



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2021 – 04:13 PM EDT

PDB ID : 3F6S
Title : Desulfovibrio desulfuricans (ATCC 29577) oxidized flavodoxin alternate conformers
Authors : Guelker, M.; Shamoo, Y.
Deposited on : 2008-11-06
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

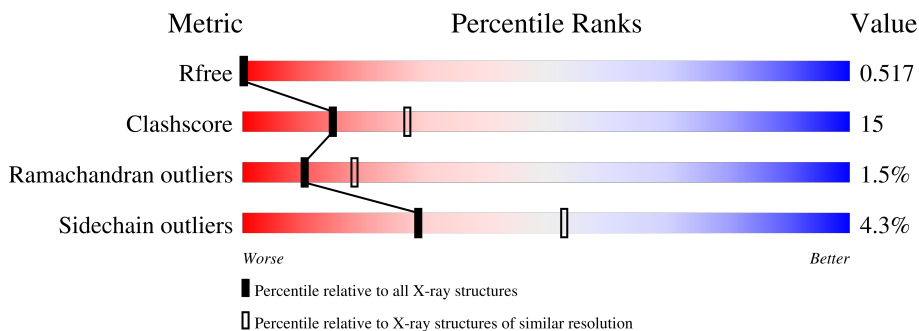
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	148	77% 17% 5% ..
1	B	148	74% 20% ..
1	D	148	72% 26% ..
1	E	148	70% 25% 5% ..
1	F	148	66% 31% ..
1	G	148	77% 18% ..
1	H	148	64% 33% ..

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Mol	Chain	Length	Quality of chain
1	I	148	 72% 26% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9299 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 Flavodoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	147	1093	683	175	230	5	0	0	0
1	B	147	1093	683	175	230	5	0	0	0
1	D	147	1093	683	175	230	5	0	0	0
1	E	147	1093	683	175	230	5	0	0	0
1	F	147	1093	683	175	230	5	0	0	0
1	H	147	1093	683	175	230	5	0	0	0
1	I	147	1093	683	175	230	5	0	0	0
1	G	147	1093	683	175	230	5	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	79	ASP	ASN	engineered mutation	UNP P26492
B	79	ASP	ASN	engineered mutation	UNP P26492
D	79	ASP	ASN	engineered mutation	UNP P26492
E	79	ASP	ASN	engineered mutation	UNP P26492
F	79	ASP	ASN	engineered mutation	UNP P26492
H	79	ASP	ASN	engineered mutation	UNP P26492
I	79	ASP	ASN	engineered mutation	UNP P26492
G	79	ASP	ASN	engineered mutation	UNP P26492

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	E	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	F	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	H	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	I	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	G	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total	O	0	0
			47	47		
3	B	68	Total	O	0	0
			68	68		
3	D	17	Total	O	0	0
			17	17		
3	E	43	Total	O	0	0
			43	43		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	F	26	Total O 26 26	0	0
3	H	34	Total O 34 34	0	0
3	I	32	Total O 32 32	0	0
3	G	40	Total O 40 40	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. 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. 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: Flavodoxin

Chain A: 



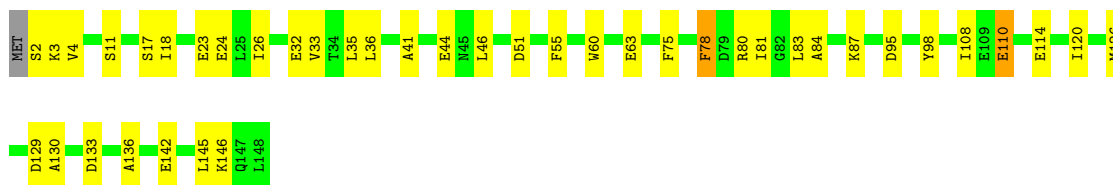
- Molecule 1: Flavodoxin

Chain B: 



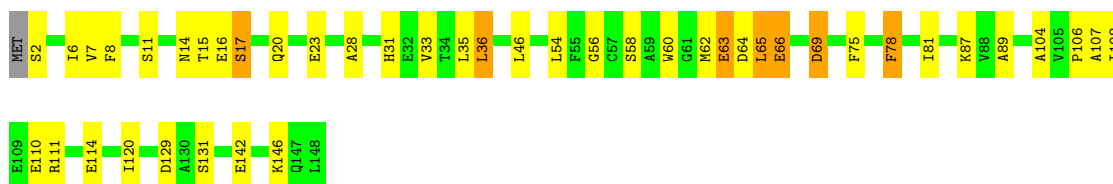
- Molecule 1: Flavodoxin

Chain D: 



- Molecule 1: Flavodoxin

Chain E: 



- Molecule 1: Flavodoxin

Chain F: 





- Molecule 1: Flavodoxin

Chain H: 64% 33%



- Molecule 1: Flavodoxin

Chain I: 72% 26%



- Molecule 1: Flavodoxin

Chain G: 77% 18%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	94.89Å 94.89Å 238.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.89 – 2.50 19.89 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.89-2.50) 99.8 (19.89-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.10 (at 2.50Å)	Xtrriage
Refinement program	PHENIX (phenix.refine), CNS	Depositor
R, R_{free}	0.220 , 0.279 0.517 , 0.517	Depositor DCC
R_{free} test set	4386 reflections (10.06%)	wwPDB-VP
Wilson B-factor (Å ²)	10.6	Xtrriage
Anisotropy	0.659	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 73.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.053 for -h,-k,l	Xtrriage
Reported twinning fraction	0.071 for H, K, L 0.929 for -h,-k,l	Depositor
Outliers	13 of 43606 reflections (0.030%)	Xtrriage
F_o, F_c correlation	0.50	EDS
Total number of atoms	9299	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 70.32 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.1875e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.40	0/1108	0.57	0/1494
1	B	0.40	0/1108	0.55	0/1494
1	D	0.30	0/1108	0.44	0/1494
1	E	0.41	0/1108	0.56	0/1494
1	F	0.32	0/1108	0.44	0/1494
1	G	0.39	0/1108	0.55	0/1494
1	H	0.31	0/1108	0.44	0/1494
1	I	0.31	0/1108	0.45	0/1494
All	All	0.36	0/8864	0.50	0/11952

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	1093	0	1038	31	0
1	B	1093	0	1038	31	0
1	D	1093	0	1038	31	0
1	E	1093	0	1038	36	0
1	F	1093	0	1038	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1093	0	1038	28	0
1	H	1093	0	1038	39	0
1	I	1093	0	1038	35	0
2	A	31	0	19	3	0
2	B	31	0	19	0	0
2	D	31	0	19	1	0
2	E	31	0	19	2	0
2	F	31	0	19	0	0
2	G	31	0	19	0	0
2	H	31	0	19	0	0
2	I	31	0	19	2	0
3	A	47	0	0	1	0
3	B	68	0	0	2	0
3	D	17	0	0	0	0
3	E	43	0	0	1	0
3	F	26	0	0	0	0
3	G	40	0	0	2	0
3	H	34	0	0	0	0
3	I	32	0	0	0	0
All	All	9299	0	8456	265	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 15.

