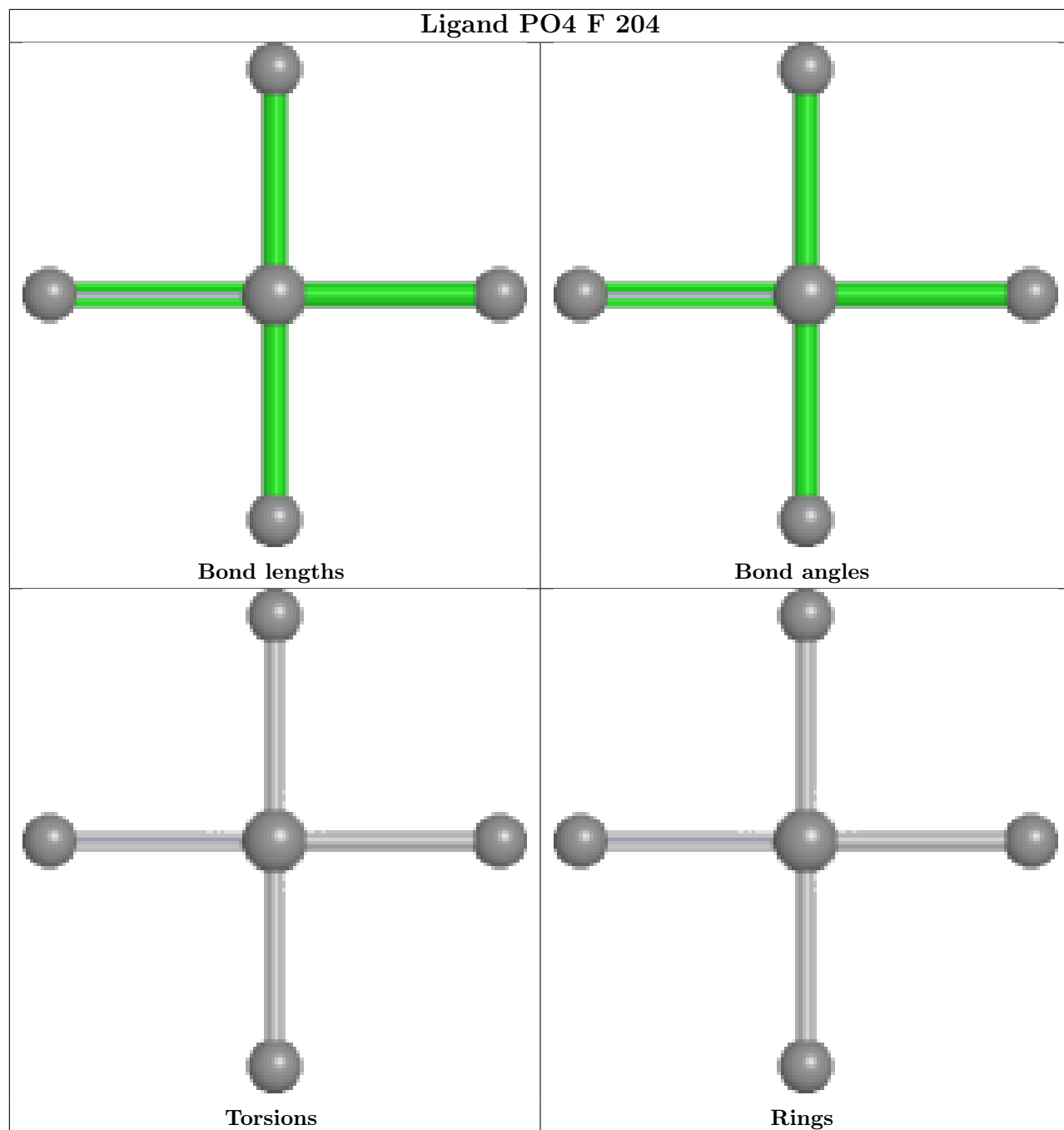


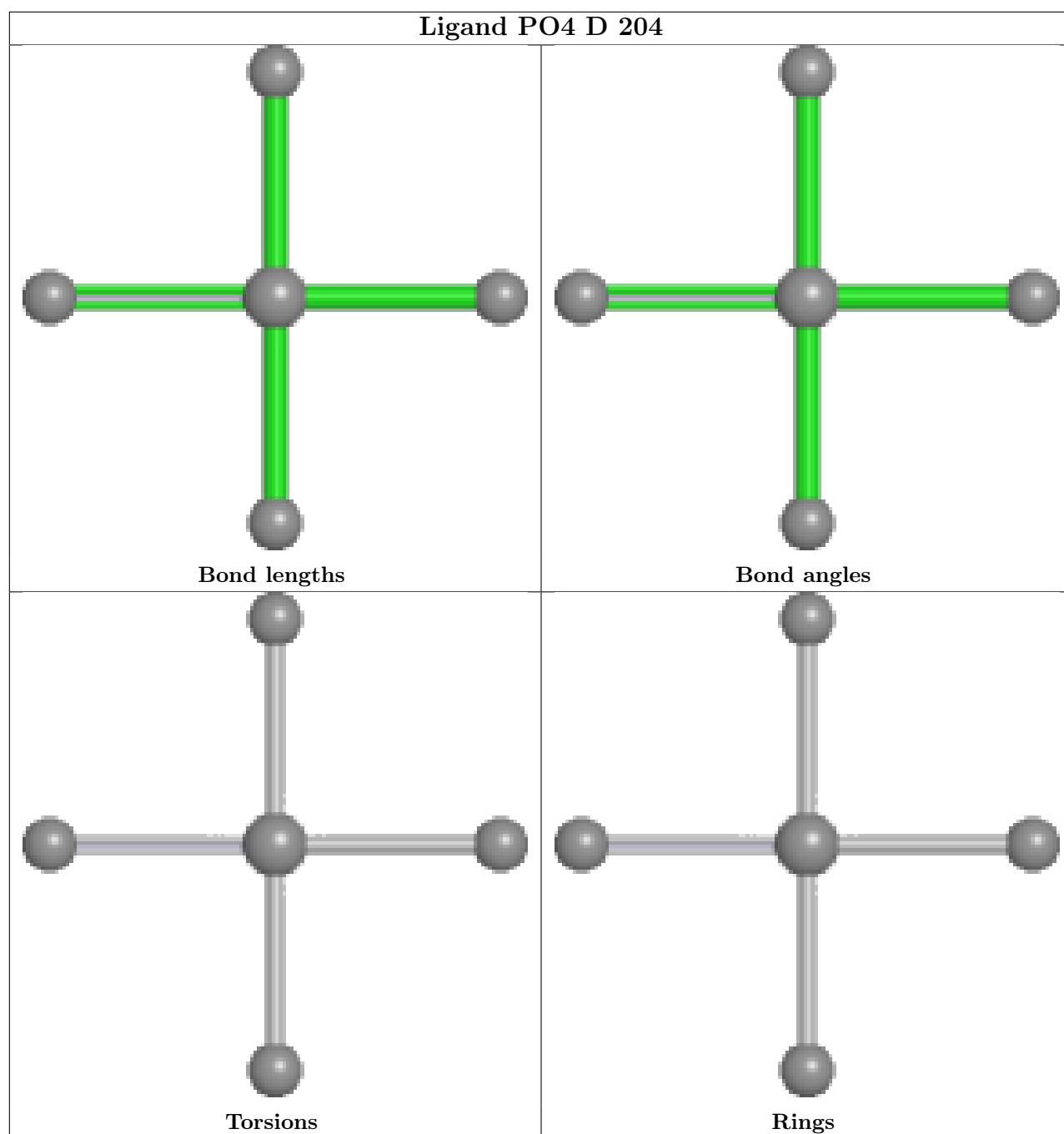


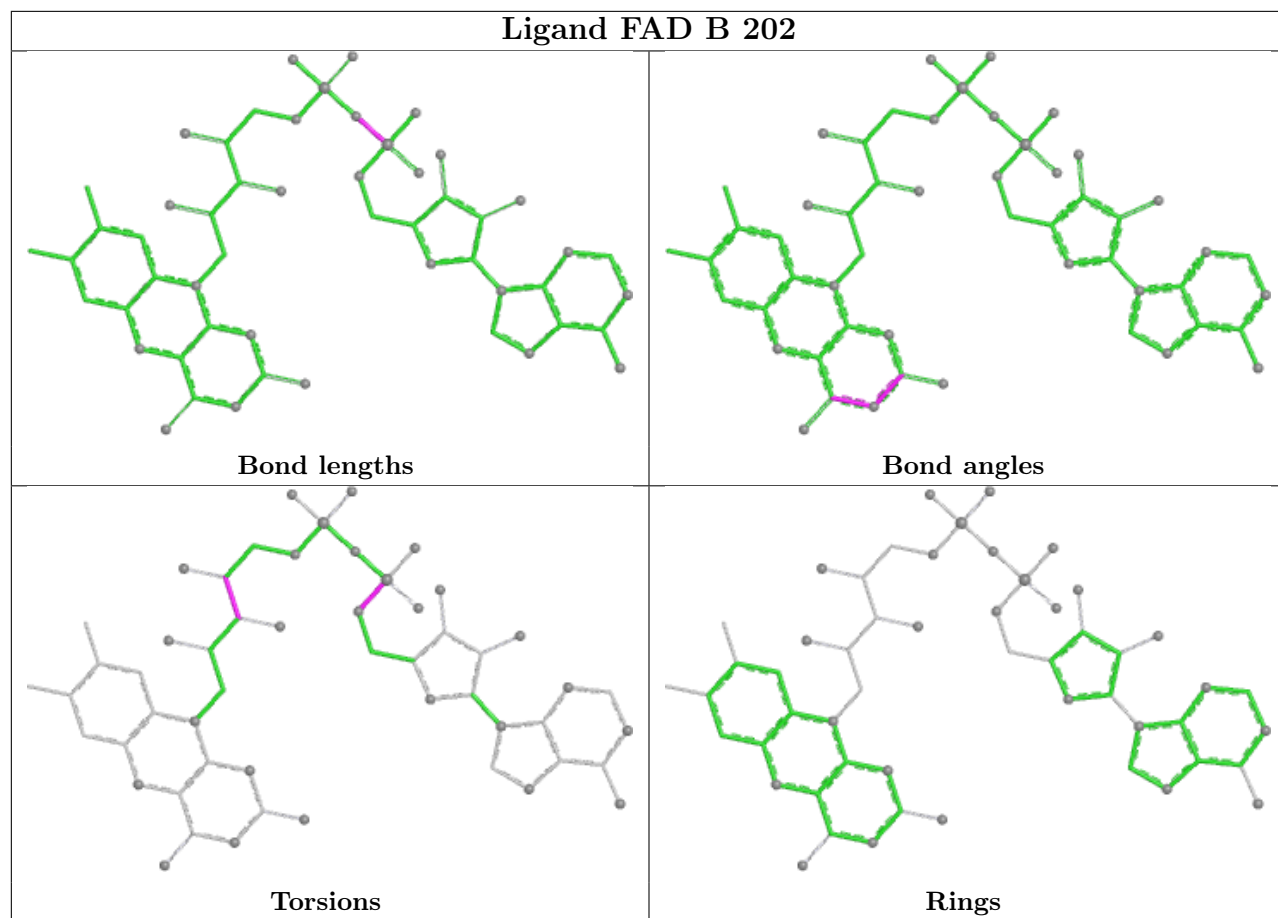


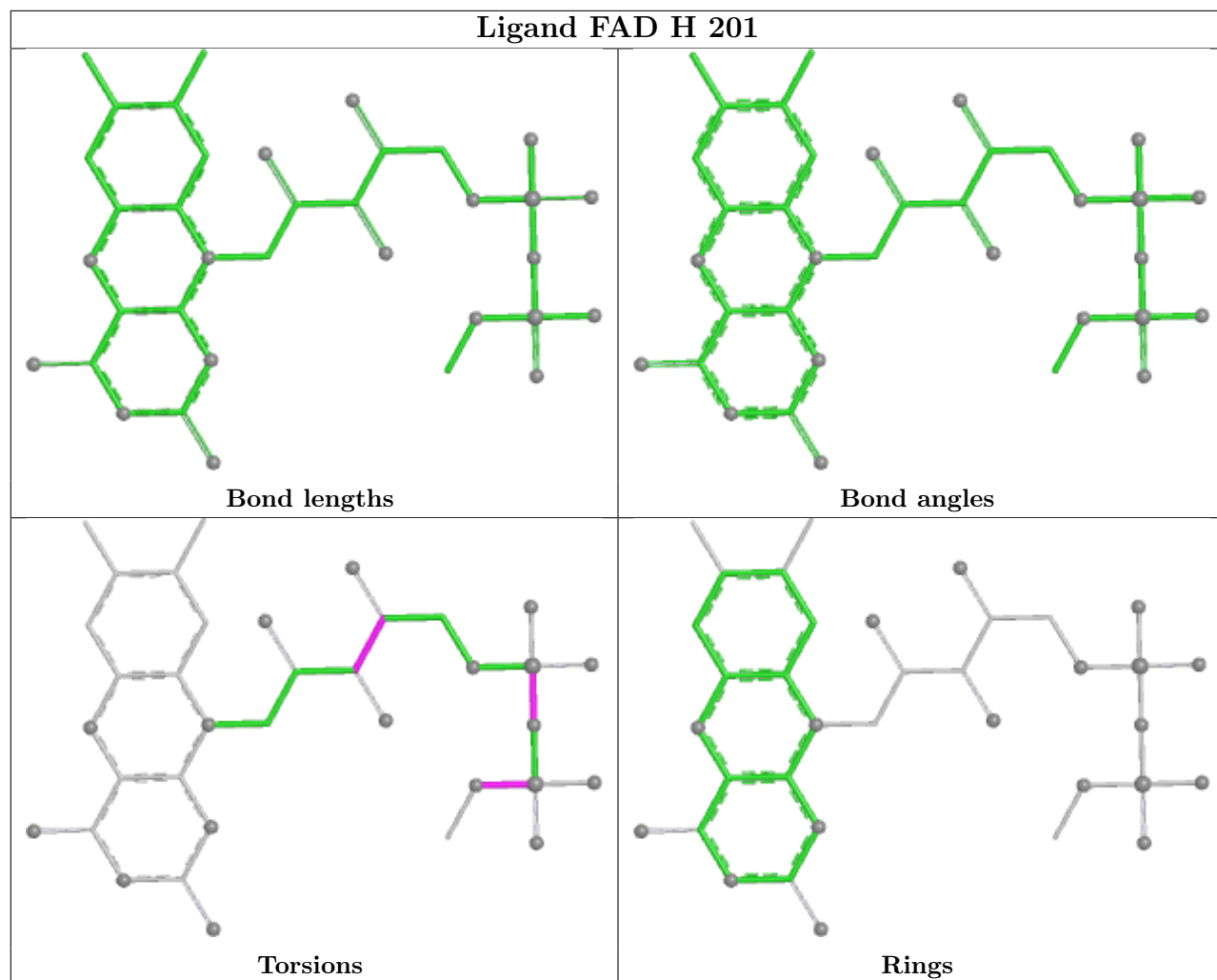


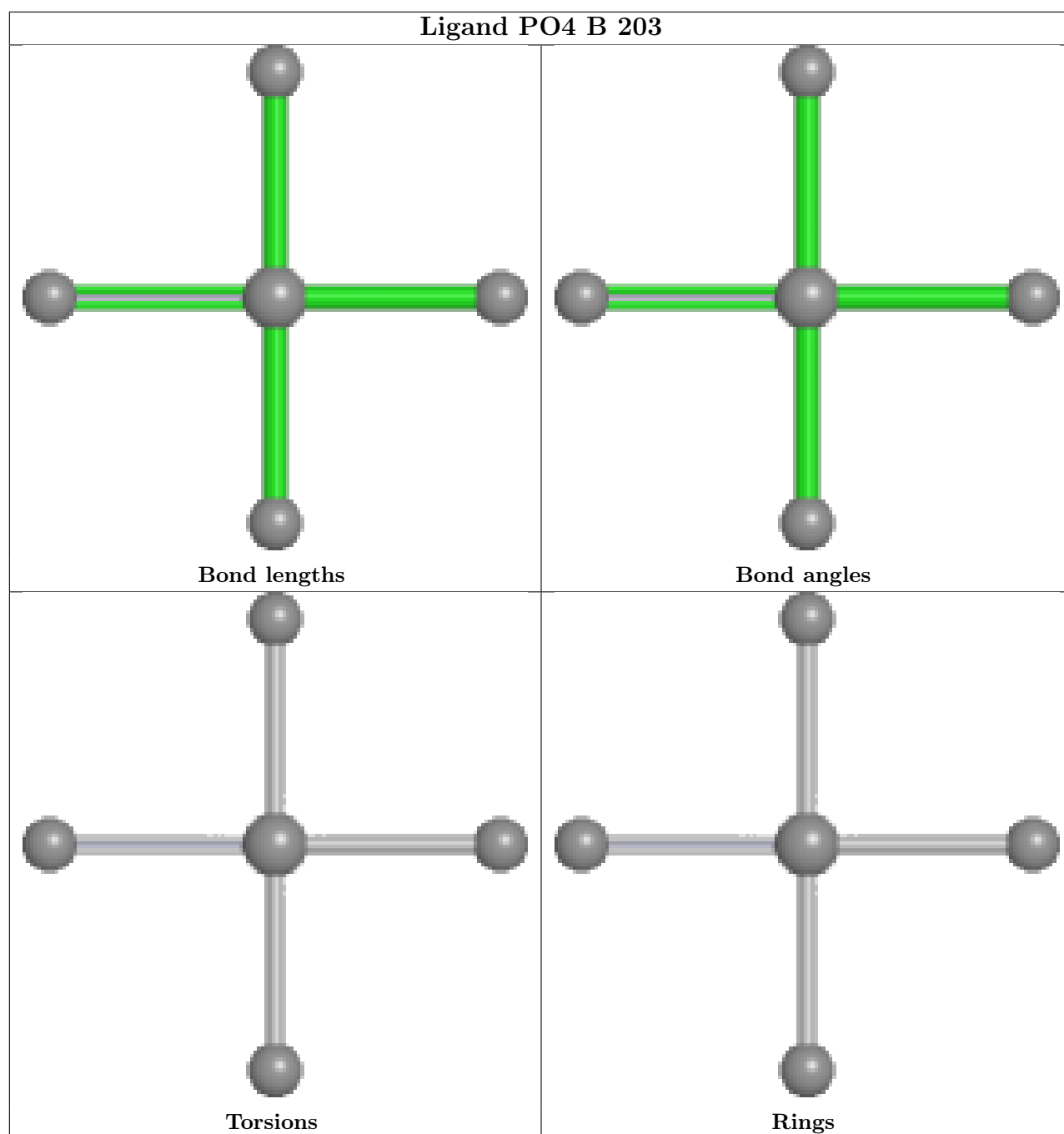


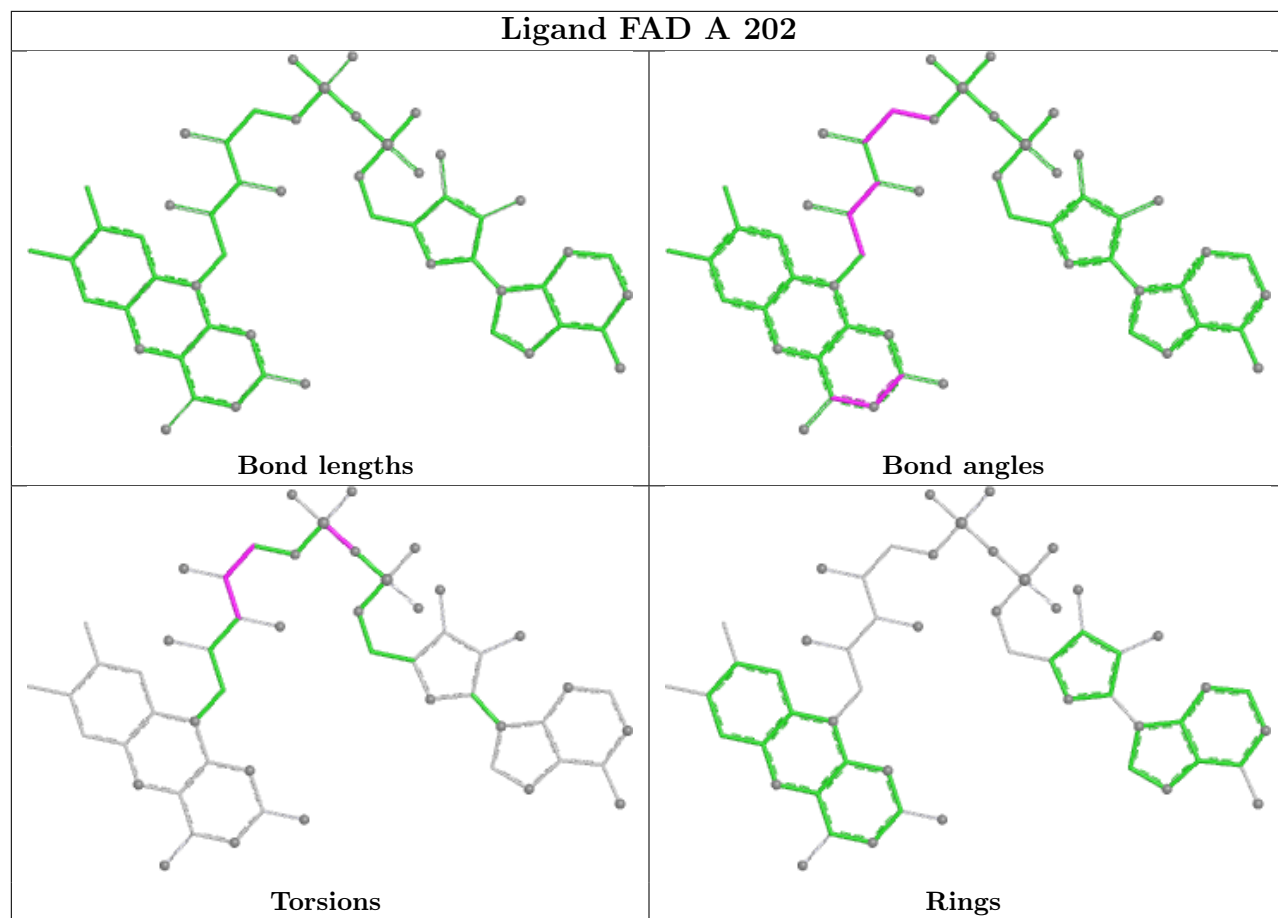


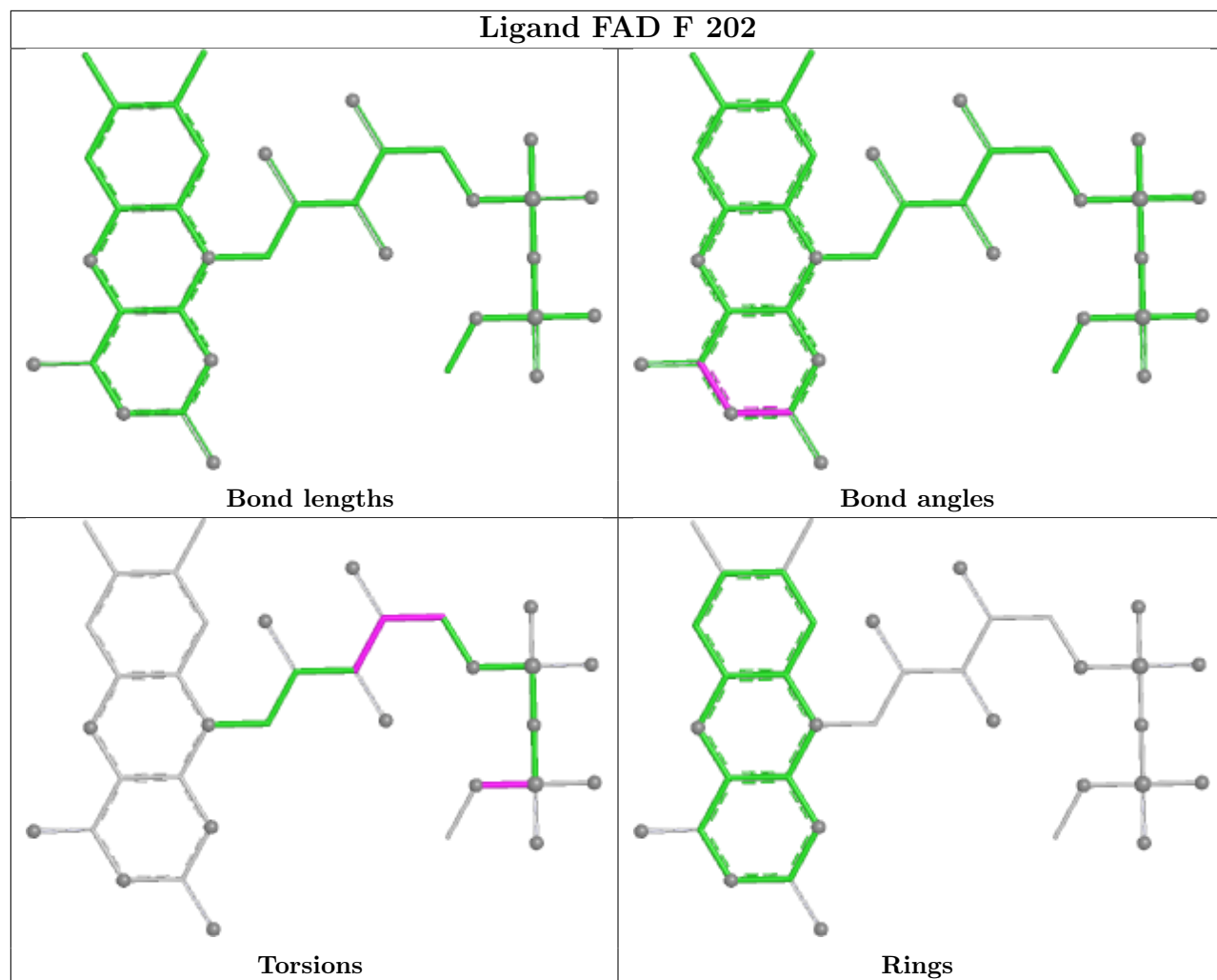


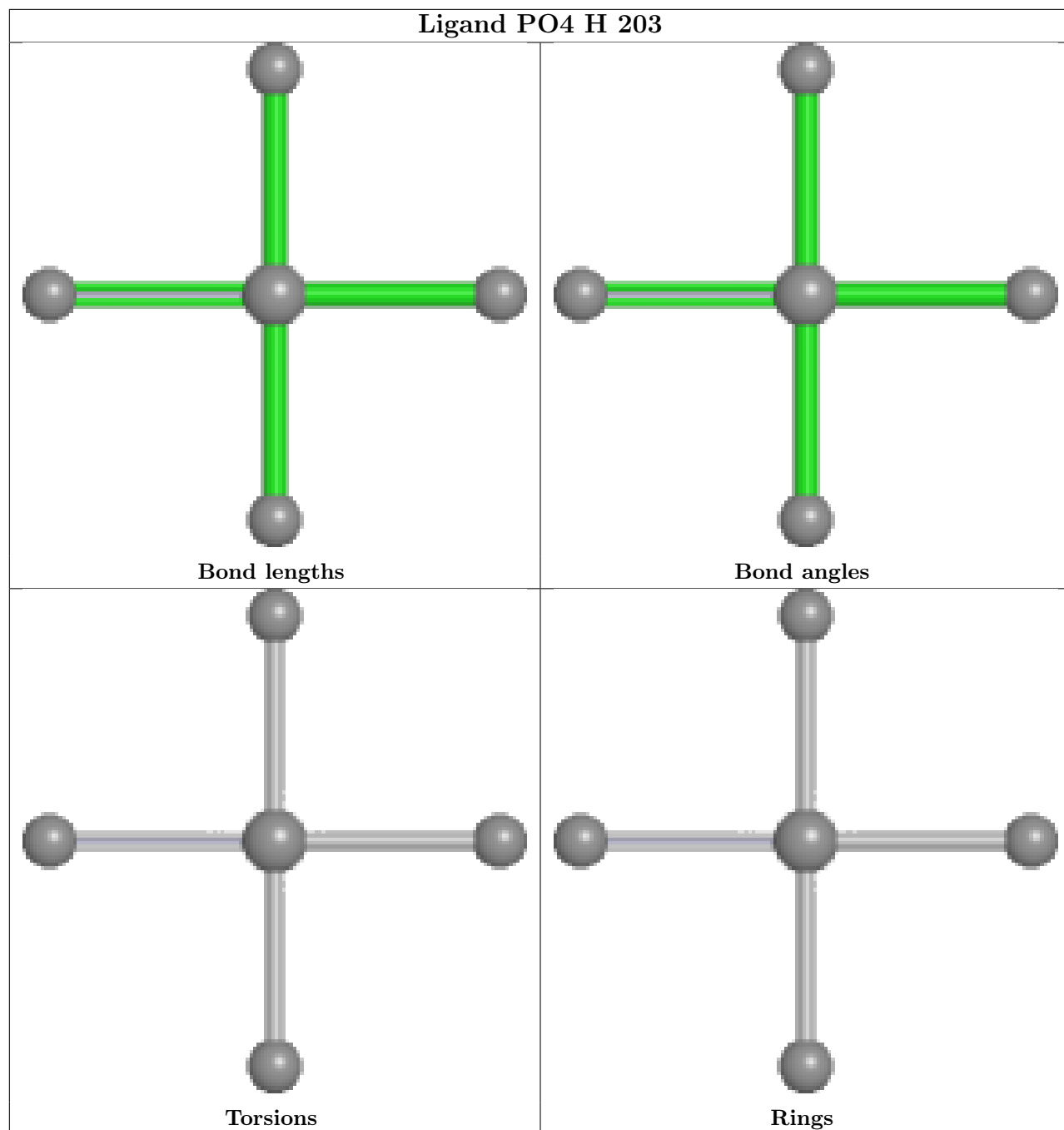


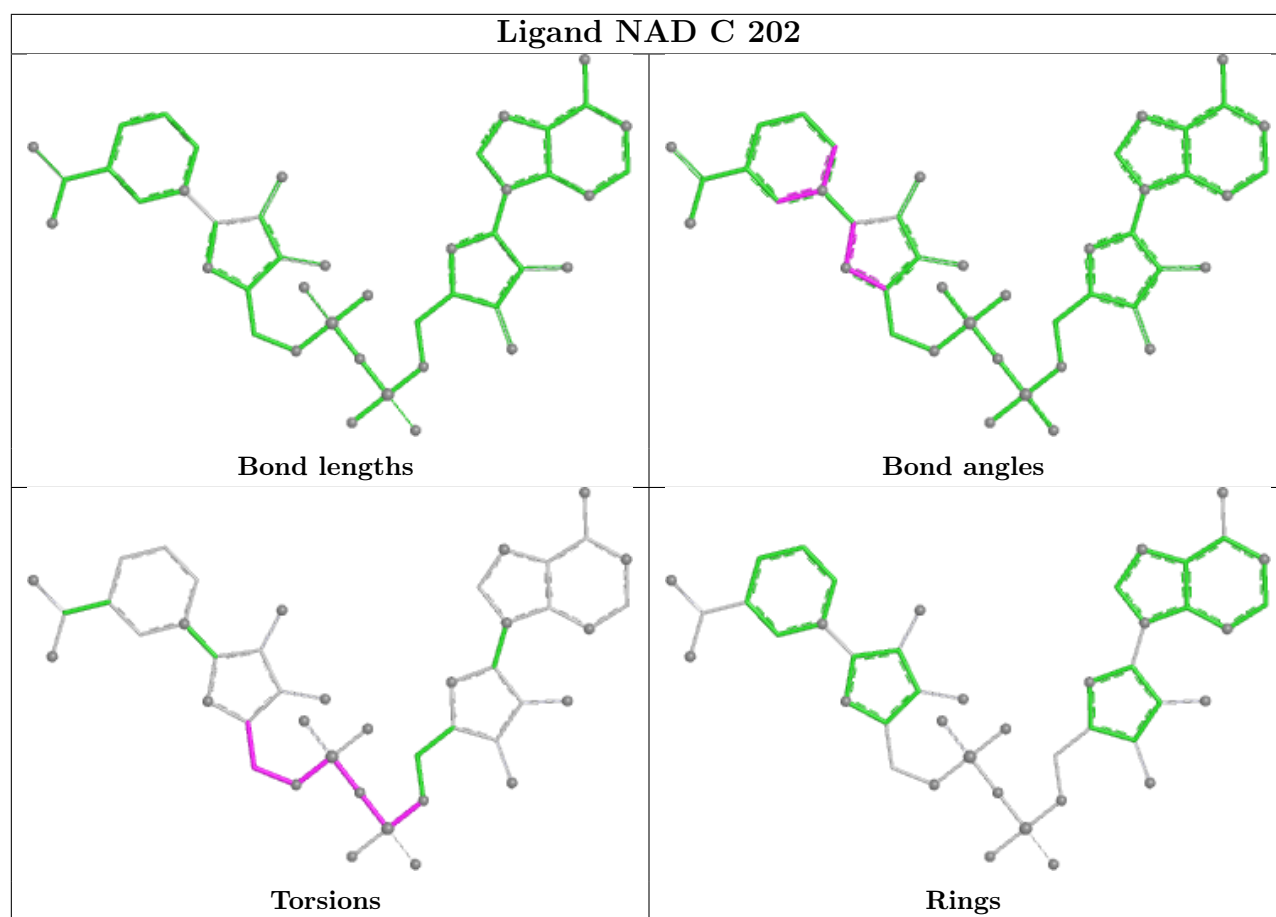


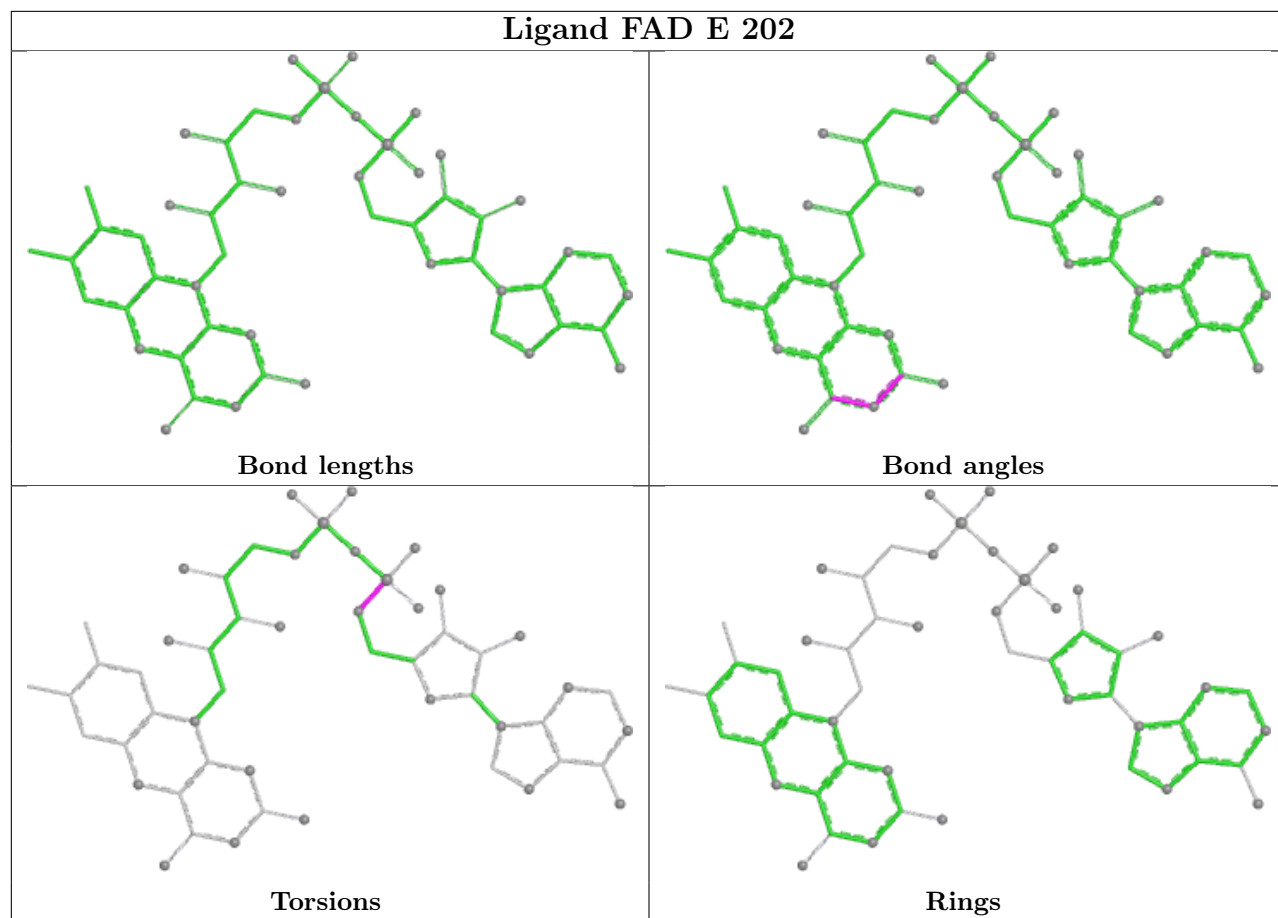


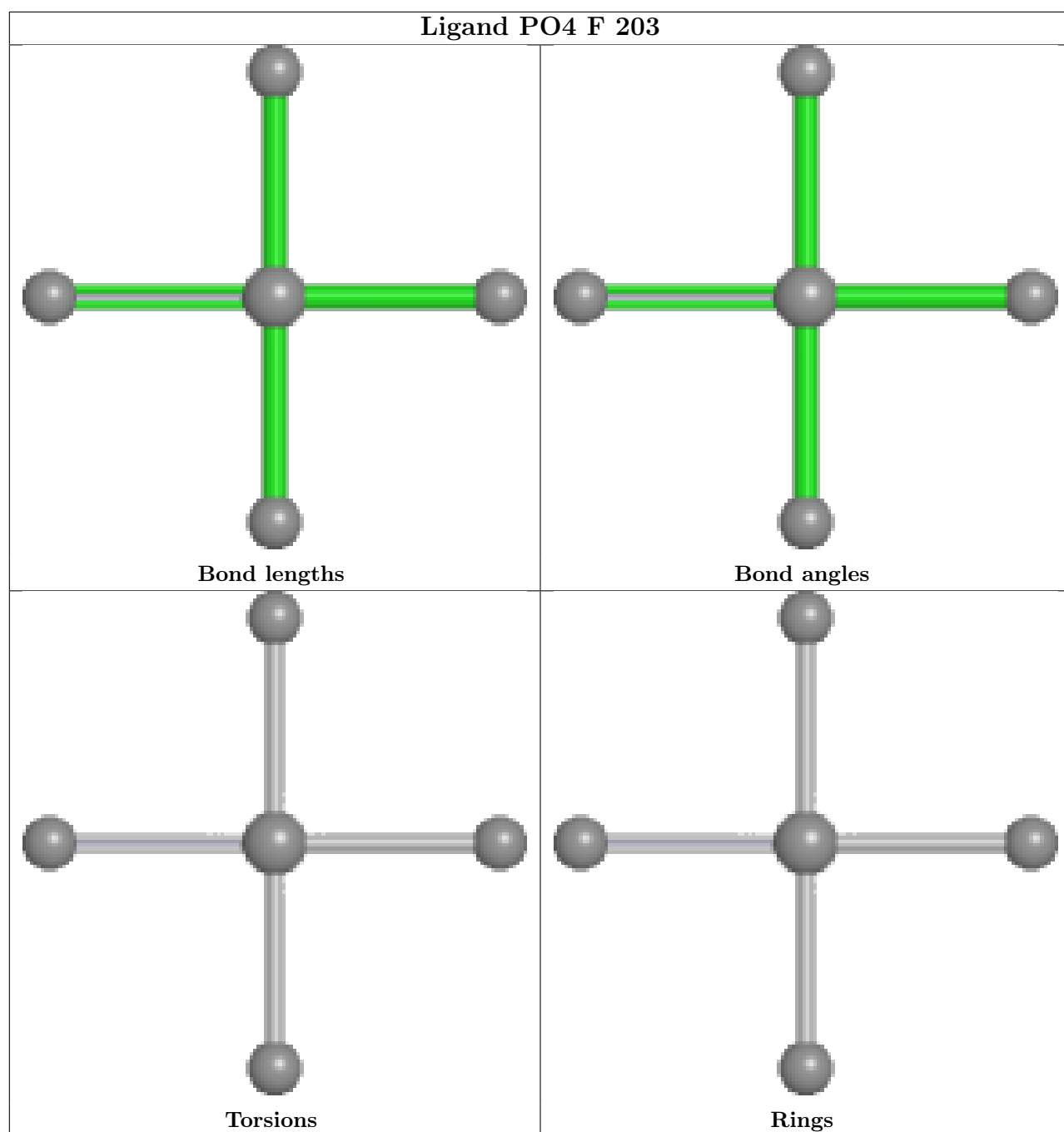


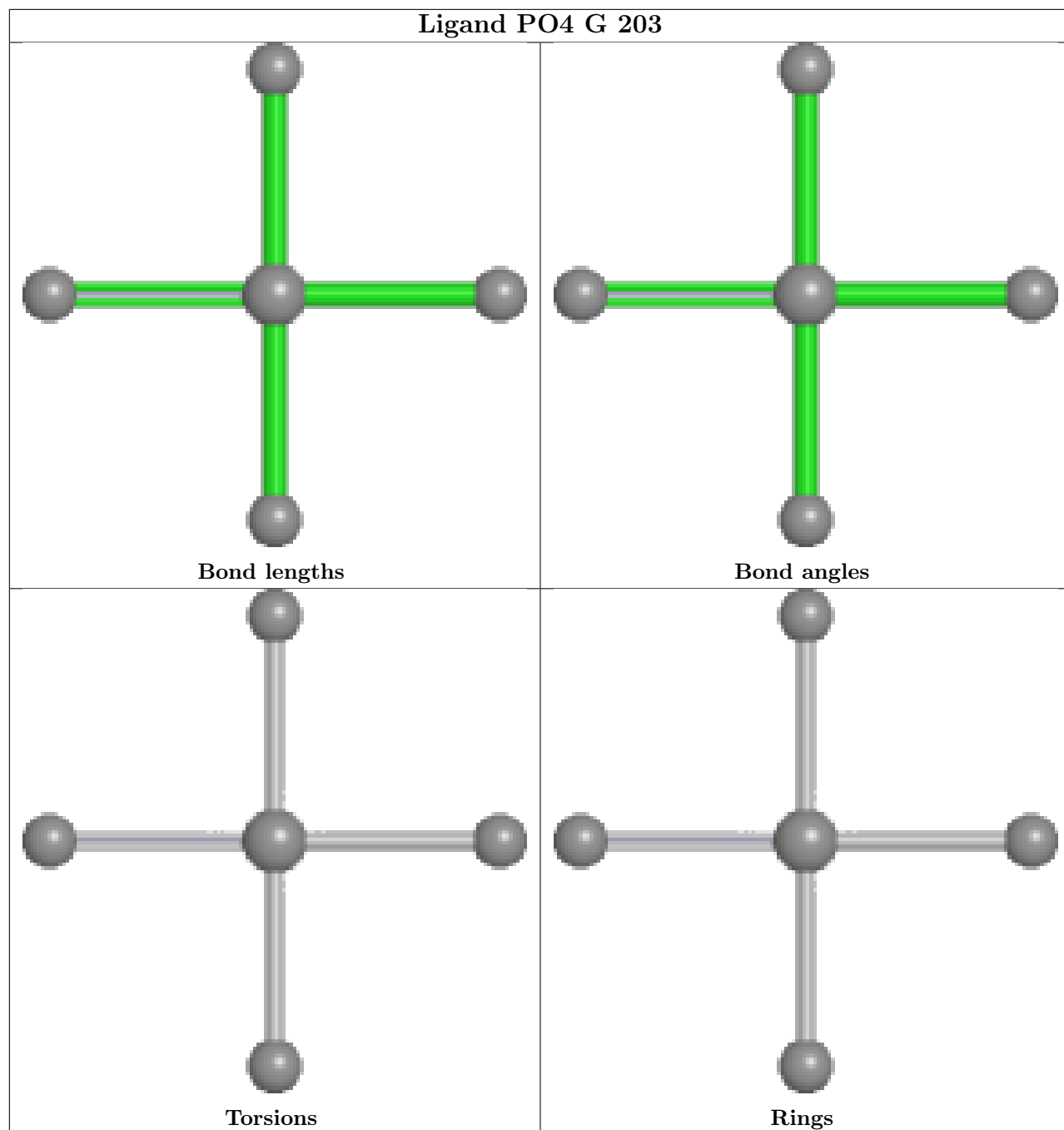


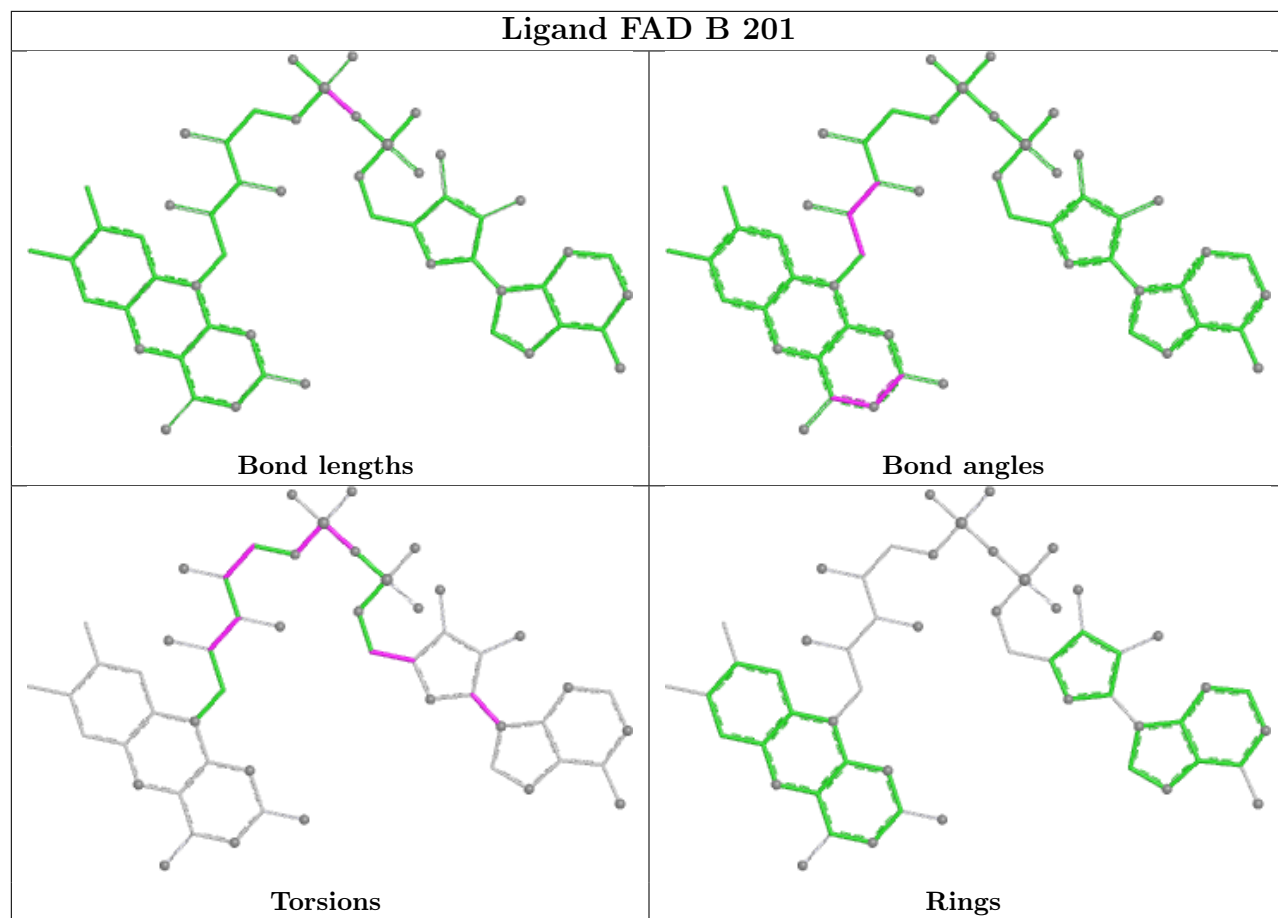


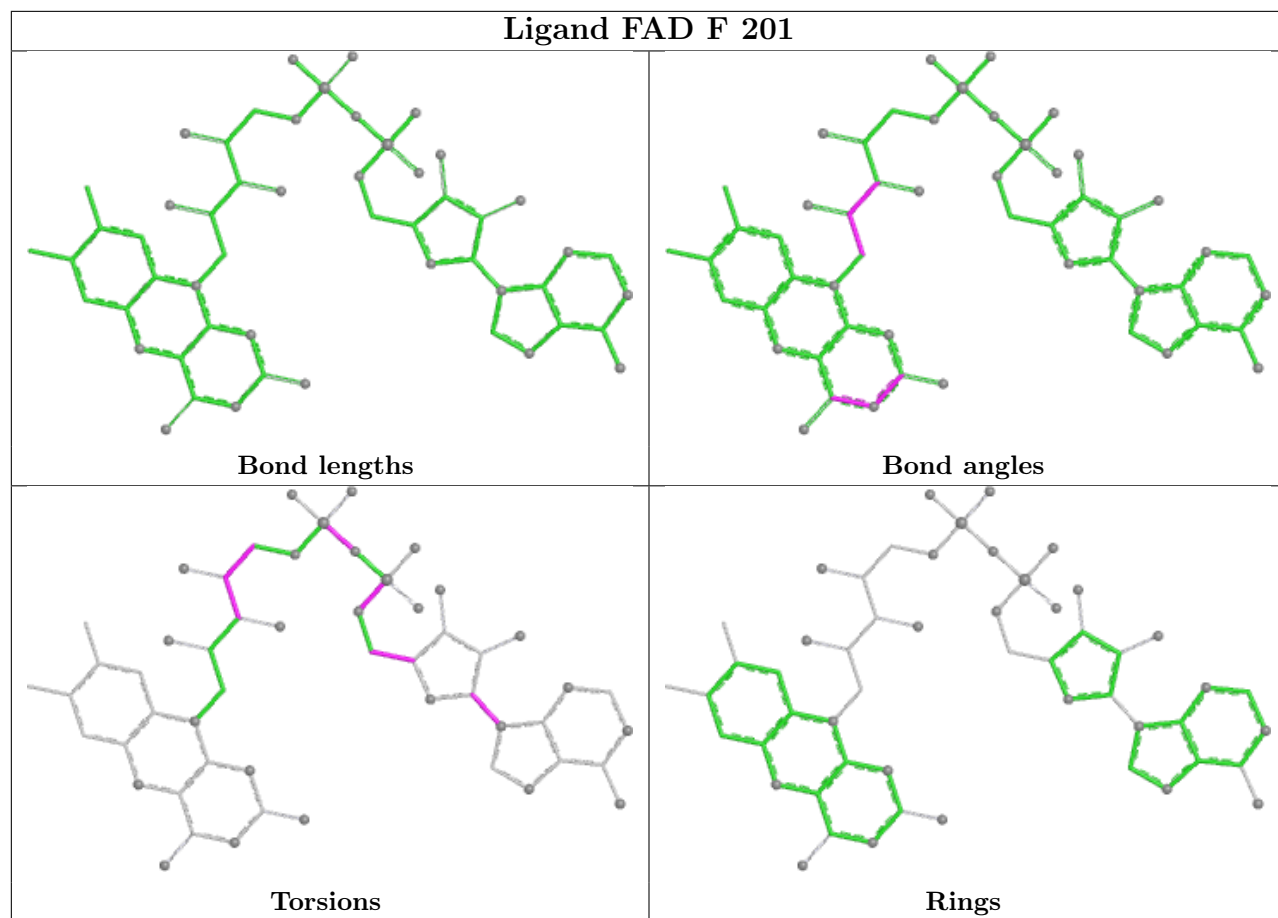


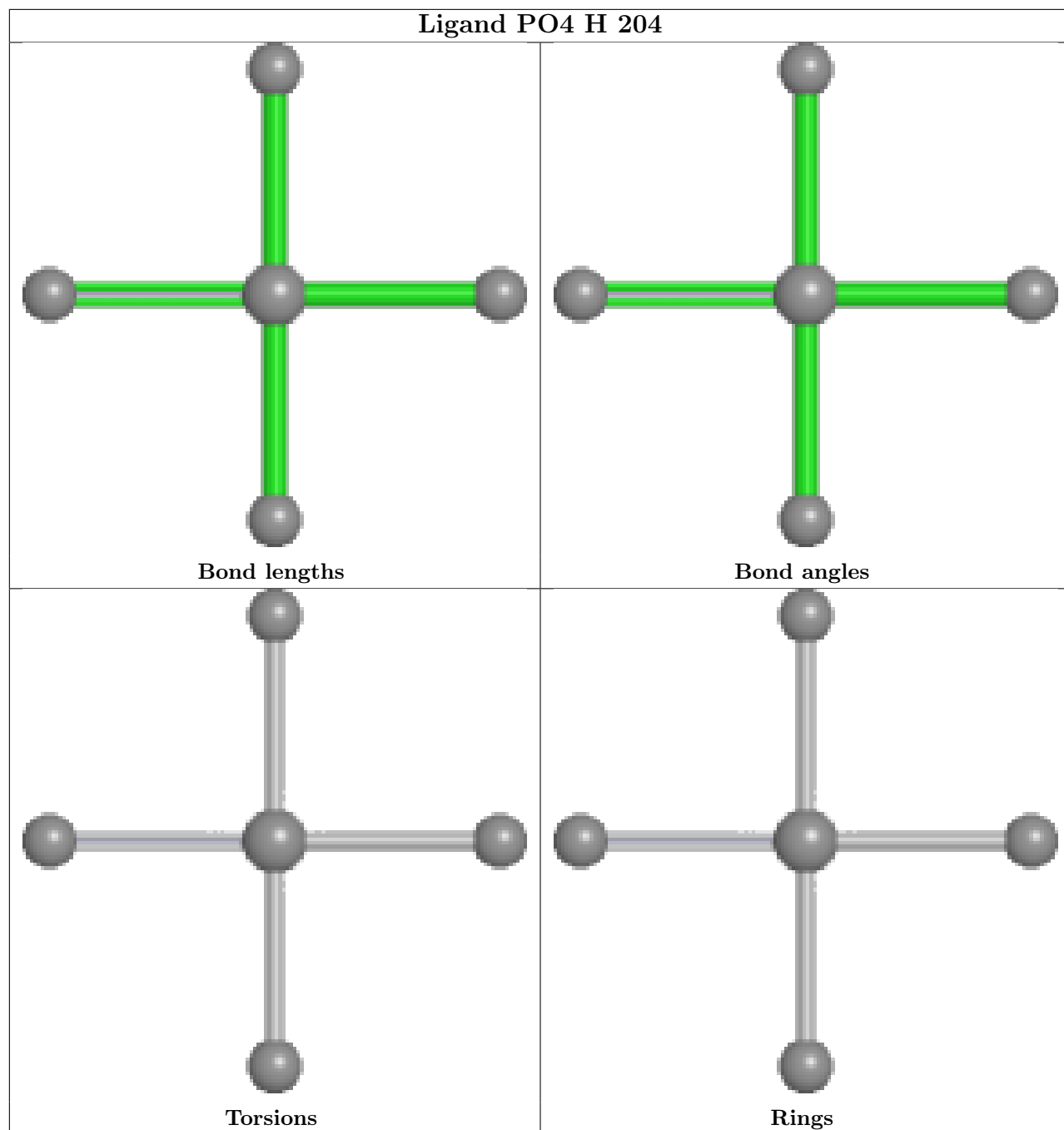


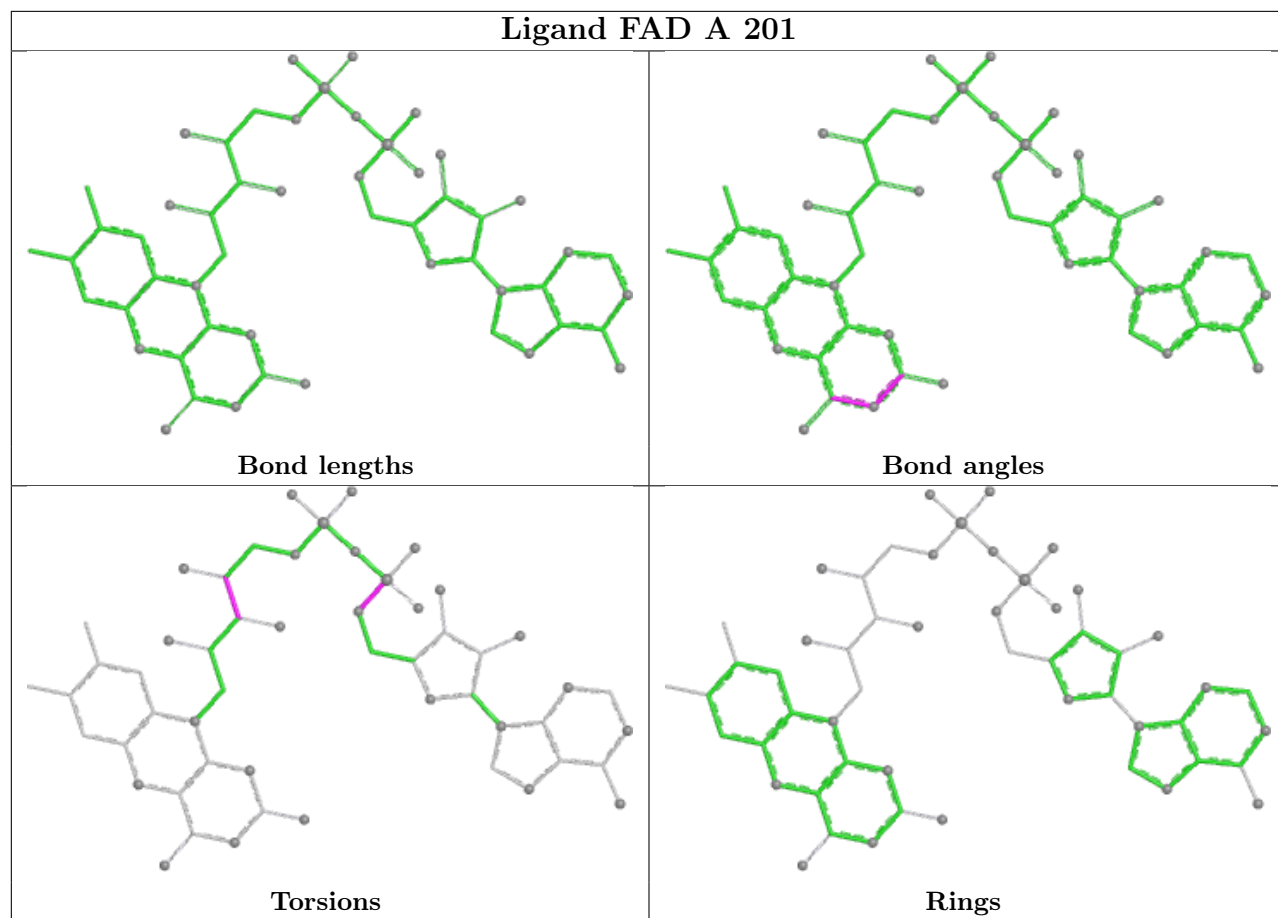


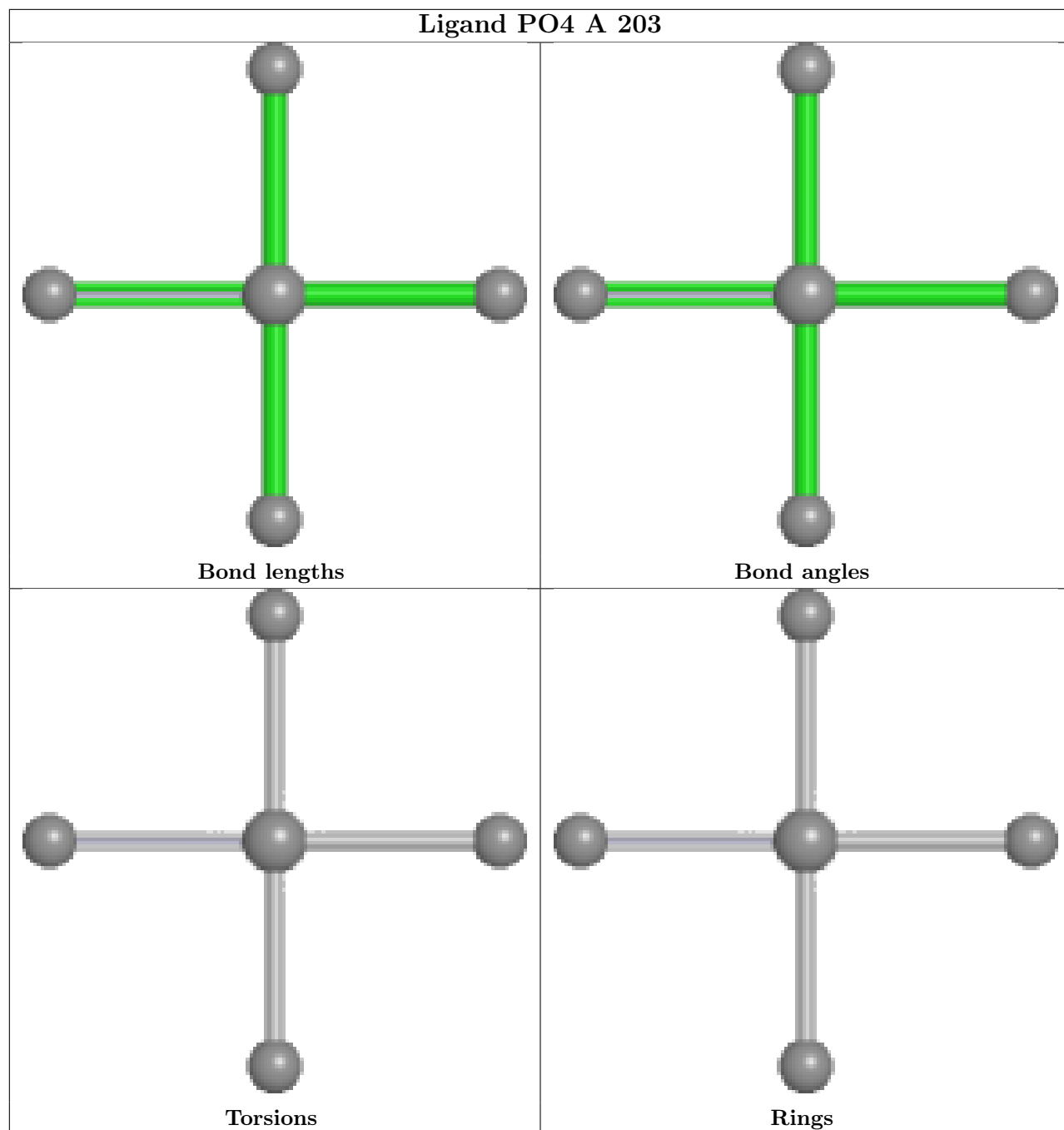


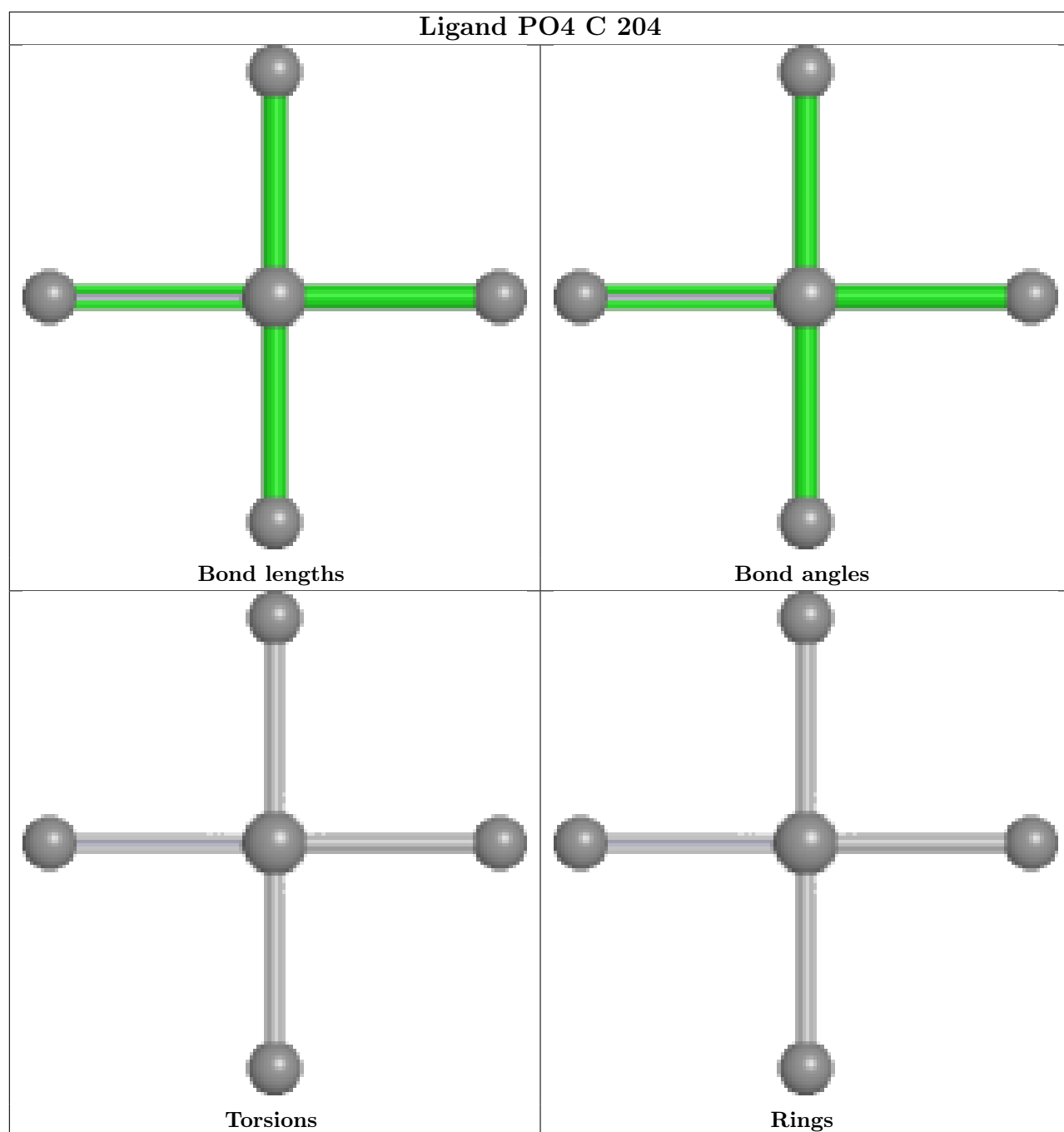


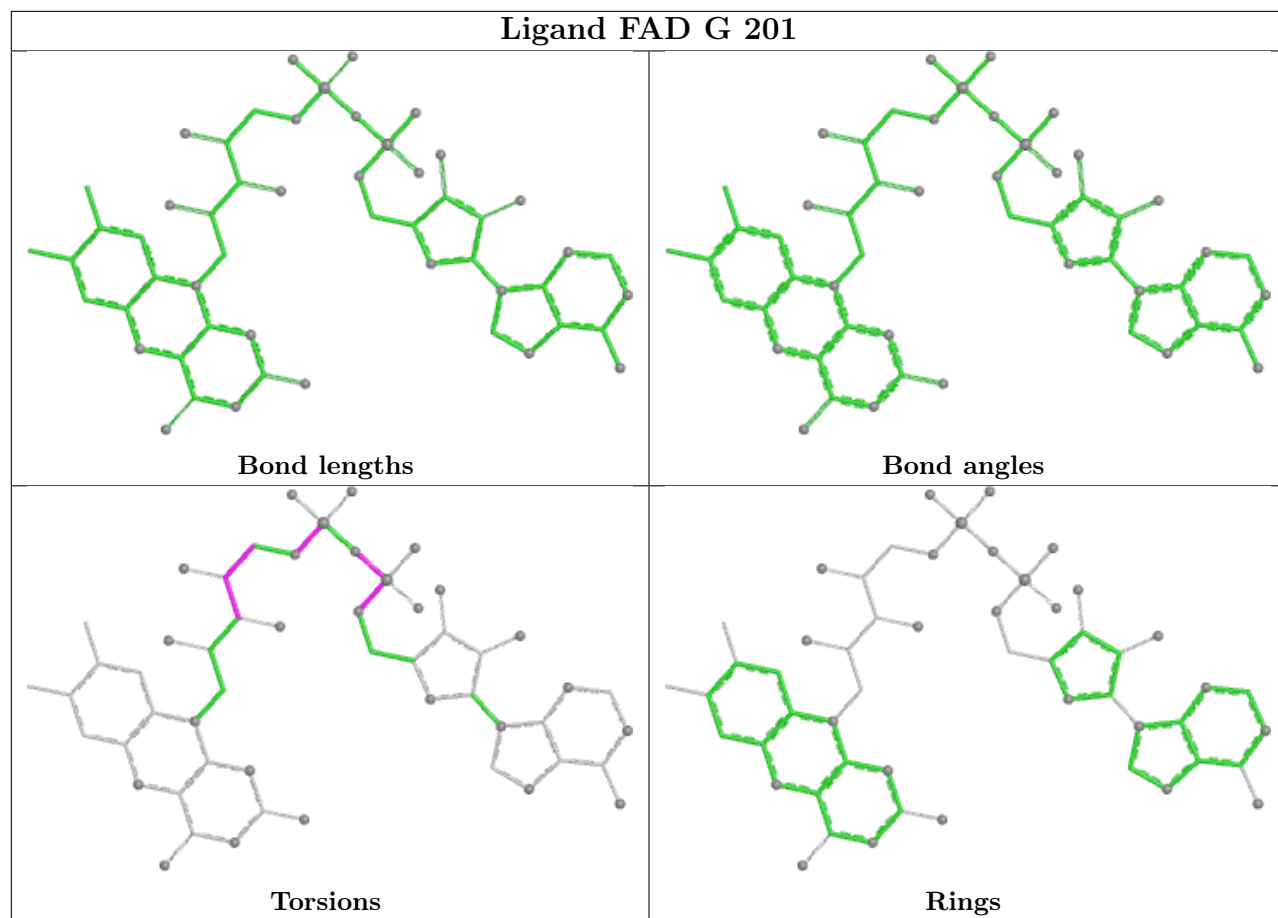


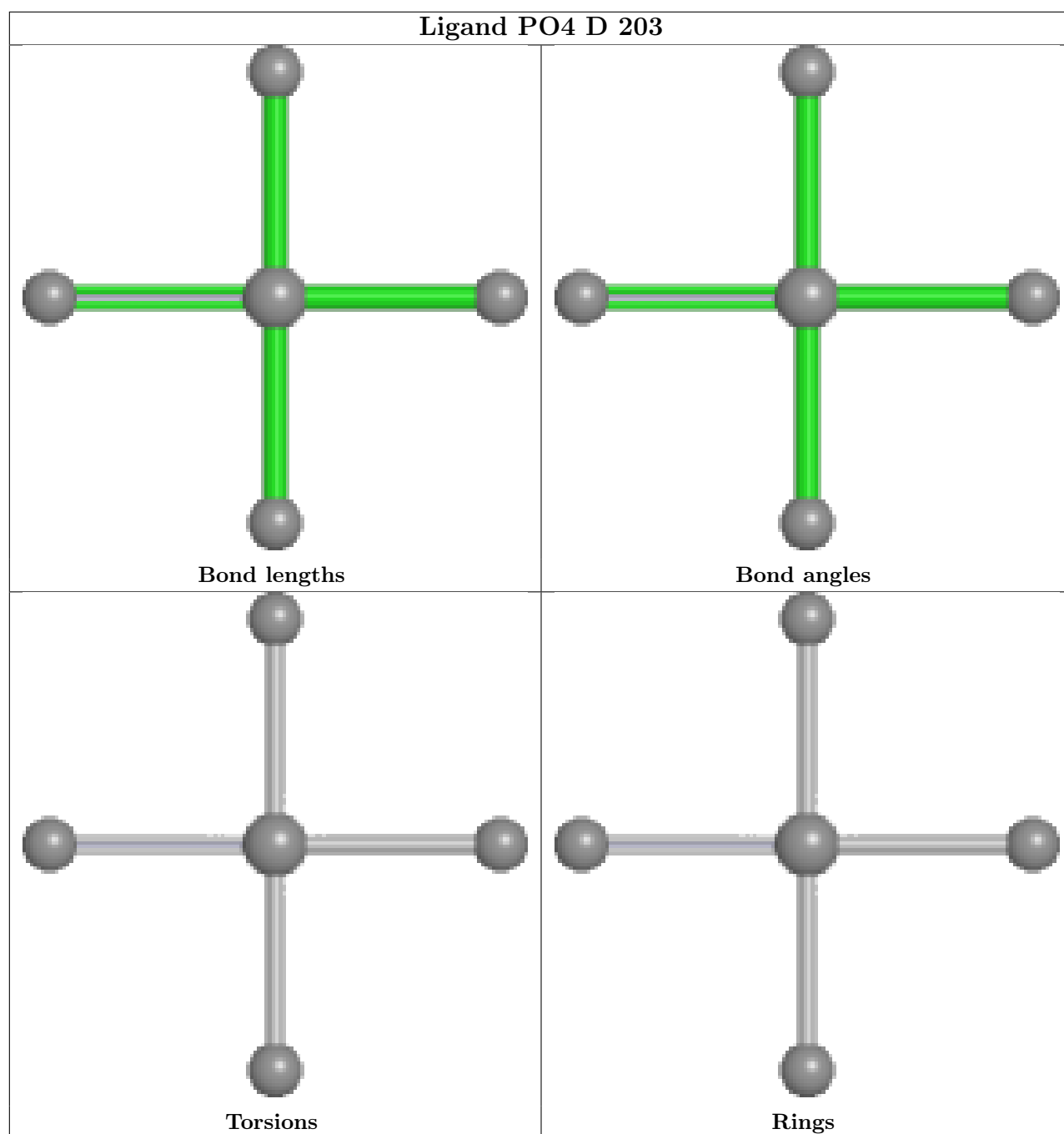