All (265) 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:H:124:LEU:HD21	1:H:126:MET:HE3	1.46	0.96
1:D:4:VAL:HB	1:D:33:VAL:HG12	1.49	0.93
1:E:142:GLU:HG2	1:E:146:LYS:HE3	1.52	0.92
1:H:124:LEU:HD11	1:H:126:MET:HE2	1.54	0.86
1:D:126:MET:HE2	1:D:133:ASP:HB3	1.56	0.86
1:E:58:SER:HG	1:E:60:TRP:HE1	1.27	0.83
1:F:95:ASP:HB3	1:F:98:TYR:HD1	1.43	0.83
1:B:65:LEU:HD23	3:B:234:HOH:O	1.81	0.81
1:G:142:GLU:HG2	1:G:146:LYS:HE3	1.64	0.80
1:F:36:LEU:HD21	1:F:41:ALA:HB2	1.63	0.79
1:F:124:LEU:HD21	1:F:126:MET:HE3	1.64	0.79
1:H:7:VAL:HG13	1:H:36:LEU:HD22	1.65	0.78
1:H:23:GLU:HG3	1:H:33:VAL:HG21	1.66	0.78
1:H:36:LEU:HD21	1:H:41:ALA:HB2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:23:GLU:HG3	1:D:33:VAL:HG21	1.69	0.74
1:A:32:GLU:HG3	1:F:35:LEU:HD23	1.70	0.73
1:H:4:VAL:HB	1:H:33:VAL:HG12	1.69	0.72
1:H:124:LEU:HD11	1:H:126:MET:CE	2.20	0.71
1:F:46:LEU:HB3	1:F:81:ILE:HG23	1.71	0.71
1:A:20:GLN:HG2	1:F:32:GLU:HG2	1.73	0.71
1:B:142:GLU:HG2	1:B:146:LYS:HE3	1.73	0.71
1:D:23:GLU:HG3	1:D:33:VAL:CG2	2.22	0.70
1:F:7:VAL:HG13	1:F:36:LEU:HD22	1.73	0.70
1:F:142:GLU:O	1:F:146:LYS:HG2	1.91	0.70
1:I:95:ASP:HB3	1:I:98:TYR:HD1	1.55	0.69
1:D:36:LEU:HD21	1:D:41:ALA:HB2	1.73	0.69
1:A:120:ILE:HB	1:A:147:GLN:HG3	1.73	0.68
1:B:16:GLU:O	1:B:20:GLN:HG3	1.92	0.68
1:E:58:SER:HB2	2:E:152:FMN:O4'	1.95	0.67
1:H:95:ASP:HB3	1:H:98:TYR:HD1	1.58	0.67
1:E:106:PRO:O	1:E:110:GLU:HG3	1.94	0.66
1:D:95:ASP:HB3	1:D:98:TYR:HD1	1.60	0.66
1:I:4:VAL:HB	1:I:33:VAL:HG12	1.78	0.66
1:D:36:LEU:CD2	1:D:41:ALA:HB2	2.26	0.65
1:F:54:LEU:HD22	1:F:89:ALA:HB3	1.79	0.65
1:D:126:MET:CE	1:D:136:ALA:HB3	2.27	0.64
1:H:46:LEU:HB3	1:H:81:ILE:HG23	1.78	0.64
1:I:23:GLU:HG3	1:I:33:VAL:HG21	1.79	0.63
1:D:95:ASP:HB3	1:D:98:TYR:CD1	2.33	0.63
1:B:142:GLU:O	1:B:146:LYS:HG2	1.98	0.63
1:E:2:SER:N	1:E:31:HIS:HD1	1.97	0.63
1:F:124:LEU:HD11	1:F:126:MET:CE	2.28	0.62
1:A:14:ASN:O	1:A:17:SER:HB3	2.00	0.62
1:D:87:LYS:HB3	1:D:120:ILE:HG21	1.82	0.61
1:D:46:LEU:HB3	1:D:81:ILE:HG23	1.83	0.61
1:A:111:ARG:HD3	3:A:293:HOH:O	2.01	0.61
1:E:106:PRO:O	1:E:110:GLU:CG	2.49	0.60
1:H:23:GLU:HG3	1:H:33:VAL:CG2	2.31	0.60
1:A:36:LEU:HD13	1:A:41:ALA:HB2	1.82	0.60
1:F:95:ASP:HB3	1:F:98:TYR:CD1	2.33	0.59
1:F:124:LEU:HD11	1:F:126:MET:HE2	1.83	0.59
1:F:17:SER:HA	1:F:20:GLN:OE1	2.03	0.59
1:H:47:ALA:HB1	1:H:86:ARG:HD3	1.84	0.59
1:H:142:GLU:O	1:H:146:LYS:HG2	2.03	0.59
1:I:124:LEU:HD11	1:I:126:MET:HE3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:GLU:O	1:D:146:LYS:HG2	2.03	0.58
1:I:36:LEU:HD21	1:I:41:ALA:HB2	1.85	0.58
1:H:44:GLU:HB2	1:H:80:ARG:NH2	2.19	0.58
1:B:36:LEU:HD22	1:B:37:ASN:O	2.03	0.58
1:G:36:LEU:HD22	1:G:37:ASN:O	2.02	0.58
1:F:131:SER:O	1:F:134:PRO:HD3	2.04	0.58
1:I:95:ASP:HB3	1:I:98:TYR:CD1	2.36	0.58
1:A:62:MET:O	1:A:64:ASP:N	2.37	0.58
1:H:17:SER:HA	1:H:20:GLN:OE1	2.03	0.58
1:B:23:GLU:HG3	1:B:33:VAL:HB	1.86	0.57
1:H:120:ILE:HB	1:H:147:GLN:HG3	1.85	0.57
1:F:36:LEU:CD2	1:F:41:ALA:HB2	2.31	0.57
1:I:126:MET:CE	1:I:136:ALA:HB3	2.34	0.57
1:G:106:PRO:O	1:G:110:GLU:HG3	2.04	0.57
1:H:54:LEU:HD22	1:H:89:ALA:HB3	1.86	0.57
1:G:87:LYS:HB3	1:G:120:ILE:HG21	1.87	0.57
1:B:142:GLU:CG	1:B:146:LYS:HE3	2.36	0.56
1:B:62:MET:O	1:B:64:ASP:N	2.38	0.56
1:I:126:MET:HE2	1:I:136:ALA:HB3	1.87	0.56
1:I:142:GLU:O	1:I:146:LYS:HG2	2.05	0.56
1:A:106:PRO:O	1:A:110:GLU:HG3	2.04	0.56
1:F:36:LEU:HD23	1:F:37:ASN:O	2.05	0.56
1:F:3:LYS:HG2	1:F:32:GLU:HB2	1.88	0.55
1:F:44:GLU:HB2	1:F:80:ARG:HH21	1.70	0.55
1:E:62:MET:O	1:E:64:ASP:N	2.40	0.55
1:A:36:LEU:HD22	1:A:37:ASN:O	2.07	0.54
1:B:135:GLU:CG	1:E:64:ASP:OD2	2.56	0.54
1:I:56:GLY:HA2	1:I:91:PHE:O	2.08	0.54
1:B:111:ARG:HH11	1:B:111:ARG:HG2	1.73	0.54
1:I:124:LEU:HD11	1:I:126:MET:CE	2.36	0.54
1:G:62:MET:O	1:G:64:ASP:N	2.40	0.54
1:G:6:ILE:HB	1:G:35:LEU:HD12	1.90	0.54
1:I:75:PHE:HA	1:I:78:PHE:CD1	2.43	0.53
1:B:110:GLU:O	1:B:114:GLU:HG3	2.07	0.53
1:I:26:ILE:HA	1:I:145:LEU:HD21	1.89	0.53
1:G:46:LEU:HB3	1:G:81:ILE:HG23	1.90	0.53
1:D:24:GLU:HG3	1:E:28:ALA:HB2	1.90	0.53
1:A:95:ASP:HB3	1:A:98:TYR:HD1	1.73	0.53
1:B:64:ASP:O	1:B:66:GLU:N	2.42	0.53
1:D:60:TRP:CZ2	2:D:151:FMN:H5'2	2.43	0.53
1:I:54:LEU:HD22	1:I:89:ALA:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:LEU:HB2	1:B:72:LEU:CD2	2.39	0.53
1:E:75:PHE:HA	1:E:78:PHE:CD1	2.44	0.53
1:I:141:ALA:O	1:I:145:LEU:HG	2.09	0.53
1:A:64:ASP:O	1:A:66:GLU:N	2.42	0.52
1:E:87:LYS:HB3	1:E:120:ILE:HD13	1.91	0.52
1:F:110:GLU:O	1:F:114:GLU:HG3	2.10	0.52
1:D:44:GLU:HB2	1:D:80:ARG:NH2	2.24	0.52
1:F:39:ALA:HB2	1:F:70:ASP:CG	2.30	0.52
1:I:23:GLU:HG3	1:I:33:VAL:CG2	2.39	0.52
1:G:64:ASP:O	1:G:66:GLU:N	2.43	0.52
1:A:105:VAL:HB	1:A:106:PRO:CD	2.39	0.51
1:D:26:ILE:HA	1:D:145:LEU:HD21	1.92	0.51
1:E:16:GLU:O	1:E:20:GLN:HG3	2.11	0.51
1:D:110:GLU:O	1:D:114:GLU:HG3	2.10	0.51
1:H:95:ASP:HB3	1:H:98:TYR:CD1	2.41	0.51
1:E:46:LEU:HB3	1:E:81:ILE:HG23	1.93	0.51
1:H:39:ALA:HB2	1:H:70:ASP:CG	2.31	0.51
1:D:17:SER:OG	1:D:129:ASP:HB2	2.11	0.51
1:H:131:SER:O	1:H:134:PRO:HD3	2.10	0.51
1:I:139:SER:O	1:I:142:GLU:HB3	2.11	0.51
1:I:53:VAL:O	1:I:88:VAL:HA	2.10	0.50
1:E:62:MET:O	1:E:63:GLU:C	2.51	0.50
1:E:62:MET:HB2	3:E:154:HOH:O	2.11	0.50
1:A:142:GLU:O	1:A:146:LYS:HG2	2.12	0.50
1:H:145:LEU:HD23	1:H:148:LEU:HD12	1.94	0.50
1:A:62:MET:O	1:A:63:GLU:C	2.50	0.49
1:H:75:PHE:HA	1:H:78:PHE:CD1	2.47	0.49
1:E:36:LEU:HD12	1:E:46:LEU:HD11	1.93	0.49
1:G:14:ASN:O	1:G:18:ILE:HG13	2.13	0.49
1:G:62:MET:HB2	3:G:167:HOH:O	2.13	0.49
1:D:75:PHE:HA	1:D:78:PHE:CD1	2.48	0.49
1:A:75:PHE:HA	1:A:78:PHE:CD1	2.48	0.49
1:E:64:ASP:O	1:E:66:GLU:N	2.46	0.48
1:H:54:LEU:CD2	1:H:89:ALA:HB3	2.43	0.48
1:E:6:ILE:HB	1:E:35:LEU:HD12	1.96	0.48
1:F:5:LEU:HB2	1:F:50:TYR:CE2	2.48	0.48
1:G:62:MET:O	1:G:63:GLU:C	2.51	0.48
1:D:11:SER:HB2	1:D:60:TRP:CZ2	2.48	0.48
1:G:8:PHE:CE1	1:G:16:GLU:HG3	2.48	0.48
1:A:62:MET:HB3	1:A:63:GLU:H	1.52	0.48
2:A:149:FMN:C8M	1:G:139:SER:HA	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:MET:O	1:B:63:GLU:C	2.52	0.48
1:D:3:LYS:HG2	1:D:32:GLU:HB2	1.95	0.48
1:E:87:LYS:HB3	1:E:120:ILE:HG21	1.95	0.48
1:G:56:GLY:HA2	1:G:91:PHE:O	2.14	0.48
1:A:95:ASP:HB3	1:A:98:TYR:CD1	2.49	0.47
1:B:111:ARG:HG2	1:B:111:ARG:NH1	2.29	0.47
1:G:65:LEU:HB2	1:G:72:LEU:CD2	2.44	0.47
1:A:19:ALA:HB1	1:A:35:LEU:HD11	1.95	0.47
1:B:111:ARG:HD3	3:B:172:HOH:O	2.13	0.47
1:A:59:ALA:HB3	2:A:149:FMN:C2	2.45	0.47
1:E:62:MET:HB3	1:E:63:GLU:H	1.48	0.47
1:H:87:LYS:HB3	1:H:120:ILE:HD13	1.95	0.47
1:F:91:PHE:CB	1:F:124:LEU:HB3	2.45	0.47
1:I:62:MET:CE	2:I:155:FMN:HM72	2.45	0.46
1:I:88:VAL:HG12	1:I:89:ALA:N	2.30	0.46
1:D:87:LYS:HB3	1:D:120:ILE:HD13	1.97	0.46
1:F:47:ALA:HB1	1:F:86:ARG:HD3	1.97	0.46
1:H:91:PHE:CB	1:H:124:LEU:HB3	2.45	0.46
1:B:104:ALA:O	1:B:108:ILE:HG13	2.15	0.46
1:H:11:SER:HB2	1:H:60:TRP:CZ2	2.50	0.46
1:I:21:LYS:CG	1:I:137:VAL:HG11	2.45	0.46
1:A:87:LYS:HB3	1:A:120:ILE:HG21	1.97	0.46
1:I:110:GLU:O	1:I:114:GLU:HG3	2.16	0.46
1:G:65:LEU:H	1:G:65:LEU:HG	1.34	0.46
1:F:56:GLY:HA2	1:F:91:PHE:O	2.16	0.46
1:F:65:LEU:C	1:F:65:LEU:HD13	2.37	0.46
1:E:110:GLU:O	1:E:114:GLU:HG3	2.16	0.45
1:F:126:MET:HE1	1:F:136:ALA:HB3	1.98	0.45
1:H:56:GLY:HA2	1:H:91:PHE:O	2.16	0.45
1:G:113:LYS:HE2	1:G:119:ILE:CG1	2.46	0.45
1:G:142:GLU:O	1:G:146:LYS:HG2	2.16	0.45
1:F:44:GLU:HB2	1:F:80:ARG:NH2	2.30	0.45
1:B:35:LEU:HD12	1:B:35:LEU:HA	1.86	0.45
1:B:75:PHE:HA	1:B:78:PHE:CD1	2.52	0.45
1:F:87:LYS:HB3	1:F:120:ILE:HG21	1.99	0.45
1:B:62:MET:HB3	1:B:63:GLU:H	1.52	0.45
1:H:91:PHE:HB2	1:H:124:LEU:HD23	1.99	0.45
1:I:53:VAL:HG11	1:I:55:PHE:CZ	2.52	0.45
1:F:75:PHE:HA	1:F:78:PHE:CD1	2.52	0.45
1:B:21:LYS:HD2	1:B:21:LYS:HA	1.76	0.45
1:D:18:ILE:HA	1:D:130:ALA:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:43:ALA:O	1:F:81:ILE:HA	2.17	0.44
1:B:106:PRO:O	1:B:110:GLU:CG	2.65	0.44
1:D:36:LEU:C	1:D:36:LEU:HD23	2.38	0.44
1:I:7:VAL:HA	1:I:36:LEU:O	2.18	0.44
1:I:101:PHE:HA	2:I:155:FMN:O2	2.18	0.44
1:B:72:LEU:HD12	1:B:72:LEU:O	2.17	0.44
1:A:111:ARG:HG2	1:A:111:ARG:HH11	1.83	0.44
1:D:23:GLU:HB2	1:D:35:LEU:HD22	1.99	0.44
1:H:7:VAL:HG13	1:H:36:LEU:CD2	2.43	0.44
1:E:23:GLU:HG3	1:E:33:VAL:HB	1.99	0.44
1:E:107:ALA:HA	1:E:110:GLU:OE1	2.17	0.44
1:B:120:ILE:HB	1:B:147:GLN:HG3	2.00	0.44
1:E:65:LEU:H	1:E:65:LEU:HG	1.37	0.44
1:I:78:PHE:HA	1:I:81:ILE:HD12	2.00	0.44
1:F:94:GLY:O	1:F:127:GLU:HG2	2.18	0.44
1:B:113:LYS:HE2	1:B:119:ILE:CG1	2.48	0.43
1:F:109:GLU:O	1:F:113:LYS:HG3	2.19	0.43
1:G:106:PRO:O	1:G:110:GLU:CG	2.66	0.43
1:D:3:LYS:HB3	1:D:3:LYS:HE3	1.75	0.43
1:F:91:PHE:HA	1:F:124:LEU:HB3	2.00	0.43
1:I:120:ILE:O	1:I:147:GLN:HG3	2.17	0.43
1:E:14:ASN:OD1	2:E:152:FMN:H5'1	2.19	0.43
1:E:111:ARG:HA	1:E:111:ARG:HD2	1.67	0.43
1:F:5:LEU:HB2	1:F:50:TYR:CZ	2.53	0.43
1:A:32:GLU:CG	1:F:35:LEU:HD23	2.44	0.43
1:H:65:LEU:C	1:H:65:LEU:HD13	2.39	0.43
1:G:65:LEU:HD12	1:G:72:LEU:HD21	2.01	0.43
1:E:35:LEU:HD12	1:E:35:LEU:HA	1.81	0.43
1:H:50:TYR:O	1:H:86:ARG:NH1	2.52	0.43
1:A:32:GLU:HG3	1:F:35:LEU:CD2	2.45	0.42
1:D:23:GLU:HG3	1:D:33:VAL:HG23	1.99	0.42
1:G:36:LEU:HD12	1:G:46:LEU:HD11	2.01	0.42
1:I:36:LEU:C	1:I:36:LEU:HD23	2.39	0.42
1:I:55:PHE:HB2	1:I:108:ILE:HG21	2.01	0.42
1:D:2:SER:HB3	1:D:51:ASP:OD2	2.18	0.42
1:H:104:ALA:O	1:H:108:ILE:HG13	2.19	0.42
1:I:3:LYS:HE3	1:I:3:LYS:HB3	1.81	0.42
1:H:26:ILE:HA	1:H:145:LEU:HD21	2.01	0.42
1:H:109:GLU:O	1:H:113:LYS:HG3	2.19	0.42
1:G:87:LYS:HB3	1:G:120:ILE:CG2	2.48	0.42
1:B:6:ILE:HB	1:B:35:LEU:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:135:GLU:HG3	1:E:64:ASP:OD2	2.20	0.42
1:I:46:LEU:HB3	1:I:81:ILE:HG23	2.02	0.42
1:A:36:LEU:HD12	1:A:46:LEU:HD11	2.01	0.42
1:A:65:LEU:H	1:A:65:LEU:HG	1.34	0.42
1:D:87:LYS:HB3	1:D:120:ILE:CG2	2.46	0.42
1:E:8:PHE:HB2	1:E:15:THR:HG22	2.01	0.42
1:E:8:PHE:HE2	1:E:35:LEU:HG	1.84	0.42
1:F:90:ALA:HB3	1:F:105:VAL:HG13	2.00	0.42
1:F:124:LEU:HD11	1:F:126:MET:HE3	2.01	0.42
1:A:36:LEU:CD1	1:A:41:ALA:HB2	2.50	0.42
1:E:104:ALA:O	1:E:108:ILE:HG13	2.20	0.42
1:G:3:LYS:NZ	3:G:249:HOH:O	2.53	0.42
1:A:120:ILE:HB	1:A:147:GLN:CG	2.47	0.42
1:E:8:PHE:HA	1:E:56:GLY:O	2.19	0.42
1:H:2:SER:N	1:H:31:HIS:HD1	2.18	0.41
1:I:68:GLN:OE1	1:I:70:ASP:HB2	2.20	0.41
1:F:144:VAL:O	1:F:148:LEU:HG	2.20	0.41
1:I:120:ILE:HD12	1:I:147:GLN:HB2	2.02	0.41
2:A:149:FMN:HM83	1:G:139:SER:HA	2.02	0.41
1:B:2:SER:N	1:B:31:HIS:HD1	2.19	0.41
1:B:65:LEU:H	1:B:65:LEU:HG	1.35	0.41
1:G:62:MET:HB3	1:G:63:GLU:H	1.51	0.41
1:E:54:LEU:HD22	1:E:89:ALA:HB3	2.01	0.41
1:H:3:LYS:HG2	1:H:32:GLU:HB2	2.03	0.41
1:H:82:GLY:O	1:H:86:ARG:HD2	2.19	0.41
1:A:111:ARG:HD2	1:A:111:ARG:HA	1.80	0.41
1:B:93:SER:HA	1:B:126:MET:O	2.21	0.41
1:E:11:SER:HB2	1:E:60:TRP:CZ2	2.56	0.41
1:F:86:ARG:HH11	1:F:86:ARG:HG2	1.86	0.41
1:G:93:SER:HA	1:G:126:MET:O	2.20	0.41
1:H:36:LEU:HD23	1:H:36:LEU:C	2.41	0.41
1:I:21:LYS:HG2	1:I:137:VAL:HG11	2.01	0.41
1:G:113:LYS:HE2	1:G:119:ILE:HG13	2.01	0.41
1:A:146:LYS:HA	1:A:146:LYS:HD3	1.86	0.41
1:A:3:LYS:HE3	1:A:3:LYS:HB3	1.77	0.41
1:D:83:LEU:O	1:D:84:ALA:C	2.59	0.41
1:E:17:SER:OG	1:E:129:ASP:HB2	2.21	0.41
1:H:145:LEU:HA	1:H:148:LEU:HD12	2.03	0.41
1:B:8:PHE:HE2	1:B:35:LEU:HG	1.86	0.40
1:A:54:LEU:HD22	1:A:89:ALA:HB3	2.03	0.40
1:I:120:ILE:HB	1:I:147:GLN:HG3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:55:PHE:HB2	1:D:108:ILE:HG21	2.04	0.40
1:H:36:LEU:HD23	1:H:37:ASN:O	2.22	0.40
1:E:142:GLU:O	1:E:146:LYS:HG2	2.20	0.40
1:F:126:MET:HE2	1:F:126:MET:HB3	1.97	0.40
1:G:8:PHE:HA	1:G:56:GLY: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	145/148 (98%)	138 (95%)	3 (2%)	4 (3%)	5	7
1	B	145/148 (98%)	139 (96%)	2 (1%)	4 (3%)	5	7
1	D	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
1	E	145/148 (98%)	140 (97%)	1 (1%)	4 (3%)	5	7
1	F	145/148 (98%)	138 (95%)	7 (5%)	0	100	100
1	G	145/148 (98%)	138 (95%)	2 (1%)	5 (3%)	3	5
1	H	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
1	I	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
All	All	1160/1184 (98%)	1110 (96%)	33 (3%)	17 (2%)	10	18