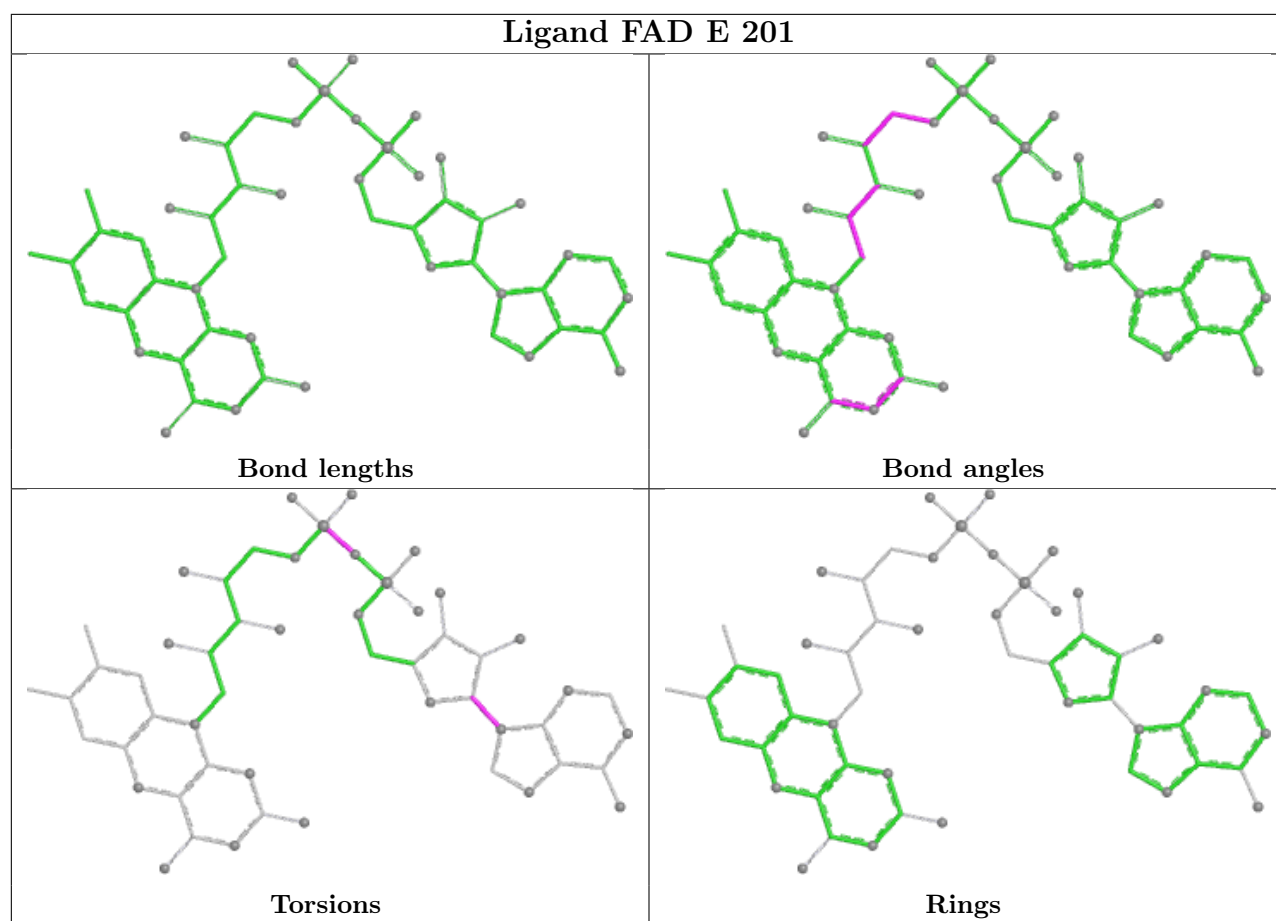


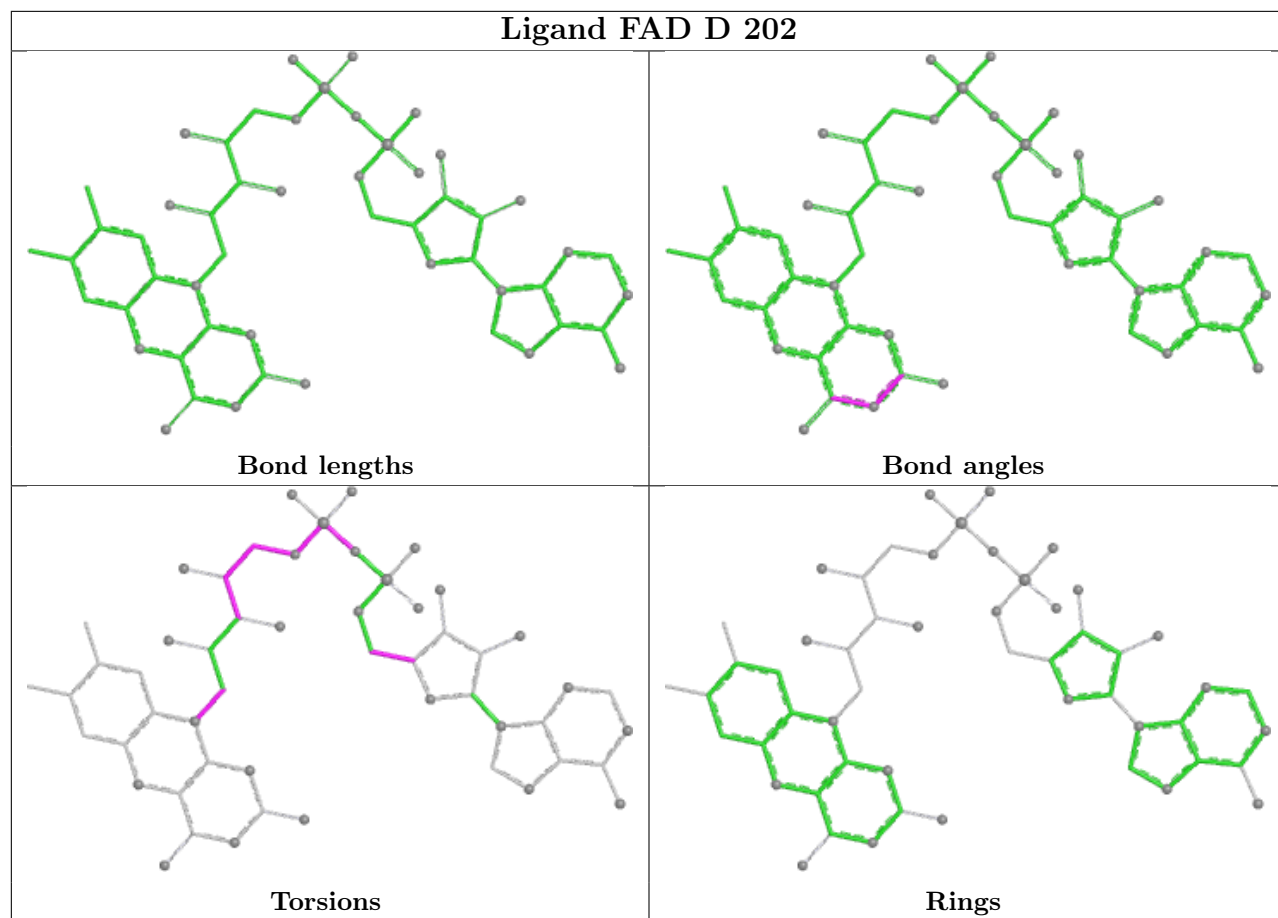












5.7 Other polymers [i](#)

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	170/199 (85%)	0.24	12 (7%)	22	19	10, 20, 45, 61	2 (1%)
1	B	171/199 (85%)	0.11	5 (2%)	53	55	12, 19, 42, 50	2 (1%)
1	C	172/199 (86%)	0.17	8 (4%)	36	35	10, 20, 38, 47	2 (1%)
1	D	172/199 (86%)	0.14	3 (1%)	69	71	12, 21, 38, 51	2 (1%)
1	E	168/199 (84%)	0.17	5 (2%)	52	53	12, 21, 37, 69	2 (1%)
1	F	175/199 (87%)	0.24	4 (2%)	61	63	11, 22, 43, 53	2 (1%)
1	G	172/199 (86%)	-0.01	4 (2%)	61	63	10, 17, 33, 46	2 (1%)
1	H	178/199 (89%)	0.26	5 (2%)	55	56	12, 22, 44, 56	2 (1%)
All	All	1378/1592 (86%)	0.17	46 (3%)	49	50	10, 20, 41, 69	16 (1%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	158	PRO	4.3
1	A	174	TRP	4.3
1	A	14	PRO	4.0
1	A	13	ALA	3.9
1	C	44	GLU	3.2
1	A	161	PRO	3.2
1	E	156	PRO	3.2
1	G	124	SER	3.0
1	F	18	ASP	3.0