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	GLU
1	A	65	LEU
1	A	66	GLU
1	B	63	GLU
1	B	65	LEU

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Mol	Chain	Res	Type
1	B	66	GLU
1	E	63	GLU
1	E	65	LEU
1	E	66	GLU
1	E	69	ASP
1	G	63	GLU
1	G	65	LEU
1	G	66	GLU
1	G	69	ASP
1	A	62	MET
1	G	62	MET
1	B	62	MET

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	110/111 (99%)	104 (94%)	6 (6%)	21	41
1	B	110/111 (99%)	104 (94%)	6 (6%)	21	41
1	D	110/111 (99%)	107 (97%)	3 (3%)	44	71
1	E	110/111 (99%)	104 (94%)	6 (6%)	21	41
1	F	110/111 (99%)	106 (96%)	4 (4%)	35	61
1	G	110/111 (99%)	105 (96%)	5 (4%)	27	51
1	H	110/111 (99%)	105 (96%)	5 (4%)	27	51
1	I	110/111 (99%)	107 (97%)	3 (3%)	44	71
All	All	880/888 (99%)	842 (96%)	38 (4%)	29	53

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	35	LEU
1	A	36	LEU

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Mol	Chain	Res	Type
1	A	66	GLU
1	A	78	PHE
1	A	111	ARG
1	B	7	VAL
1	B	32	GLU
1	B	36	LEU
1	B	66	GLU
1	B	78	PHE
1	B	111	ARG
1	D	63	GLU
1	D	78	PHE
1	D	110	GLU
1	E	7	VAL
1	E	17	SER
1	E	36	LEU
1	E	69	ASP
1	E	78	PHE
1	E	131	SER
1	F	7	VAL
1	F	33	VAL
1	F	35	LEU
1	F	80	ARG
1	H	17	SER
1	H	33	VAL
1	H	63	GLU
1	H	78	PHE
1	H	110	GLU
1	I	63	GLU
1	I	78	PHE
1	I	110	GLU
1	G	36	LEU
1	G	66	GLU
1	G	69	ASP
1	G	78	PHE
1	G	111	ARG

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 [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](#)

8 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	FMN	B	150	-	31,33,33	1.39	4 (12%)	40,50,50	1.69	7 (17%)
2	FMN	H	154	-	31,33,33	1.37	5 (16%)	40,50,50	1.51	6 (15%)
2	FMN	A	149	-	31,33,33	1.41	5 (16%)	40,50,50	1.63	6 (15%)
2	FMN	D	151	-	31,33,33	1.44	4 (12%)	40,50,50	1.58	5 (12%)
2	FMN	F	153	-	31,33,33	1.39	4 (12%)	40,50,50	1.62	7 (17%)
2	FMN	E	152	-	31,33,33	1.44	5 (16%)	40,50,50	1.86	11 (27%)
2	FMN	I	155	-	31,33,33	1.43	4 (12%)	40,50,50	1.66	5 (12%)
2	FMN	G	156	-	31,33,33	1.39	5 (16%)	40,50,50	1.88	8 (20%)

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	FMN	B	150	-	-	4/18/18/18	0/3/3/3
2	FMN	H	154	-	-	5/18/18/18	0/3/3/3
2	FMN	A	149	-	-	4/18/18/18	0/3/3/3
2	FMN	D	151	-	-	4/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FMN	F	153	-	-	4/18/18/18	0/3/3/3
2	FMN	E	152	-	-	3/18/18/18	0/3/3/3
2	FMN	I	155	-	-	7/18/18/18	0/3/3/3
2	FMN	G	156	-	-	4/18/18/18	0/3/3/3

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	151	FMN	C10-N1	4.40	1.38	1.33
2	I	155	FMN	C10-N1	4.16	1.38	1.33
2	A	149	FMN	C10-N1	4.09	1.38	1.33
2	A	149	FMN	C4A-N5	4.02	1.39	1.33
2	E	152	FMN	C4A-N5	3.87	1.38	1.33
2	F	153	FMN	C4A-N5	3.87	1.38	1.33
2	B	150	FMN	C10-N1	3.81	1.38	1.33
2	B	150	FMN	C4A-N5	3.80	1.38	1.33
2	E	152	FMN	C10-N1	3.73	1.38	1.33
2	H	154	FMN	C10-N1	3.68	1.38	1.33
2	H	154	FMN	C4A-N5	3.65	1.38	1.33
2	G	156	FMN	C4A-N5	3.64	1.38	1.33
2	G	156	FMN	C10-N1	3.59	1.37	1.33
2	F	153	FMN	C10-N1	3.55	1.37	1.33
2	I	155	FMN	C4A-N5	3.52	1.38	1.33
2	E	152	FMN	C4-N3	3.41	1.39	1.33
2	D	151	FMN	C4A-N5	3.38	1.38	1.33
2	D	151	FMN	C4-N3	3.34	1.38	1.33
2	I	155	FMN	C4-N3	3.31	1.38	1.33
2	B	150	FMN	C4-N3	3.20	1.38	1.33
2	G	156	FMN	C4-N3	3.13	1.38	1.33
2	H	154	FMN	C4-N3	3.10	1.38	1.33
2	F	153	FMN	C4-N3	3.10	1.38	1.33
2	A	149	FMN	C4-N3	2.64	1.37	1.33
2	G	156	FMN	C1'-N10	2.33	1.50	1.48
2	E	152	FMN	C1'-N10	2.30	1.50	1.48
2	A	149	FMN	C5A-N5	2.21	1.39	1.35
2	B	150	FMN	C5A-N5	2.19	1.39	1.35
2	F	153	FMN	C5A-N5	2.16	1.38	1.35
2	E	152	FMN	C5A-N5	2.14	1.38	1.35
2	H	154	FMN	C1'-N10	2.10	1.50	1.48
2	H	154	FMN	C5A-N5	2.03	1.38	1.35
2	D	151	FMN	C1'-N10	2.03	1.50	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	149	FMN	C1'-N10	2.03	1.50	1.48
2	G	156	FMN	C5A-N5	2.01	1.38	1.35
2	I	155	FMN	C1'-N10	2.00	1.50	1.48

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	155	FMN	C4-N3-C2	7.07	121.11	115.14
2	G	156	FMN	C4-N3-C2	6.67	120.78	115.14
2	B	150	FMN	C4-N3-C2	6.58	120.70	115.14
2	A	149	FMN	C4-N3-C2	6.50	120.63	115.14
2	F	153	FMN	C4-N3-C2	6.35	120.51	115.14
2	D	151	FMN	C4-N3-C2	6.26	120.42	115.14
2	H	154	FMN	C4-N3-C2	5.67	119.93	115.14
2	E	152	FMN	C4-N3-C2	5.35	119.66	115.14
2	G	156	FMN	C1'-N10-C9A	5.13	122.33	118.29
2	E	152	FMN	C4'-C3'-C2'	-4.11	104.81	113.36
2	E	152	FMN	C1'-N10-C9A	3.84	121.31	118.29
2	D	151	FMN	C1'-N10-C9A	3.52	121.07	118.29
2	H	154	FMN	C4A-N5-C5A	3.46	120.22	116.77
2	D	151	FMN	C4A-N5-C5A	3.45	120.22	116.77
2	B	150	FMN	C4A-C4-N3	-3.35	118.85	123.43
2	G	156	FMN	C4A-C4-N3	-3.33	118.88	123.43
2	F	153	FMN	C4A-N5-C5A	3.32	120.09	116.77
2	G	156	FMN	C4A-N5-C5A	3.32	120.09	116.77
2	I	155	FMN	C4A-N5-C5A	3.23	120.00	116.77
2	G	156	FMN	C5A-C9A-N10	3.23	120.05	117.72
2	A	149	FMN	C4A-N5-C5A	3.22	119.99	116.77
2	I	155	FMN	C4A-C4-N3	-3.22	119.03	123.43
2	I	155	FMN	C5A-C9A-N10	3.18	120.02	117.72
2	A	149	FMN	C5A-C9A-N10	3.17	120.01	117.72
2	E	152	FMN	C4A-N5-C5A	3.11	119.88	116.77
2	E	152	FMN	C5A-C9A-N10	3.09	119.95	117.72
2	A	149	FMN	C1'-N10-C9A	3.03	120.68	118.29
2	B	150	FMN	C4A-N5-C5A	2.97	119.74	116.77
2	F	153	FMN	C5A-C9A-N10	2.92	119.83	117.72
2	B	150	FMN	C10-C4A-N5	-2.92	119.24	121.26
2	A	149	FMN	C4A-C4-N3	-2.88	119.49	123.43
2	F	153	FMN	C4A-C4-N3	-2.85	119.54	123.43
2	D	151	FMN	C4A-C4-N3	-2.80	119.60	123.43
2	D	151	FMN	C5A-C9A-N10	2.77	119.73	117.72
2	E	152	FMN	O5'-C5'-C4'	-2.76	101.99	109.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	152	FMN	C5'-C4'-C3'	2.76	117.53	112.20
2	B	150	FMN	C1'-N10-C9A	2.74	120.45	118.29
2	H	154	FMN	C5A-C9A-N10	2.66	119.64	117.72
2	E	152	FMN	C4A-C4-N3	-2.63	119.83	123.43
2	I	155	FMN	C1'-N10-C9A	2.62	120.36	118.29
2	H	154	FMN	C4A-C4-N3	-2.62	119.86	123.43
2	H	154	FMN	C1'-N10-C9A	2.60	120.34	118.29
2	F	153	FMN	C10-C4A-N5	-2.59	119.47	121.26
2	G	156	FMN	O2P-P-O5'	2.53	113.46	106.73
2	E	152	FMN	C10-C4A-N5	-2.52	119.52	121.26
2	G	156	FMN	P-O5'-C5'	2.50	125.18	118.30
2	H	154	FMN	C10-C4A-N5	-2.48	119.54	121.26
2	F	153	FMN	C1'-N10-C9A	2.42	120.19	118.29
2	B	150	FMN	C5A-C9A-N10	2.40	119.45	117.72
2	E	152	FMN	P-O5'-C5'	2.38	124.85	118.30
2	A	149	FMN	C10-C4A-N5	-2.28	119.68	121.26
2	G	156	FMN	C10-C4A-N5	-2.18	119.75	121.26
2	E	152	FMN	O4'-C4'-C5'	-2.09	105.23	109.92
2	F	153	FMN	C4-C4A-N5	2.07	120.97	118.60
2	B	150	FMN	O3P-P-O5'	2.02	112.11	106.73

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	149	FMN	C1'-C2'-C3'-O3'
2	A	149	FMN	C1'-C2'-C3'-C4'
2	B	150	FMN	C1'-C2'-C3'-O3'
2	B	150	FMN	C1'-C2'-C3'-C4'
2	D	151	FMN	C1'-C2'-C3'-O3'
2	D	151	FMN	C1'-C2'-C3'-C4'
2	E	152	FMN	O4'-C4'-C5'-O5'
2	F	153	FMN	C1'-C2'-C3'-O3'
2	F	153	FMN	C1'-C2'-C3'-C4'
2	H	154	FMN	C1'-C2'-C3'-O3'
2	H	154	FMN	C1'-C2'-C3'-C4'
2	I	155	FMN	C1'-C2'-C3'-O3'
2	I	155	FMN	C1'-C2'-C3'-C4'
2	I	155	FMN	C5'-O5'-P-O1P
2	G	156	FMN	C1'-C2'-C3'-O3'
2	G	156	FMN	C1'-C2'-C3'-C4'
2	A	149	FMN	O2'-C2'-C3'-O3'