1	H	70	ASP	3.0
1	A	158	PRO	2.9
1	E	157	ARG	2.8
1	D	104	ASP	2.8
1	H	41	PRO	2.6
1	E	155	GLY	2.6
1	C	116	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	9	PRO	2.6
1	F	104	ASP	2.5
1	B	14	PRO	2.5
1	G	42	ASP	2.5
1	F	109	ASP	2.4
1	H	176	VAL	2.4
1	A	41	PRO	2.4
1	E	119	GLY	2.4
1	B	124	SER	2.3
1	B	118	GLY	2.3
1	A	11	ASP	2.3
1	A	160	VAL	2.3
1	A	157	ARG	2.3
1	B	175	PRO	2.3
1	C	105	ASP	2.2
1	C	176	VAL	2.2
1	F	2	PRO	2.2
1	C	40	GLY	2.2
1	C	124	SER	2.2
1	C	104	ASP	2.2
1	A	5	PRO	2.2
1	A	12	LEU	2.1
1	G	44	GLU	2.1
1	D	176	VAL	2.1
1	D	44	GLU	2.1
1	C	143	ASP	2.1
1	B	13	ALA	2.1
1	H	104	ASP	2.1
1	H	1	MET	2.0
1	G	174	TRP	2.0

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 ⓘ

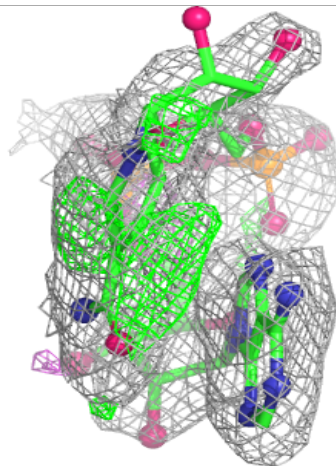
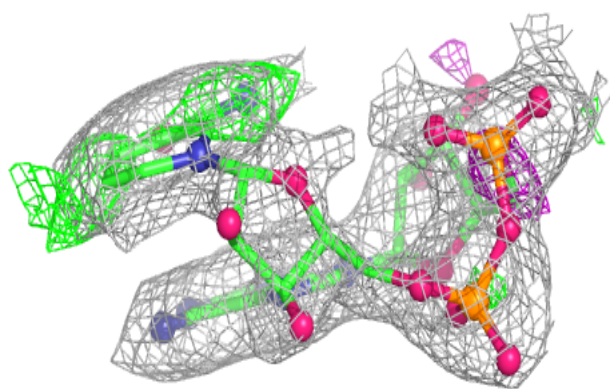
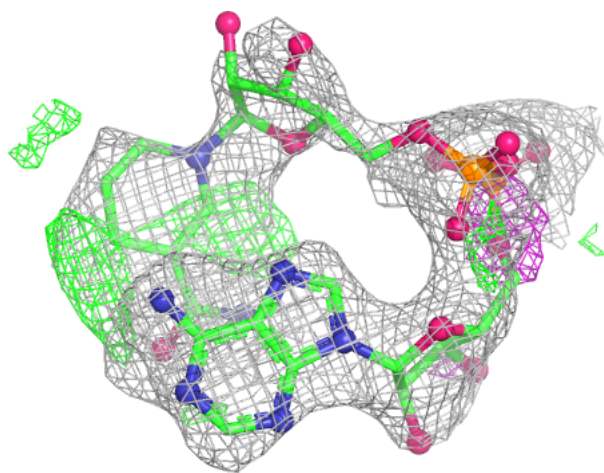
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAI	H	202	44/44	0.79	0.16	28,44,55,57	0
2	FAD	F	201	53/53	0.83	0.14	28,34,47,50	0
4	NAD	C	202	44/44	0.87	0.11	24,35,47,51	0
2	FAD	D	202	53/53	0.87	0.12	22,31,52,55	0
3	PO4	H	203	5/5	0.89	0.10	52,53,54,54	0
2	FAD	B	201	53/53	0.89	0.10	13,20,29,34	0
3	PO4	A	203	5/5	0.89	0.12	43,43,46,47	0
3	PO4	D	203	5/5	0.90	0.12	42,42,43,45	0
3	PO4	C	203	5/5	0.90	0.11	43,44,46,46	0
2	FAD	E	201	53/53	0.91	0.10	17,18,23,26	0
2	FAD	D	201	53/53	0.92	0.10	13,17,37,39	0
3	PO4	H	204	5/5	0.92	0.14	39,39,40,42	0
3	PO4	E	203	5/5	0.93	0.09	44,46,47,48	0
3	PO4	F	204	5/5	0.93	0.11	44,45,46,46	0
3	PO4	B	203	5/5	0.93	0.08	39,39,40,41	0
2	FAD	G	202	53/53	0.93	0.08	14,15,27,31	0
2	FAD	A	202	53/53	0.93	0.09	14,16,27,32	0
3	PO4	D	204	5/5	0.93	0.13	38,38,40,41	0
2	FAD	H	201	36/53	0.94	0.08	11,13,32,37	0
2	FAD	F	202	36/53	0.94	0.08	14,16,39,41	0
2	FAD	C	201	44/53	0.95	0.07	10,14,35,36	0
2	FAD	E	202	53/53	0.96	0.08	12,16,62,65	0