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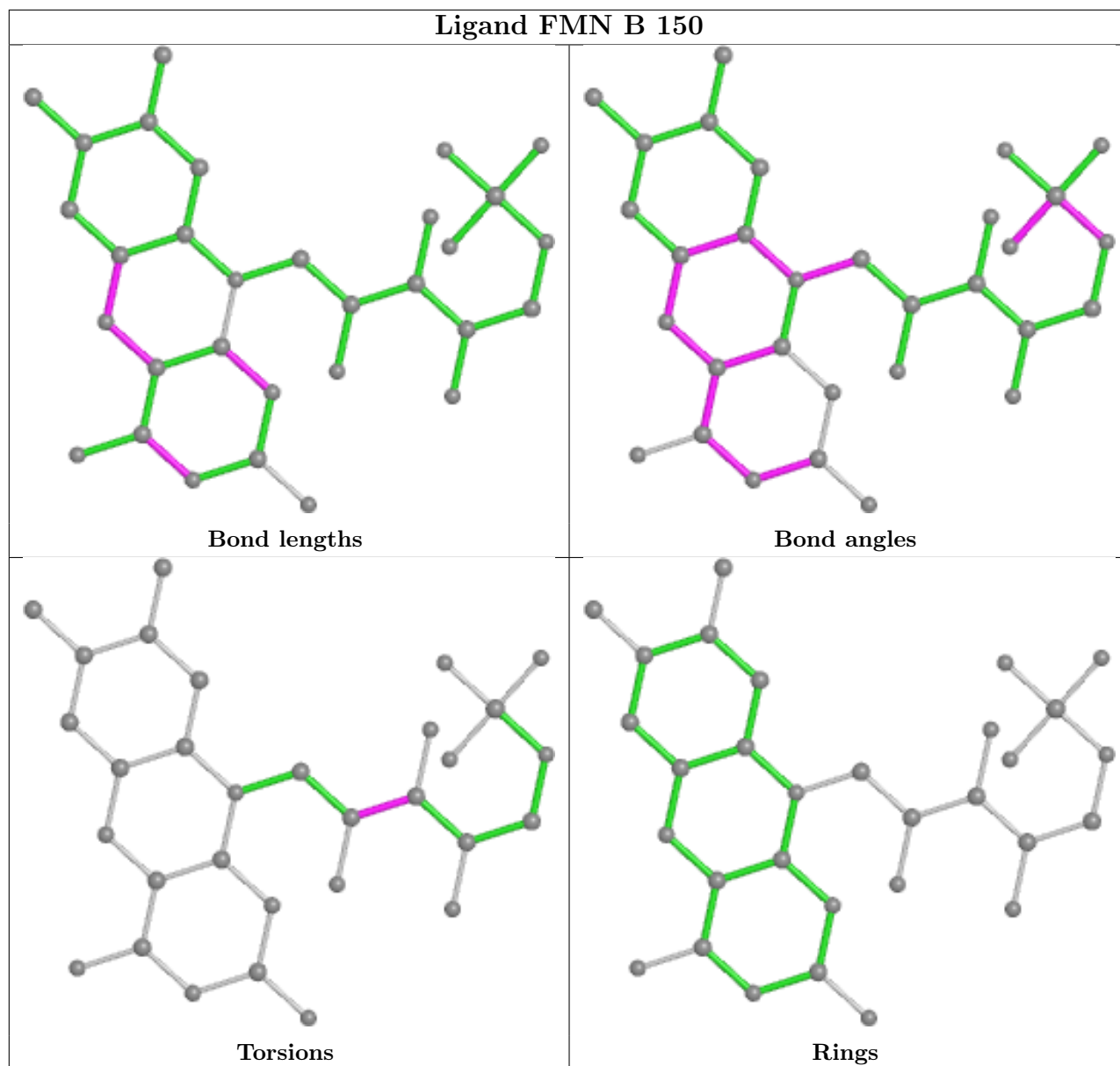
Mol	Chain	Res	Type	Atoms
2	A	149	FMN	O2'-C2'-C3'-C4'
2	B	150	FMN	O2'-C2'-C3'-C4'
2	G	156	FMN	O2'-C2'-C3'-C4'
2	G	156	FMN	O2'-C2'-C3'-O3'
2	D	151	FMN	O2'-C2'-C3'-C4'
2	H	154	FMN	O2'-C2'-C3'-C4'
2	I	155	FMN	O2'-C2'-C3'-C4'
2	F	153	FMN	O2'-C2'-C3'-C4'
2	E	152	FMN	C3'-C4'-C5'-O5'
2	D	151	FMN	O2'-C2'-C3'-O3'
2	H	154	FMN	O2'-C2'-C3'-O3'
2	I	155	FMN	O2'-C2'-C3'-O3'
2	B	150	FMN	O2'-C2'-C3'-O3'
2	I	155	FMN	C5'-O5'-P-O3P
2	H	154	FMN	C5'-O5'-P-O1P
2	F	153	FMN	O2'-C2'-C3'-O3'
2	E	152	FMN	C4'-C5'-O5'-P
2	I	155	FMN	C5'-O5'-P-O2P

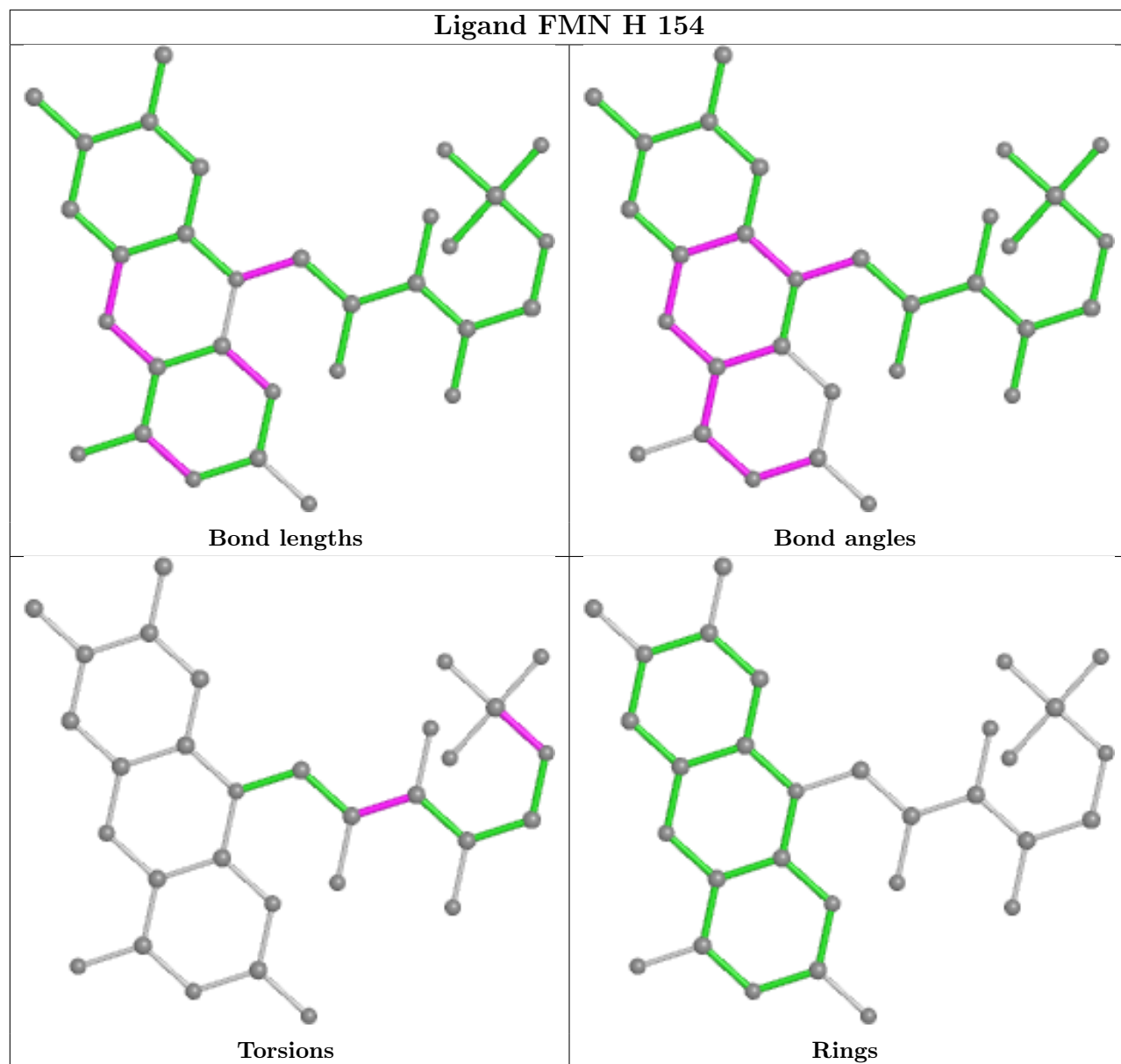
There are no ring outliers.

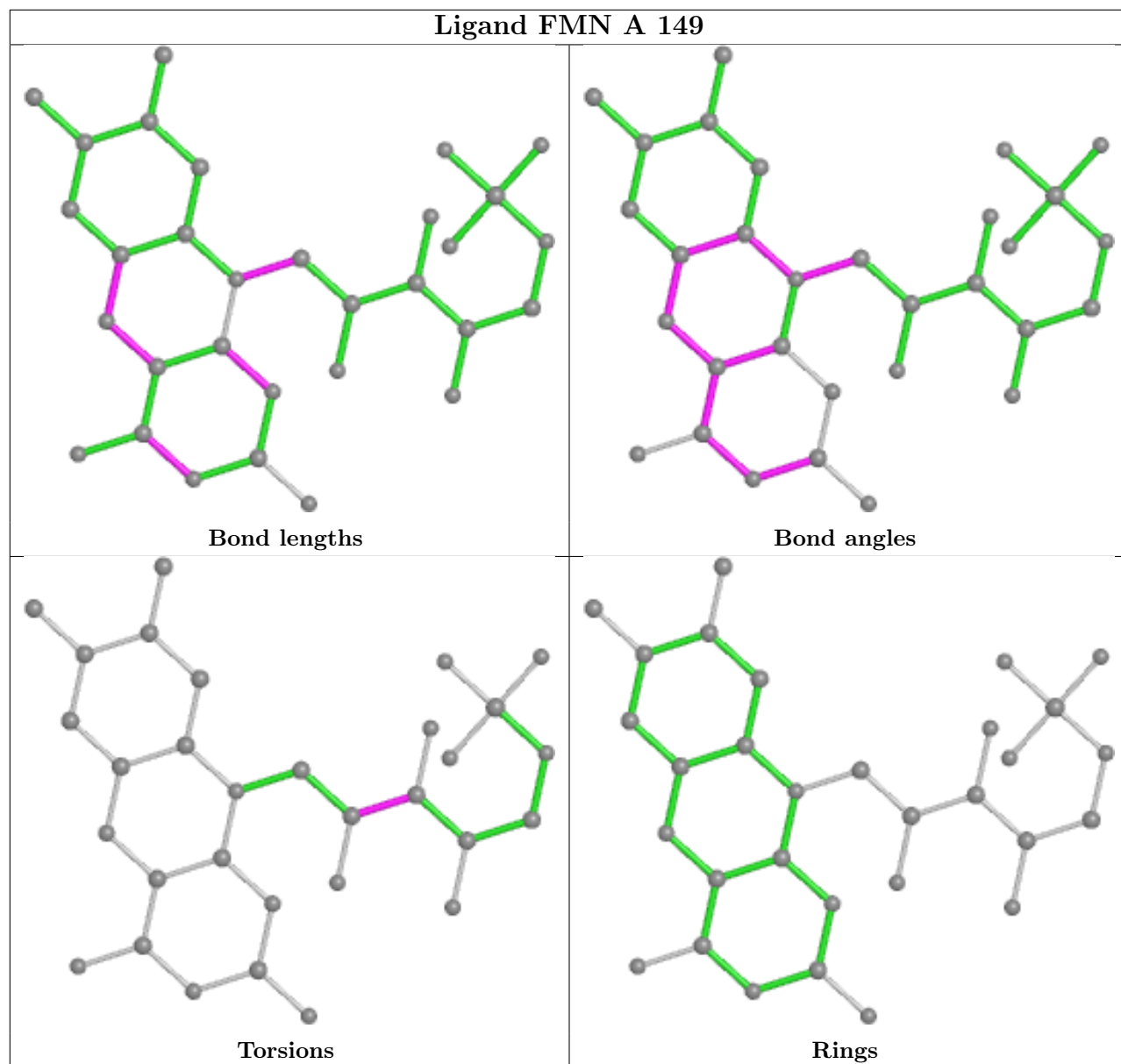
4 monomers are involved in 8 short contacts:

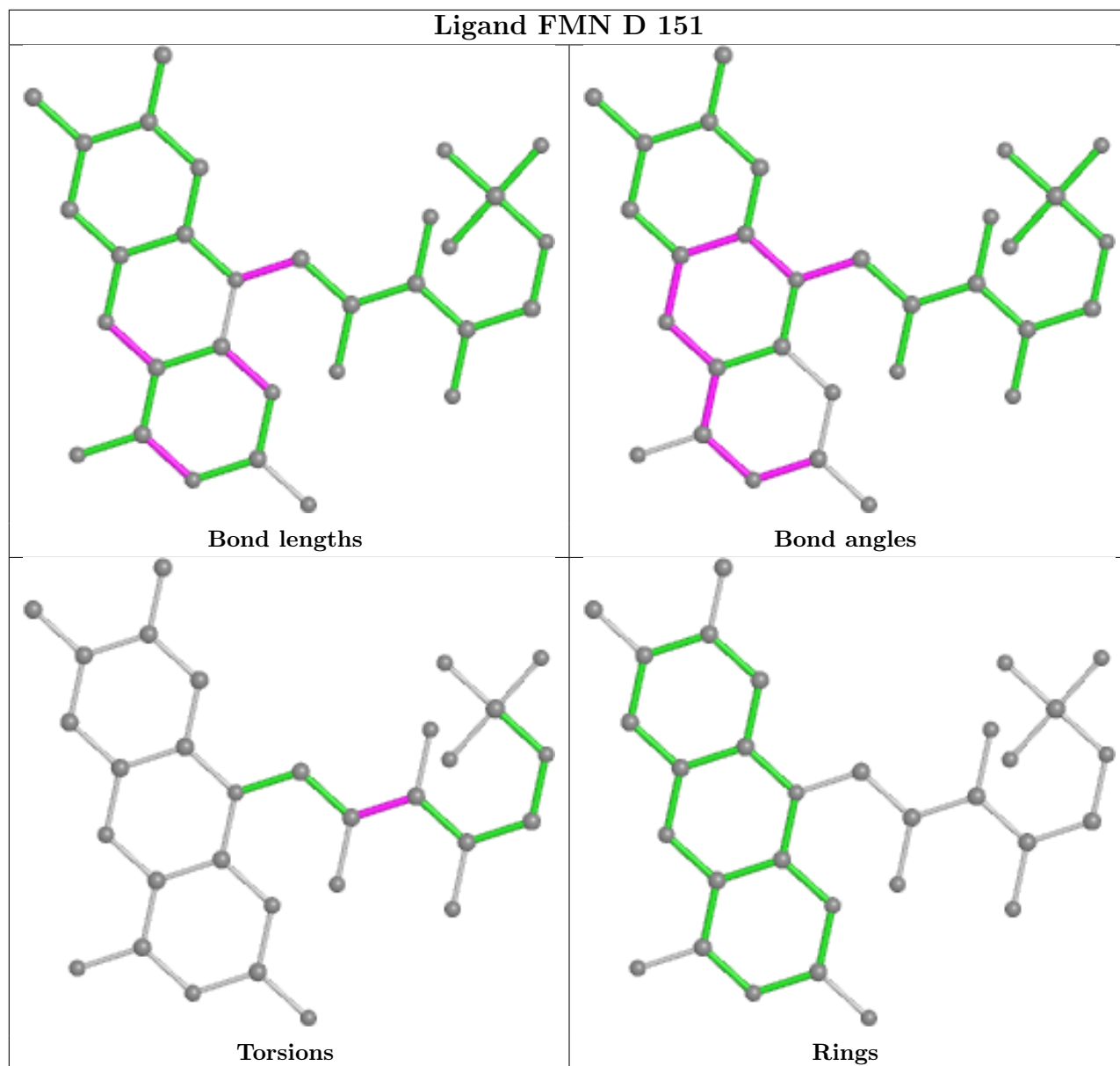
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	149	FMN	3	0
2	D	151	FMN	1	0
2	E	152	FMN	2	0
2	I	155	FMN	2	0

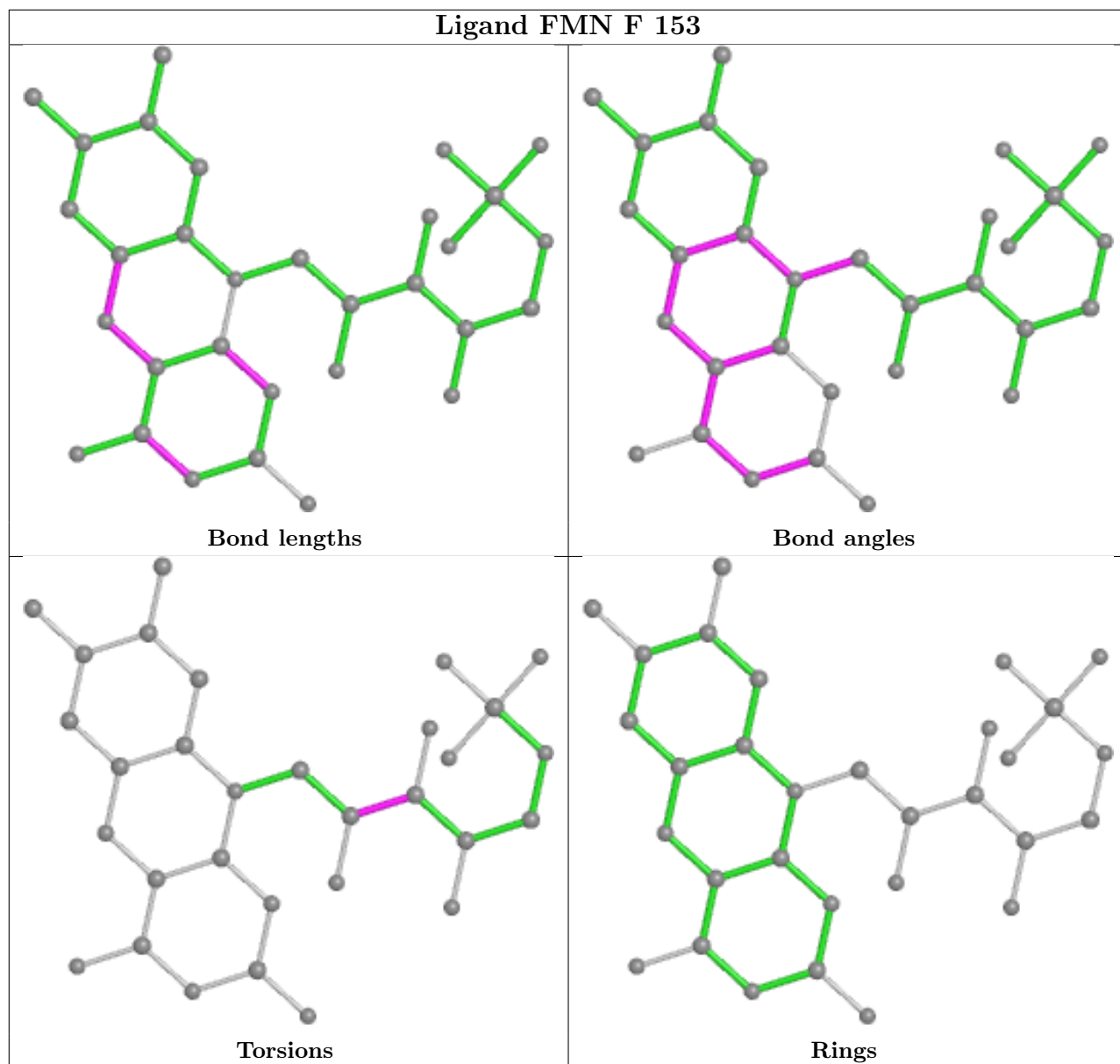
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