3	PO4	G	203	5/5	0.96	0.07	33,33,34,35	0
3	PO4	C	204	5/5	0.96	0.08	31,31,32,32	0
2	FAD	A	201	53/53	0.96	0.08	9,13,51,52	0
2	FAD	B	202	53/53	0.96	0.08	9,14,49,52	0
2	FAD	G	201	53/53	0.96	0.08	8,13,51,52	0
3	PO4	F	203	5/5	0.97	0.07	42,43,43,44	0

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

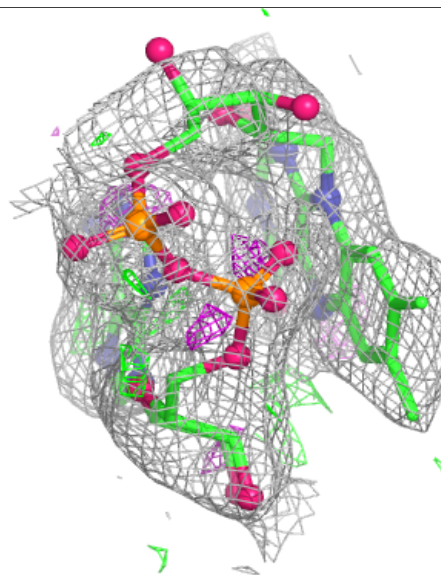
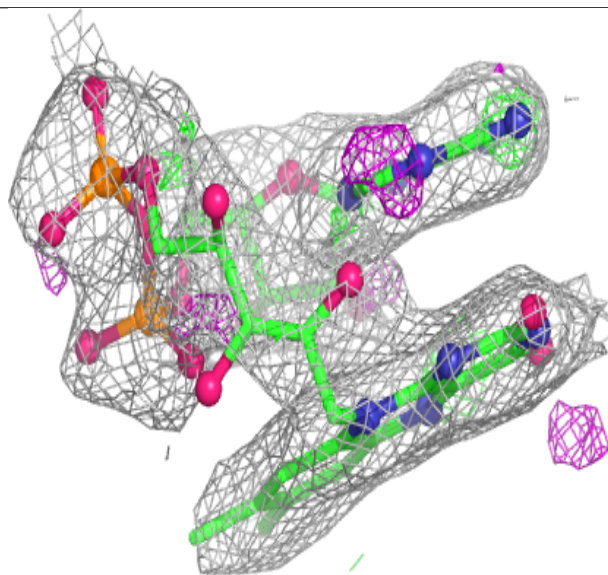
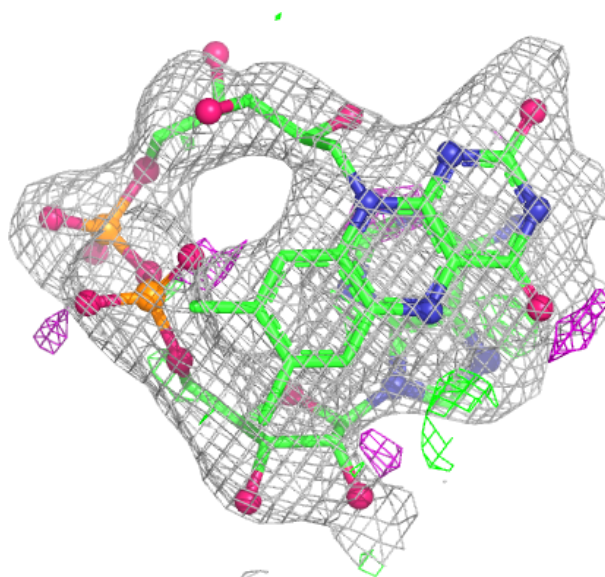
Electron density around NAI H 202:

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



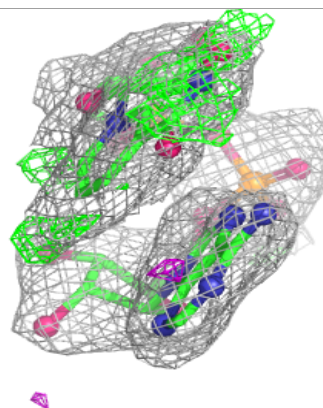
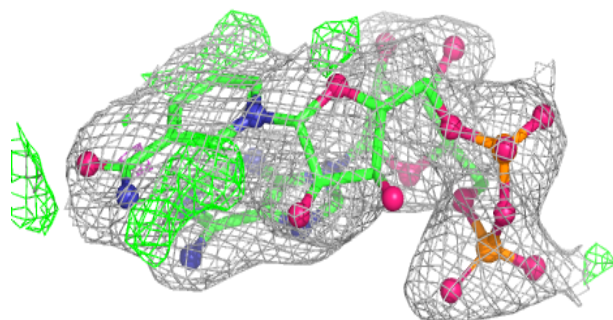
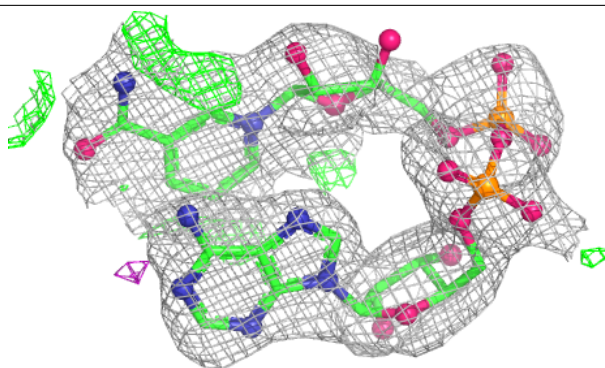
Electron density around FAD F 201:

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



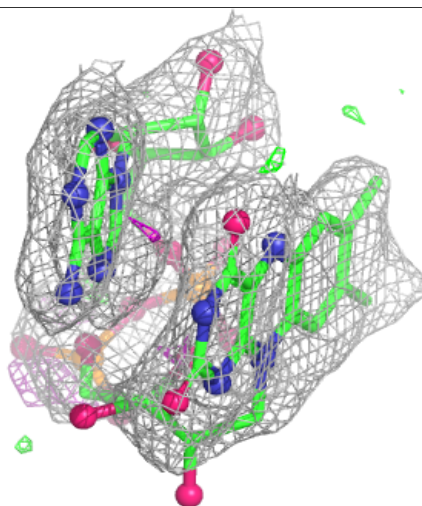
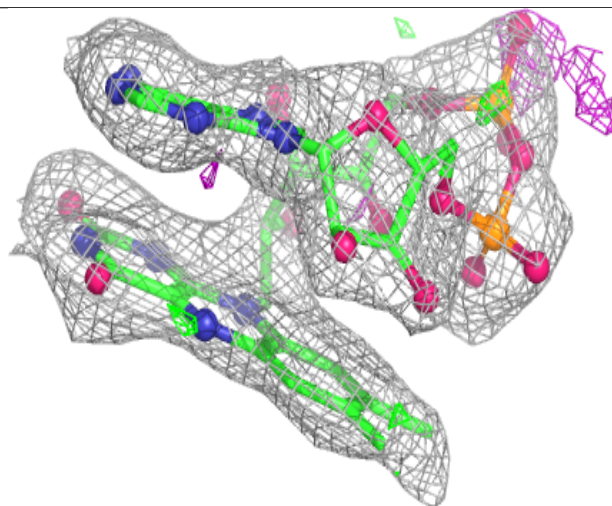
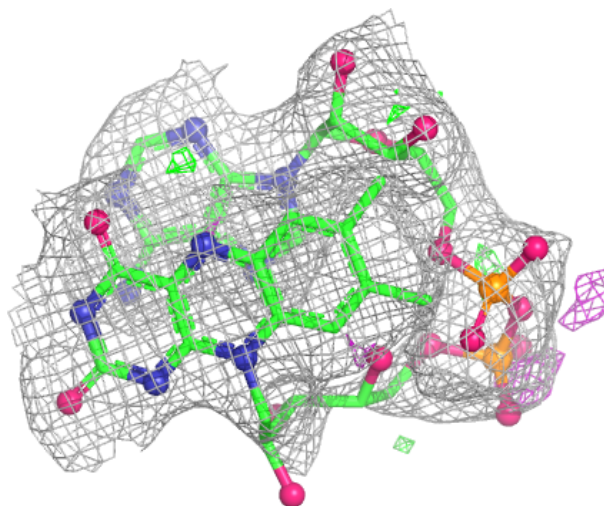
Electron density around NAD C 202:

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



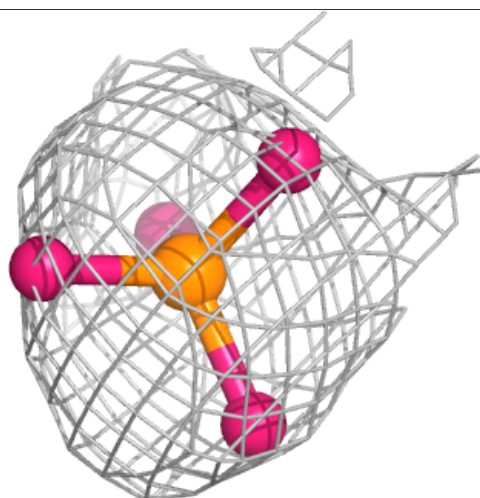
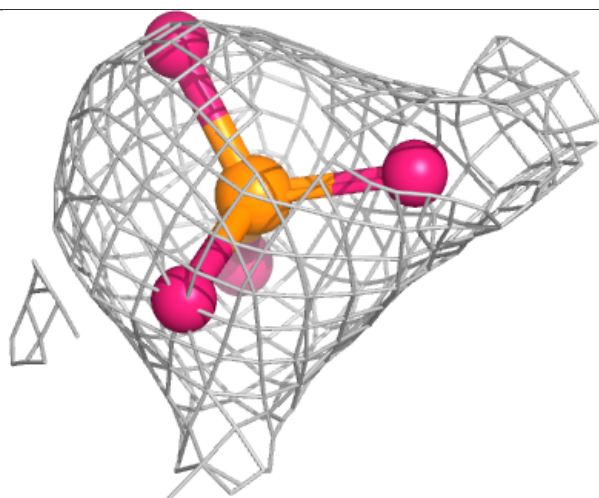
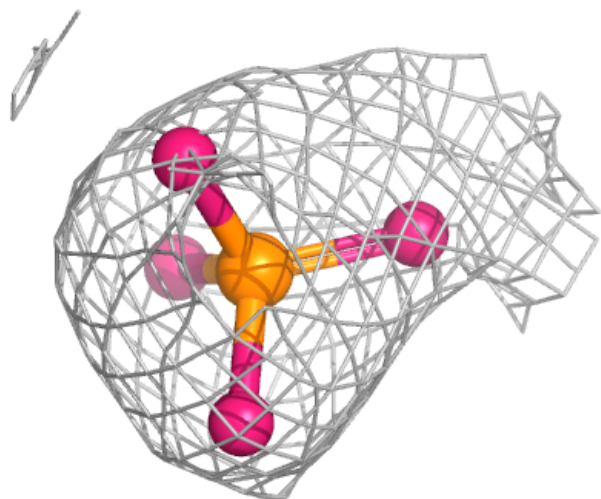
Electron density around FAD D 202:

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



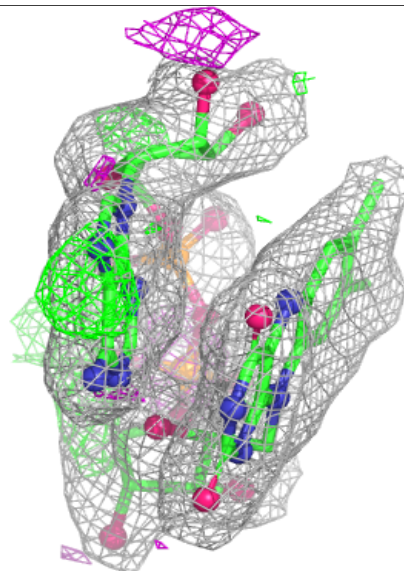
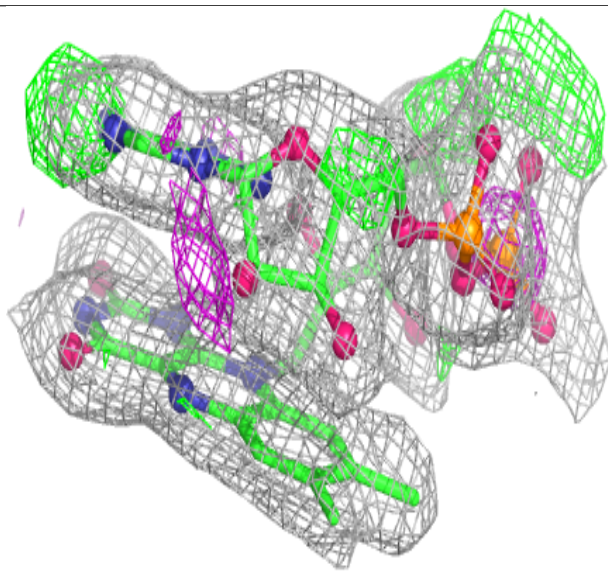
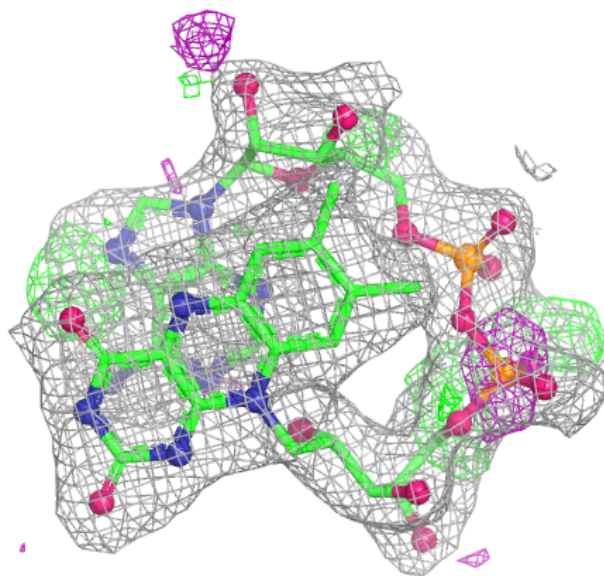
Electron density around PO4 H 203:

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



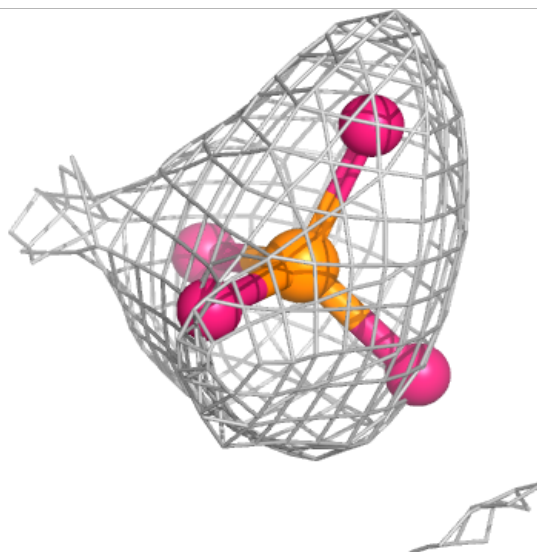
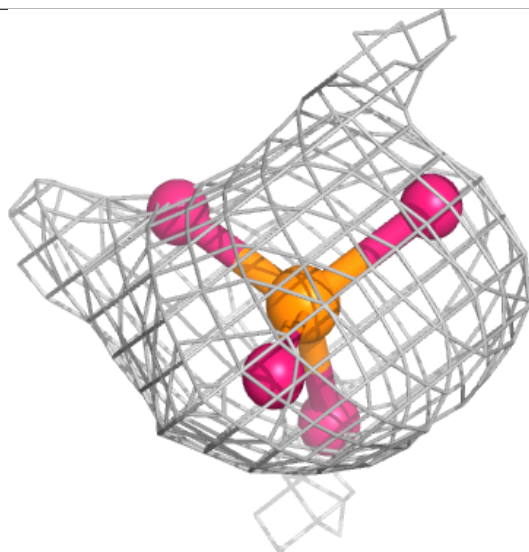
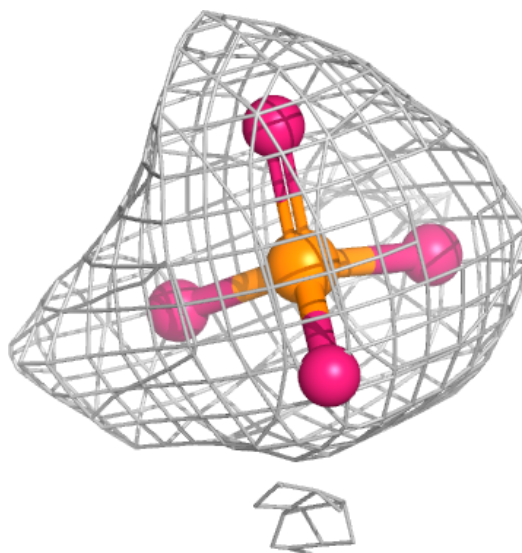
Electron density around FAD B 201:

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



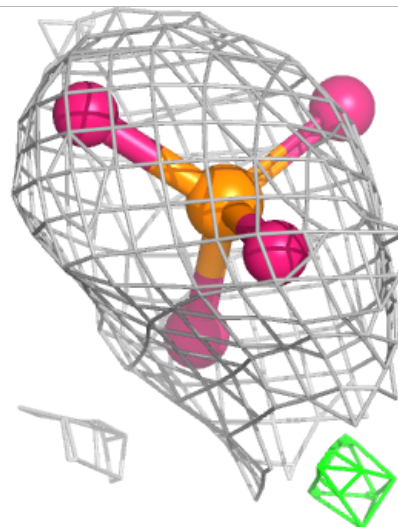
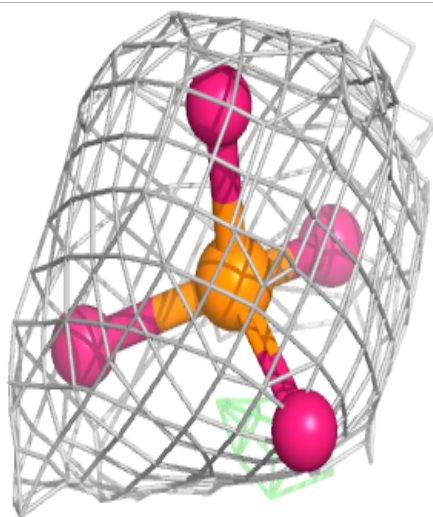
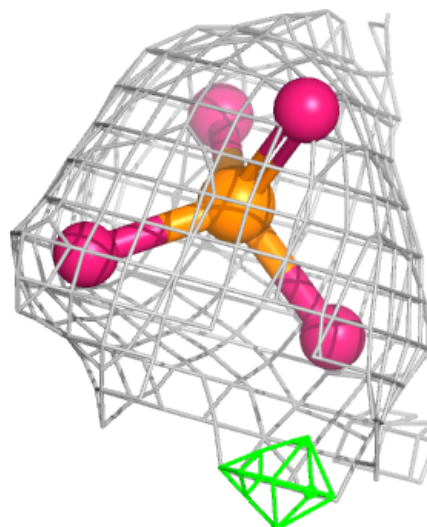
Electron density around PO4 A 203:

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



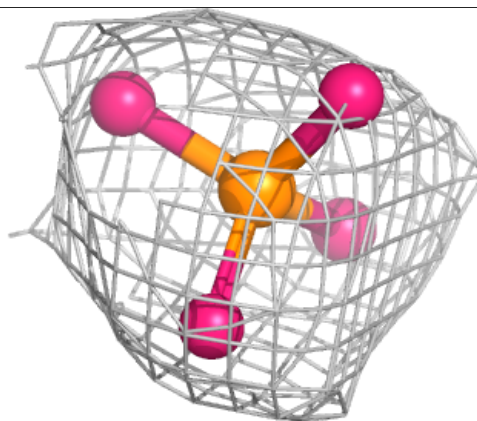
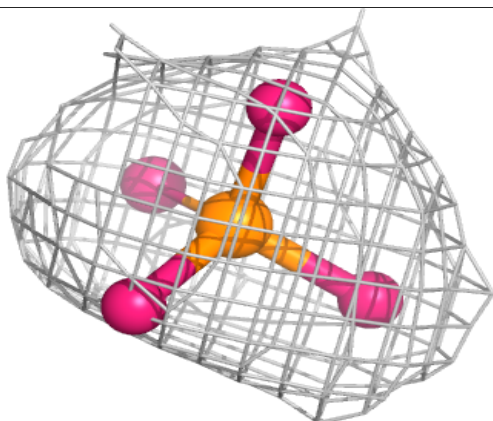
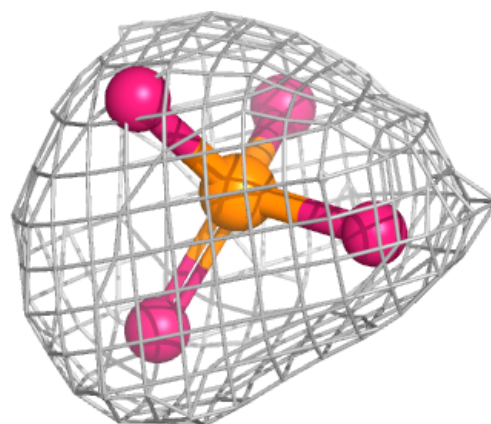
Electron density around PO4 D 203:

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



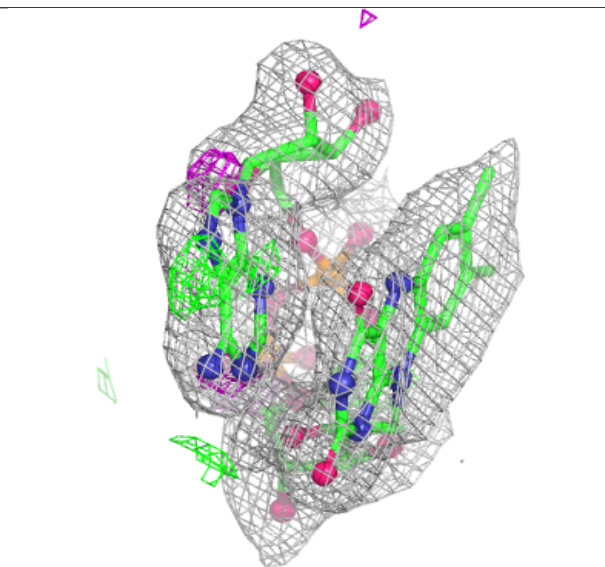
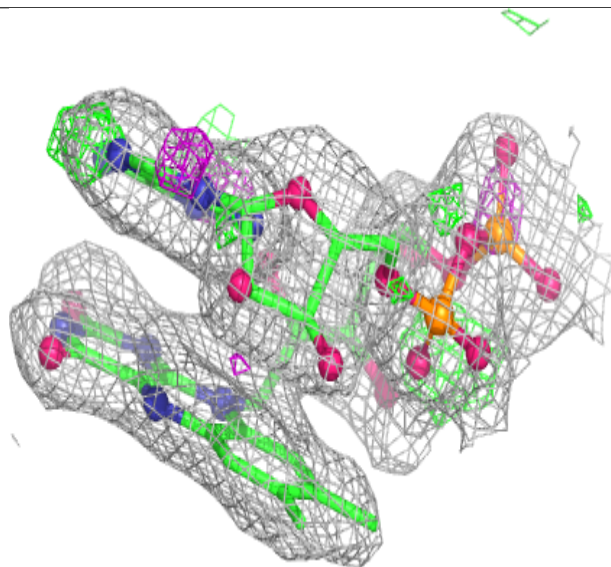
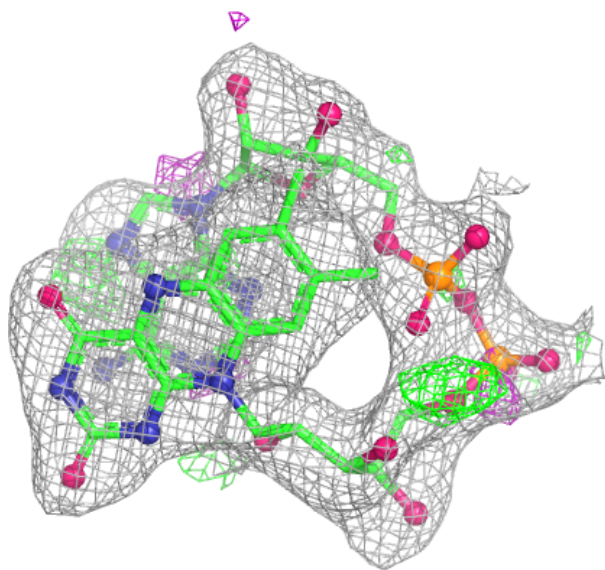
Electron density around PO4 C 203:

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



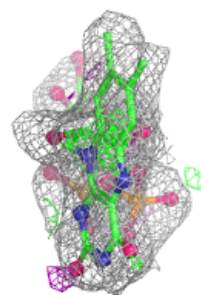
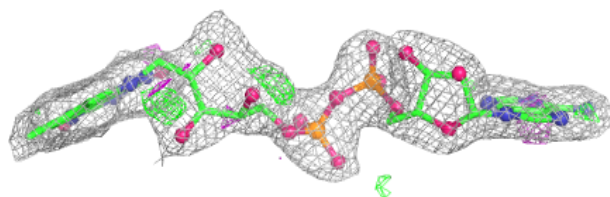
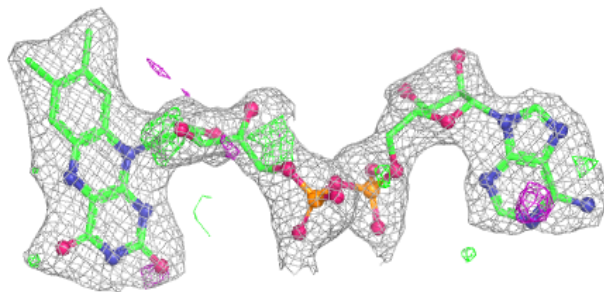
Electron density around FAD E 201:

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



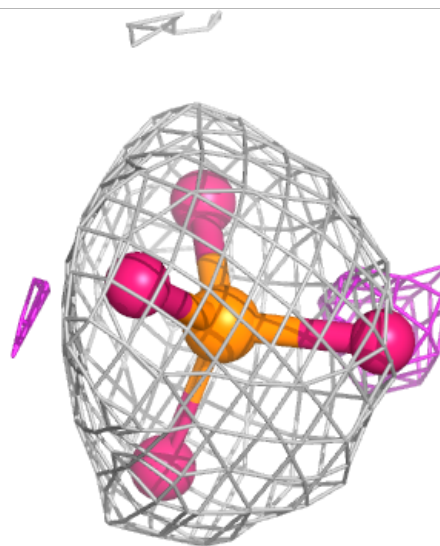
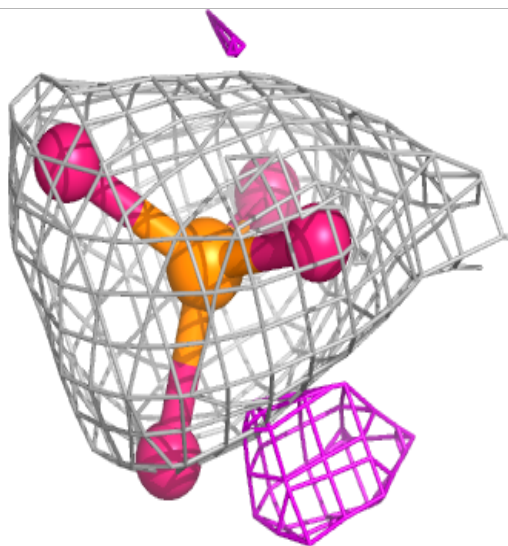
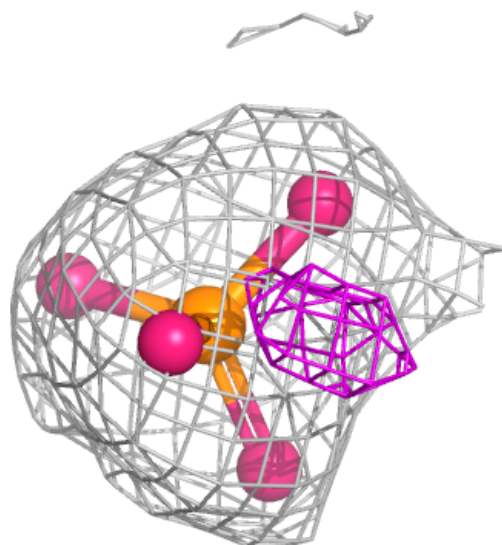
Electron density around FAD D 201:

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



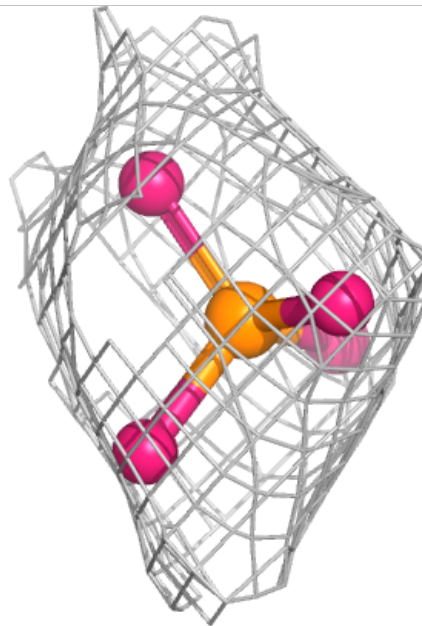
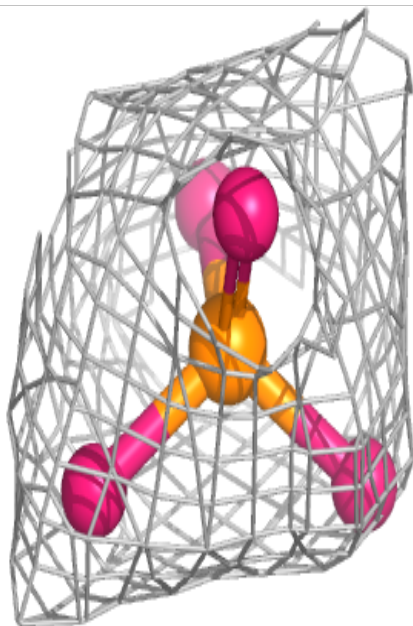
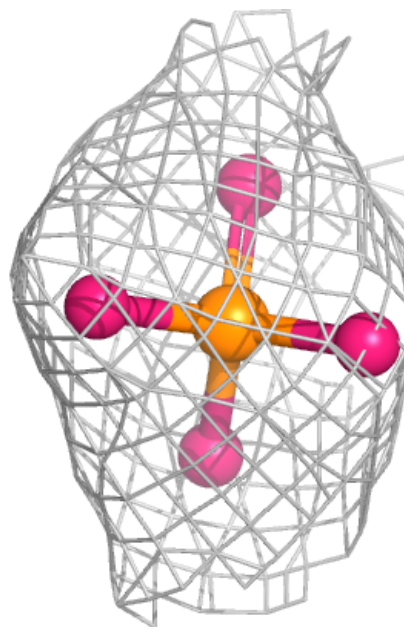
Electron density around PO4 H 204:

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



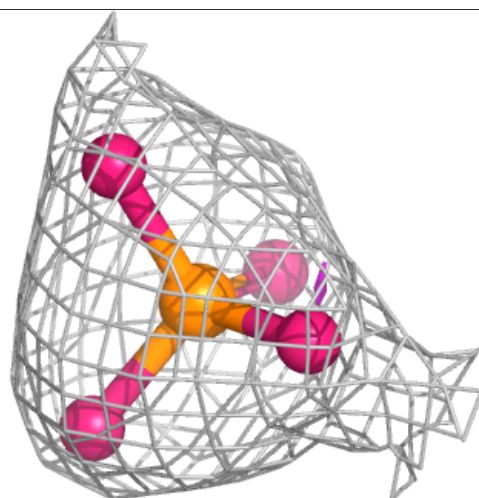
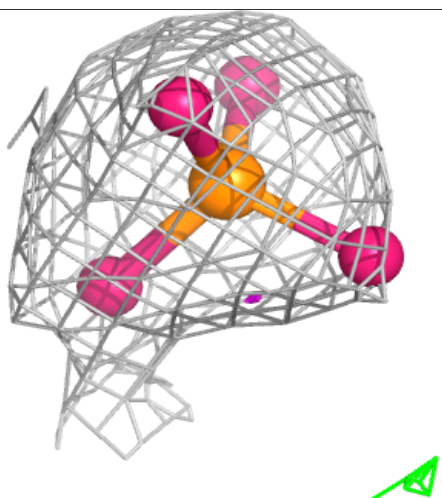
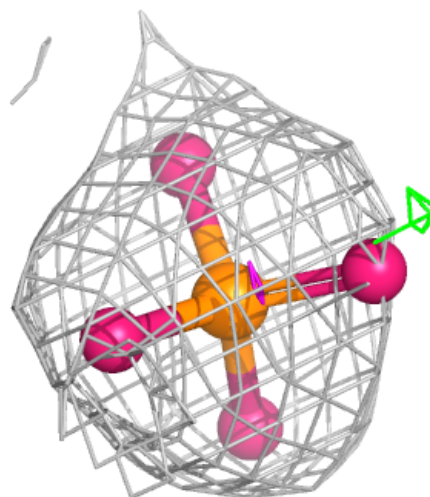
Electron density around PO4 E 203:

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



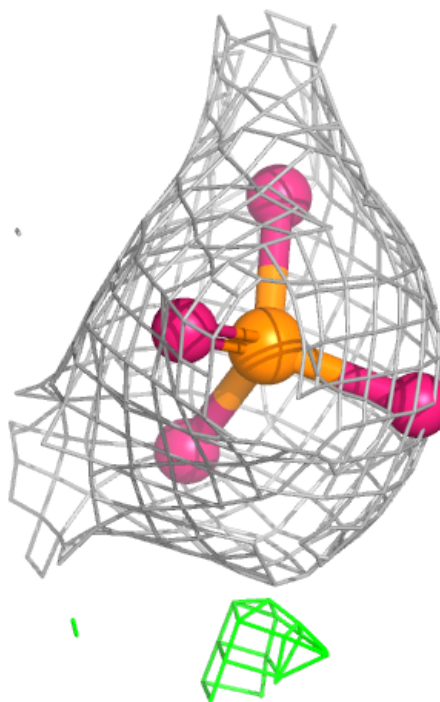
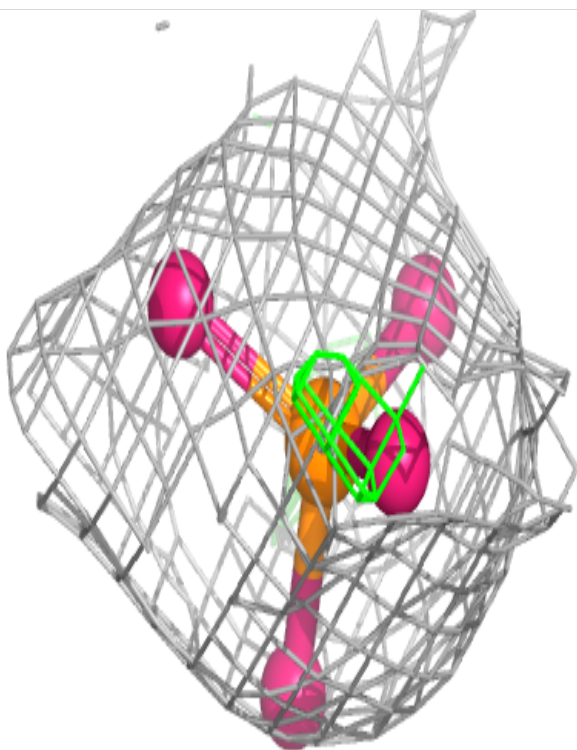
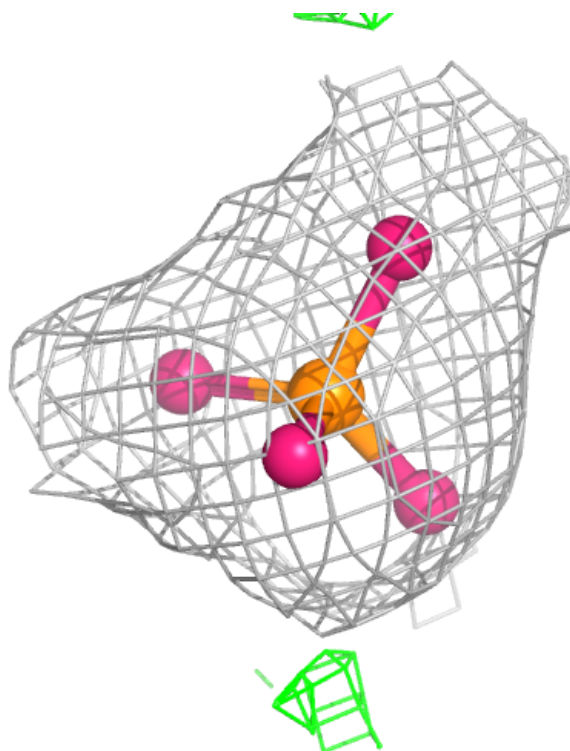
Electron density around PO4 F 204:

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



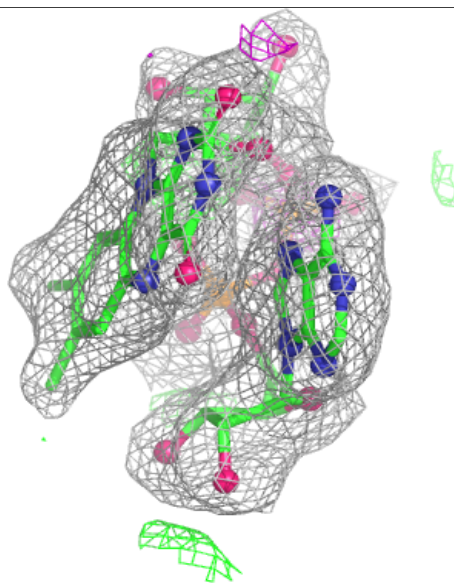
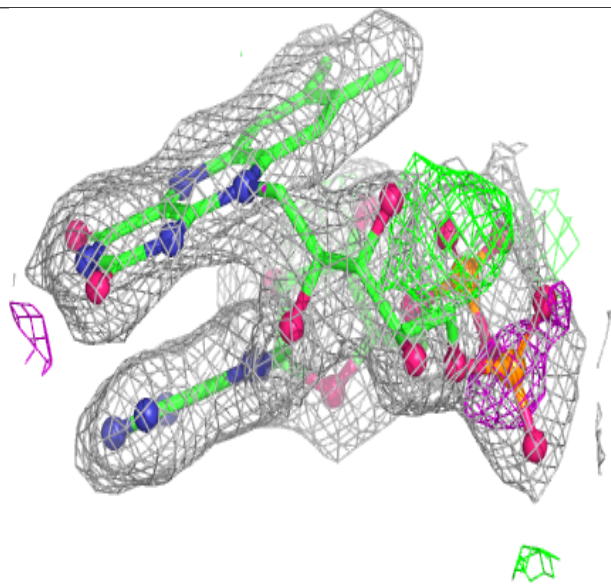
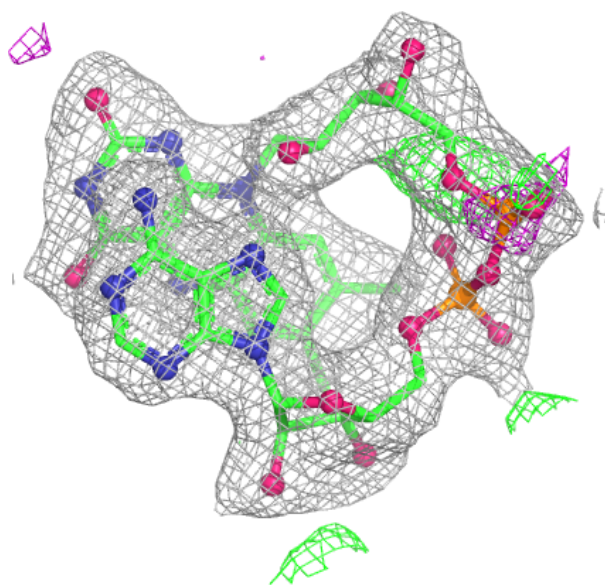
Electron density around PO4 B 203:

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



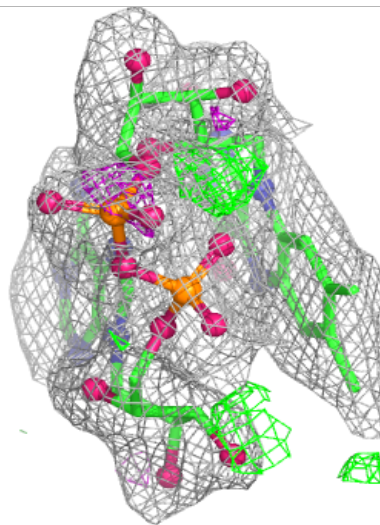
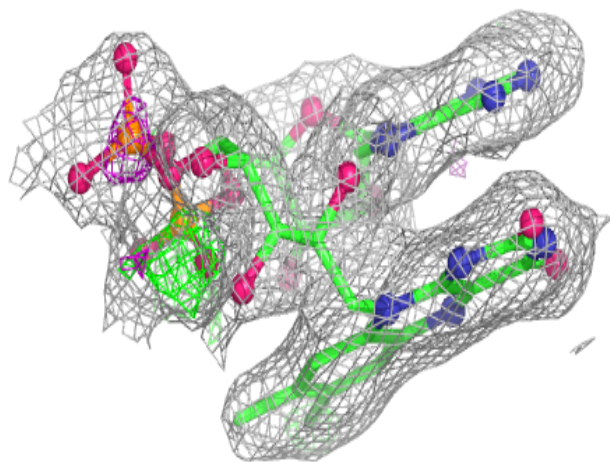
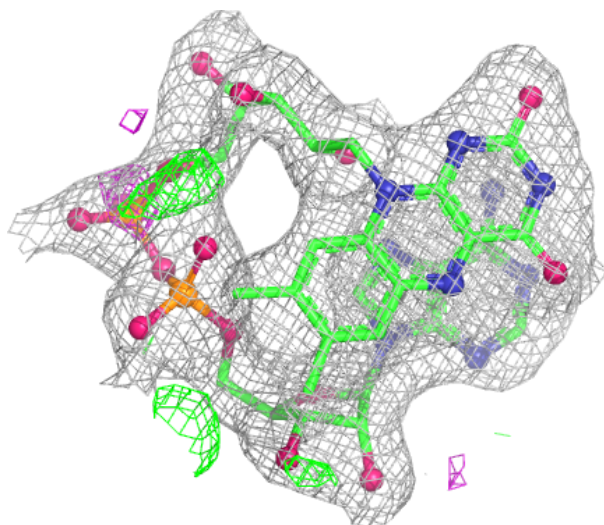
Electron density around FAD G 202:

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



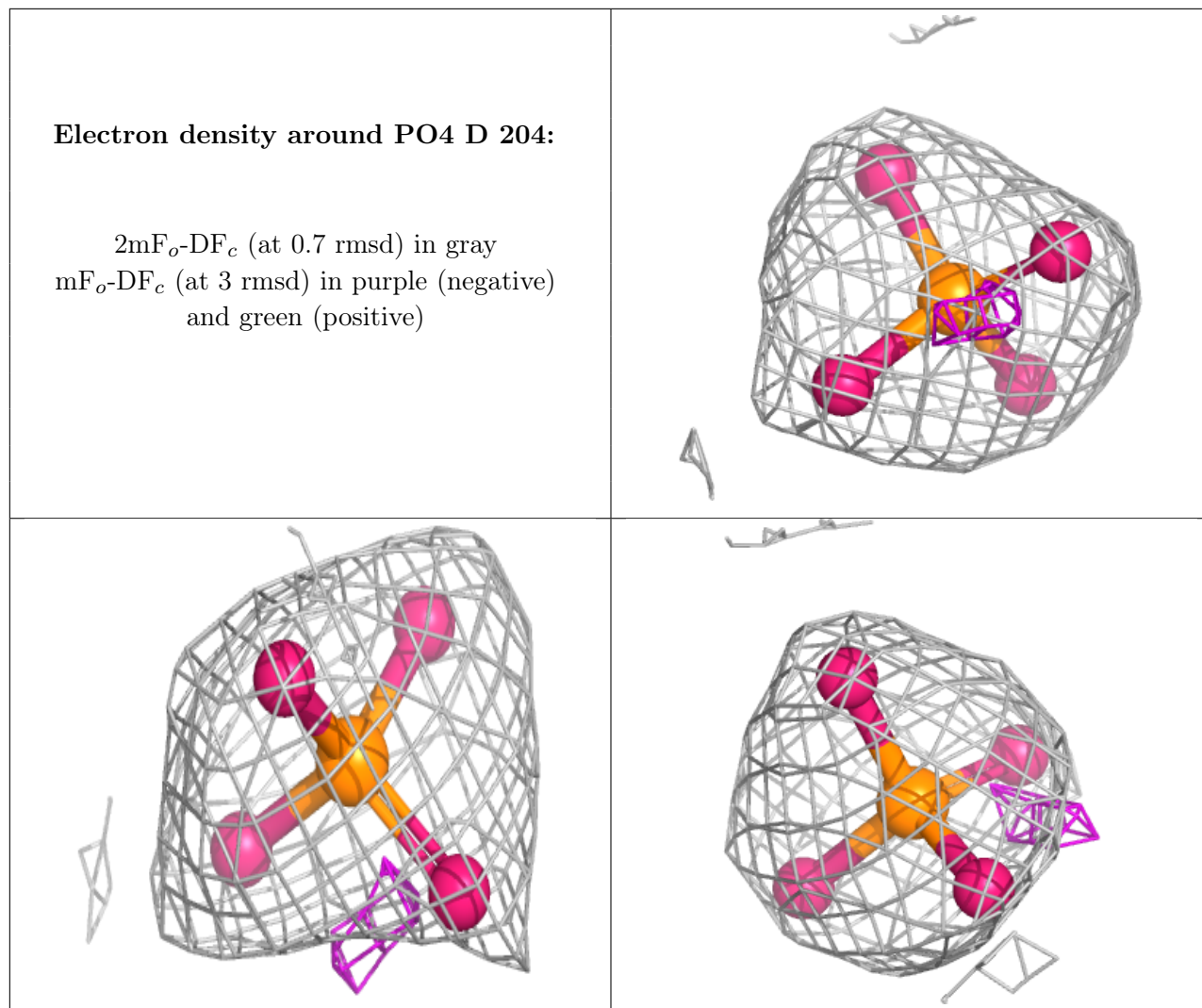
Electron density around FAD A 202:

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



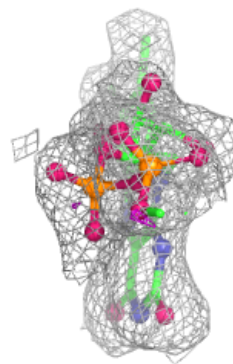
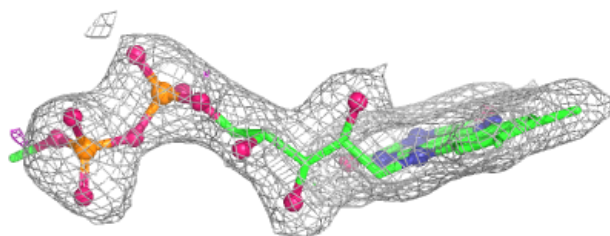
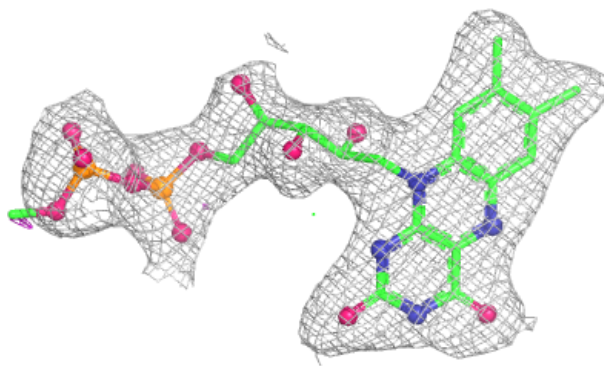
Electron density around PO4 D 204:

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

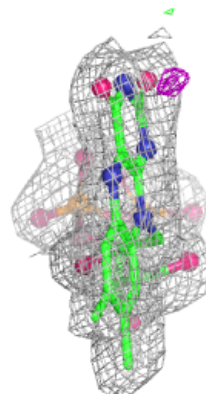
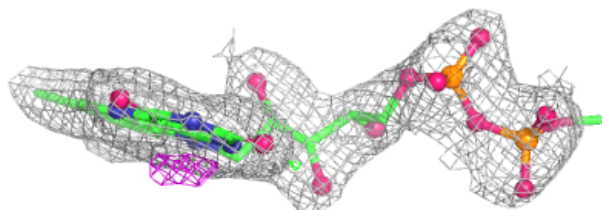
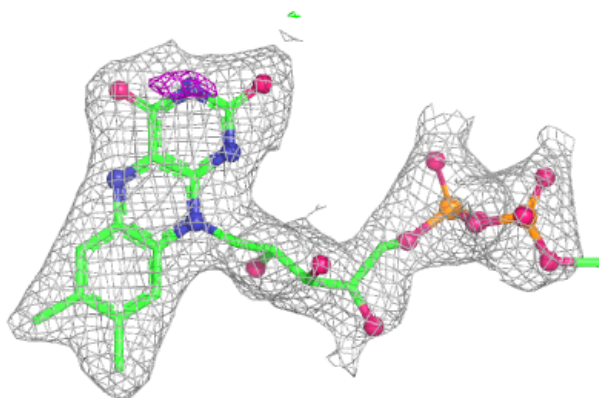


Electron density around FAD H 201:

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

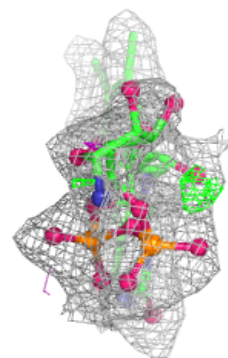
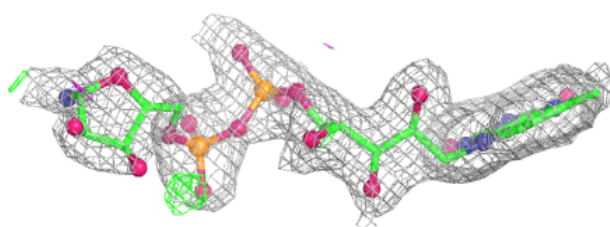
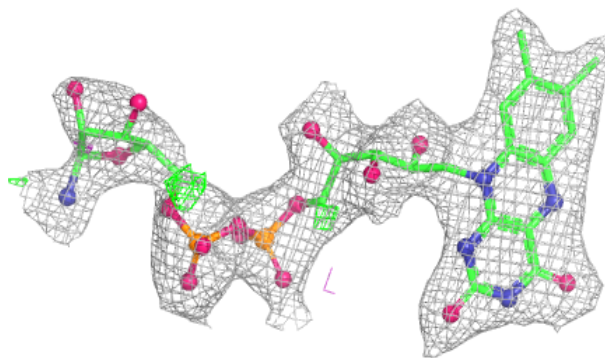
**Electron density around FAD F 202:**

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

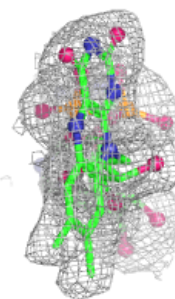
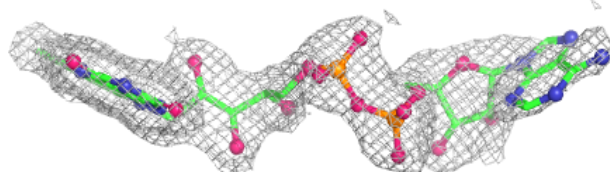
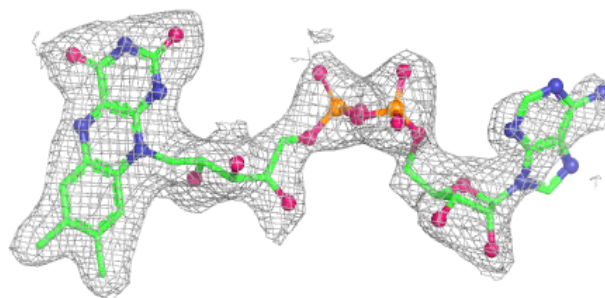


Electron density around FAD C 201:

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

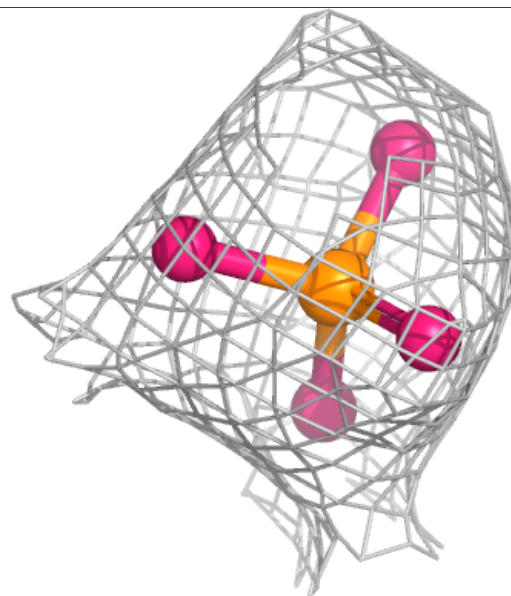
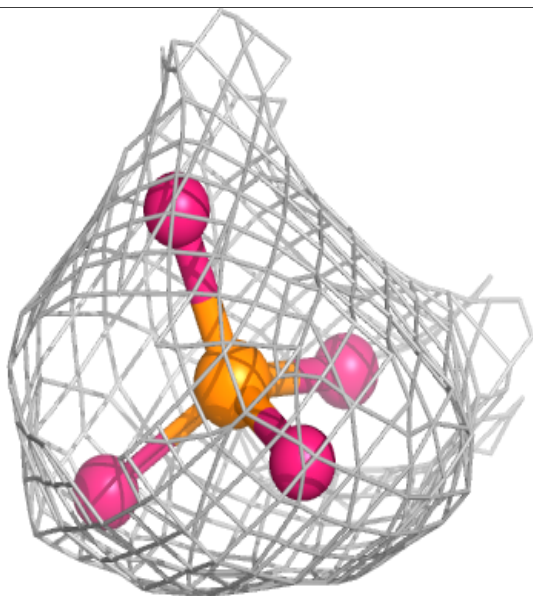
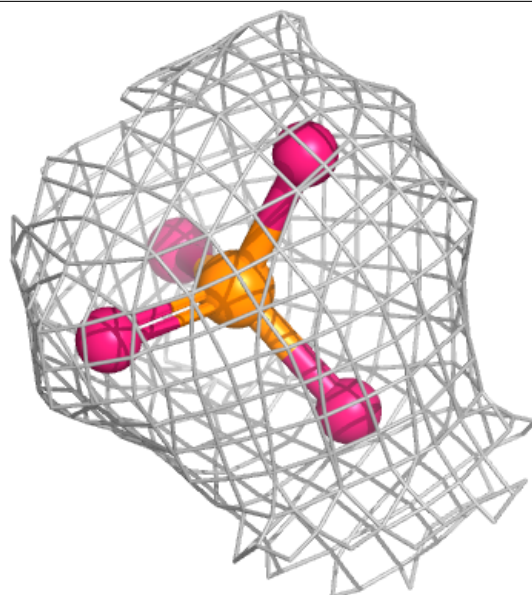
**Electron density around FAD E 202:**

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



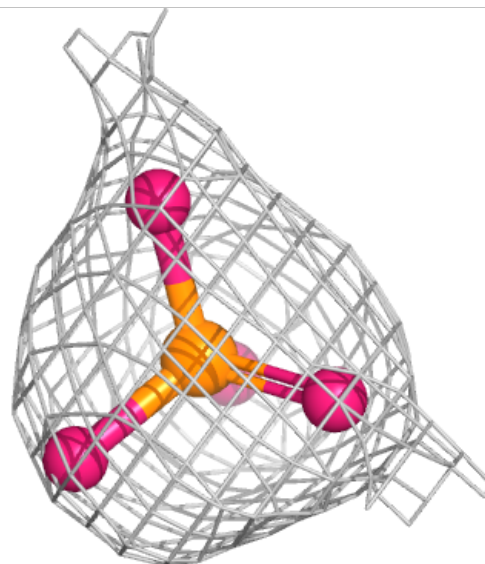
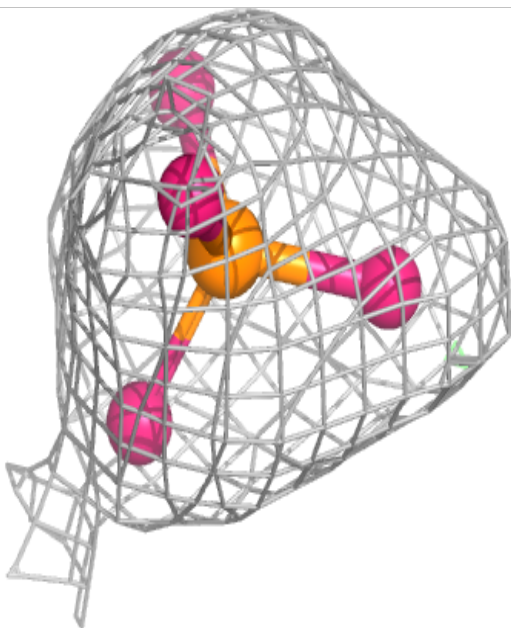
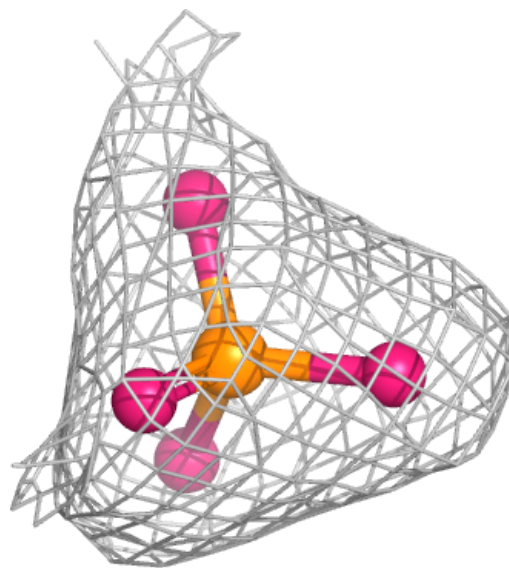
Electron density around PO4 G 203:

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



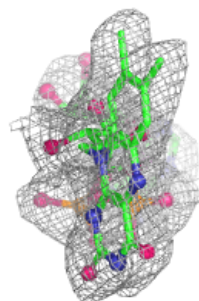
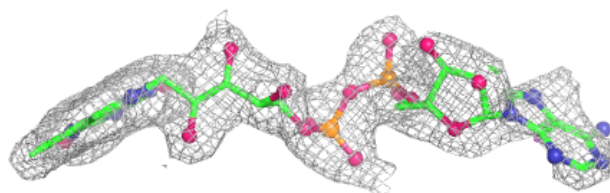
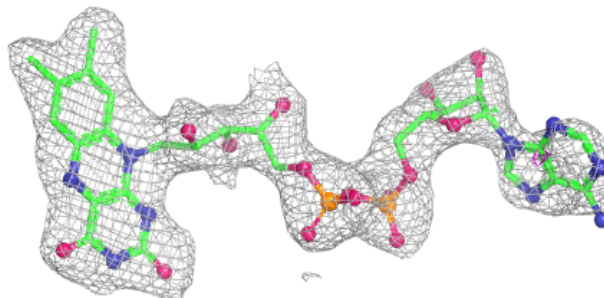
Electron density around PO4 C 204:

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

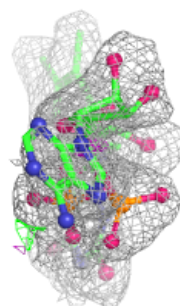
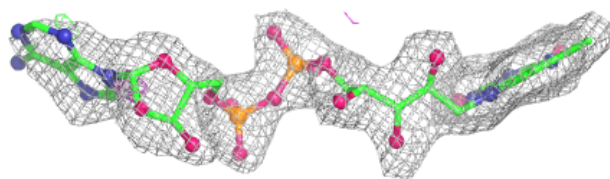
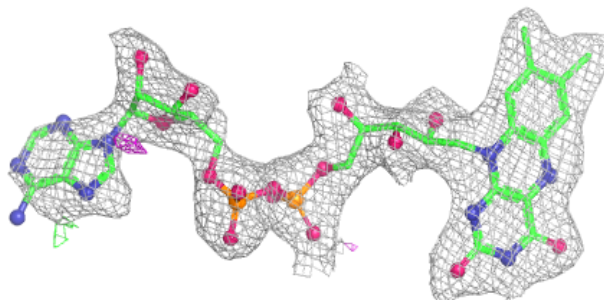


Electron density around FAD A 201:

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

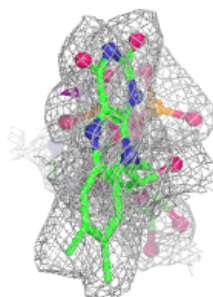
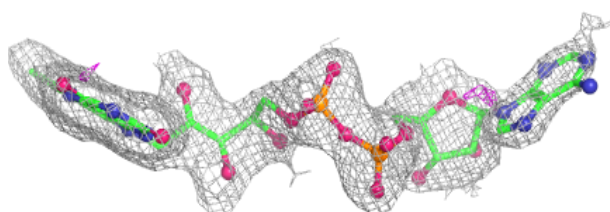
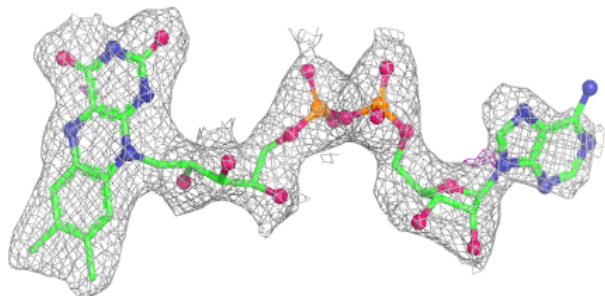
**Electron density around FAD B 202:**

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

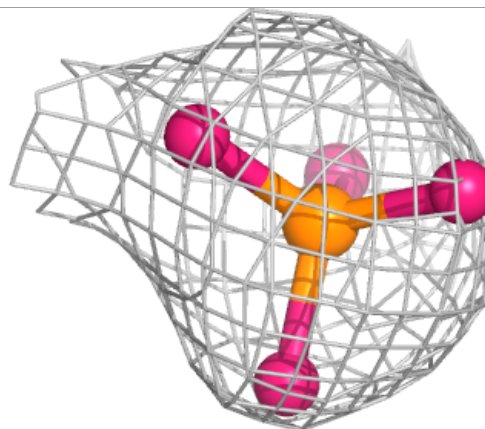
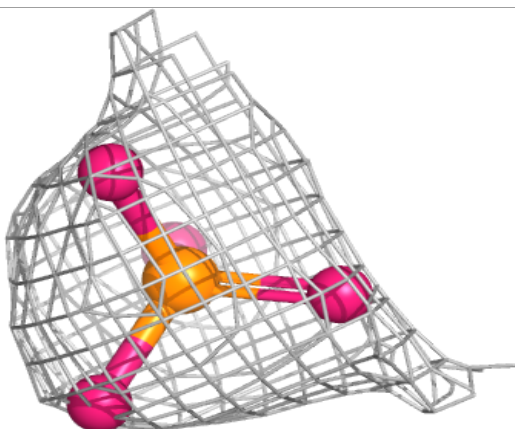
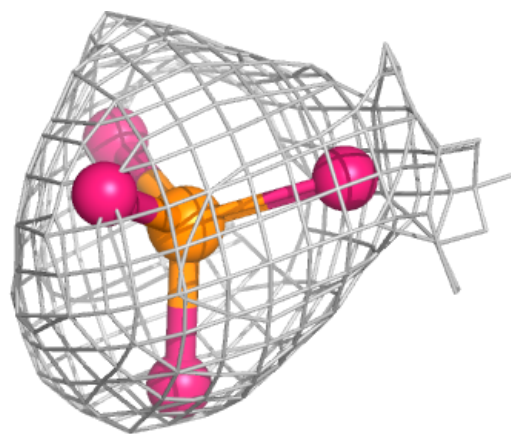


Electron density around FAD G 201:

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

**Electron density around PO4 F 203:**

$2mF_o-DF_c$ (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.