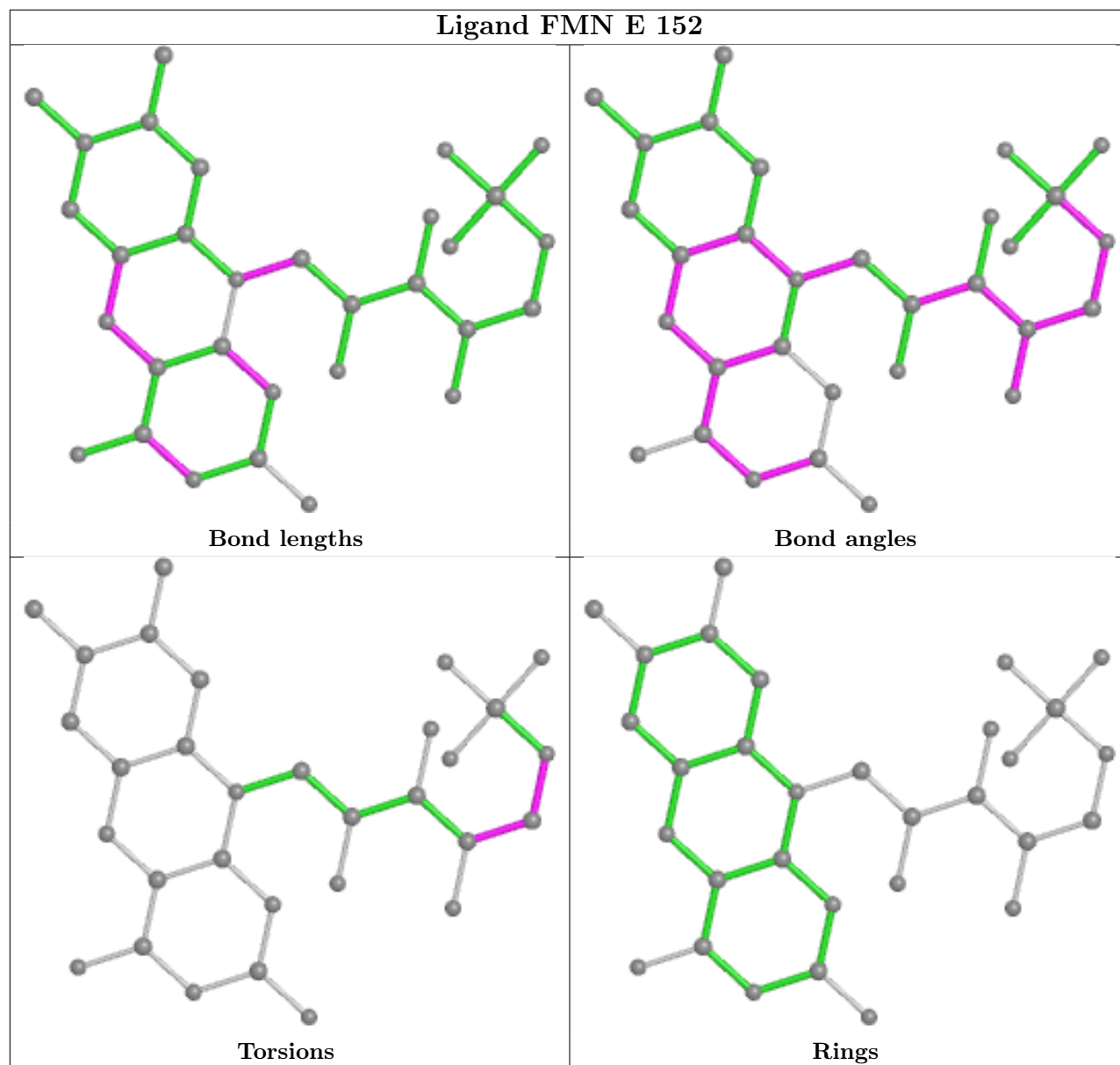


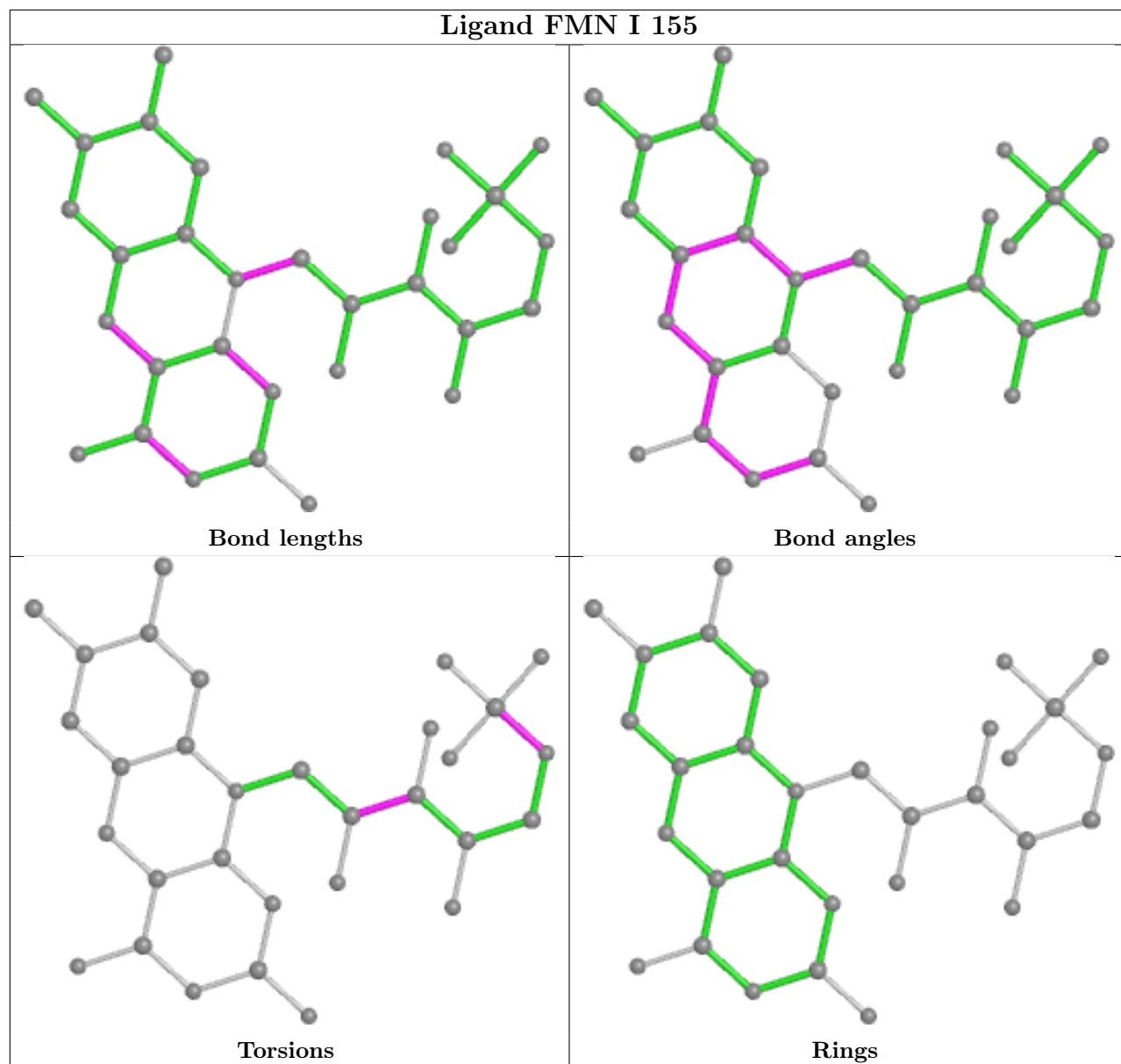


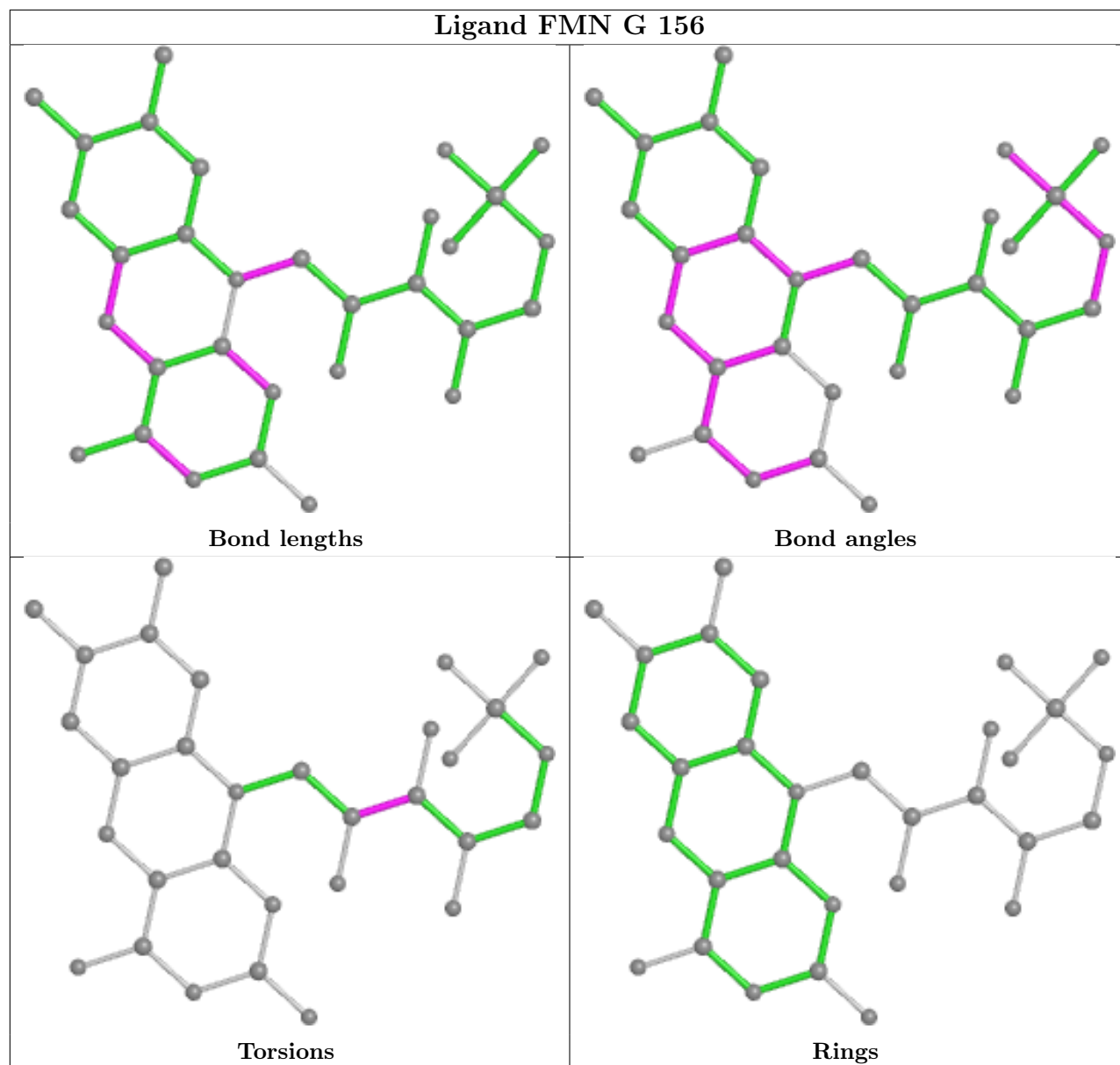












5.7 Other polymers [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

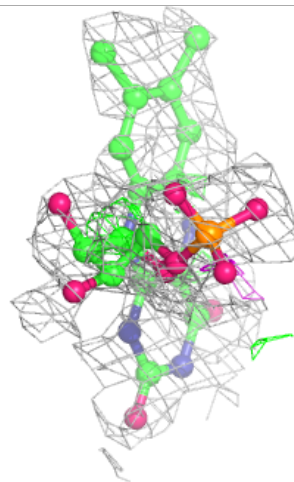
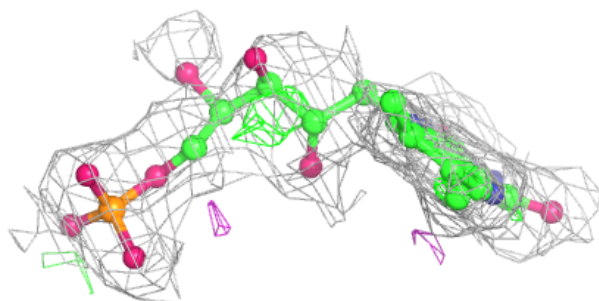
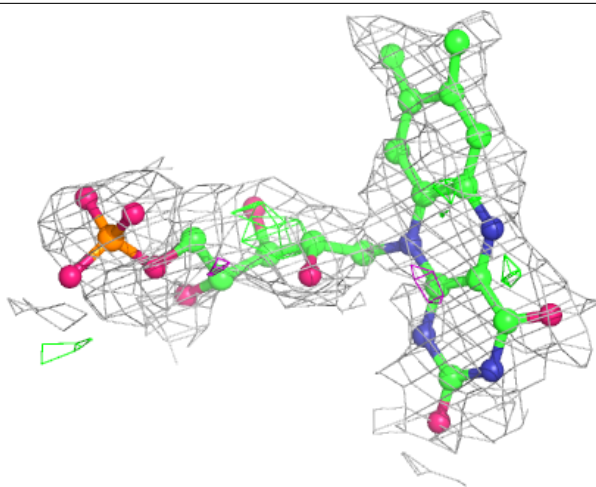
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

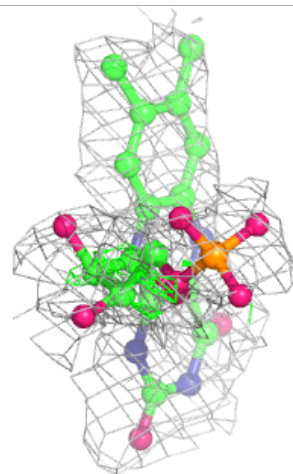
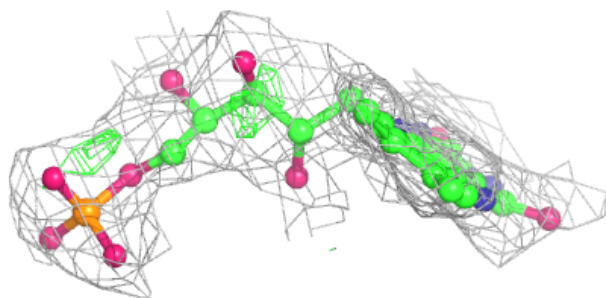
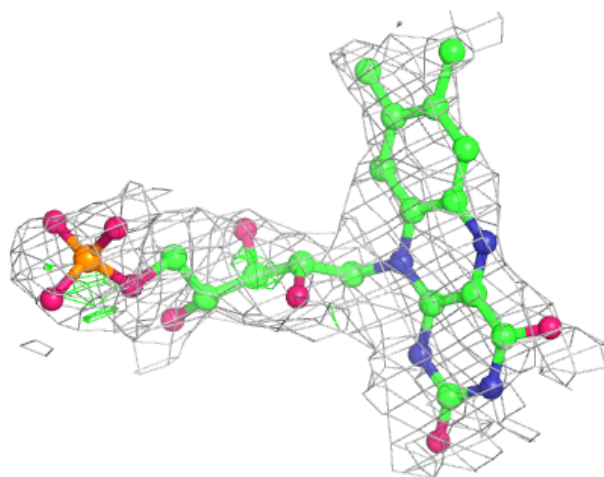
Electron density around FMN A 149:

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



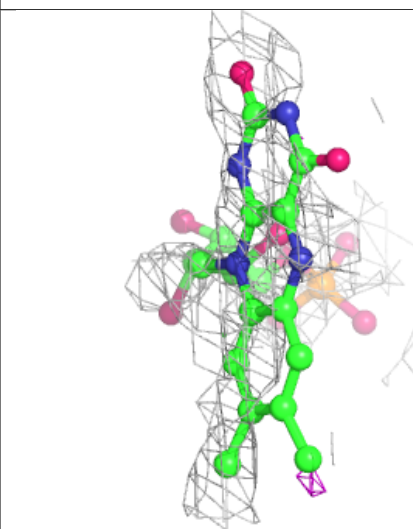
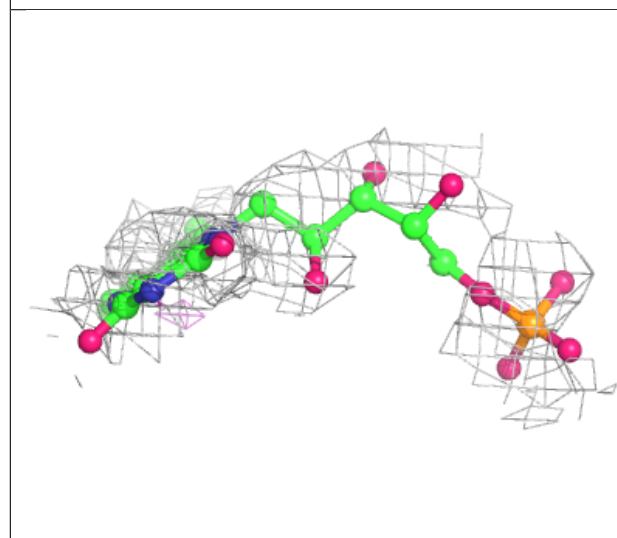
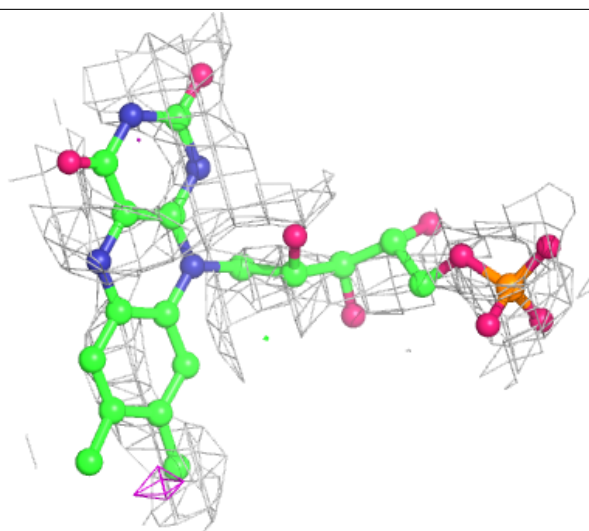
Electron density around FMN B 150:

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



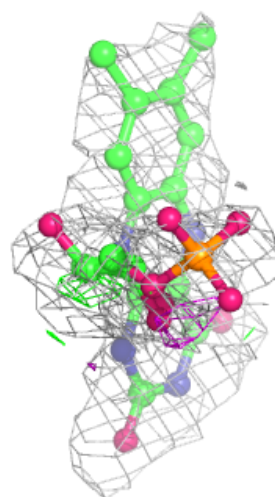
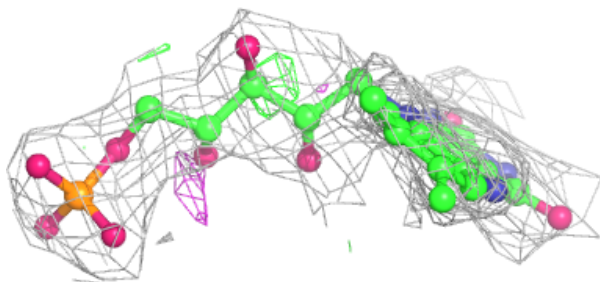
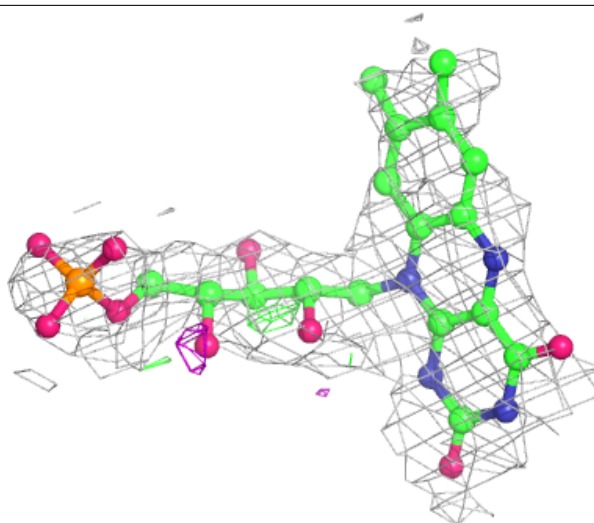
Electron density around FMN D 151:

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



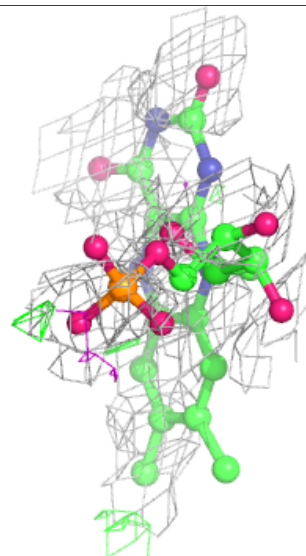
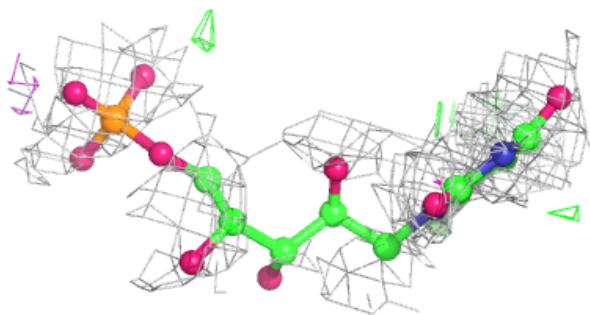
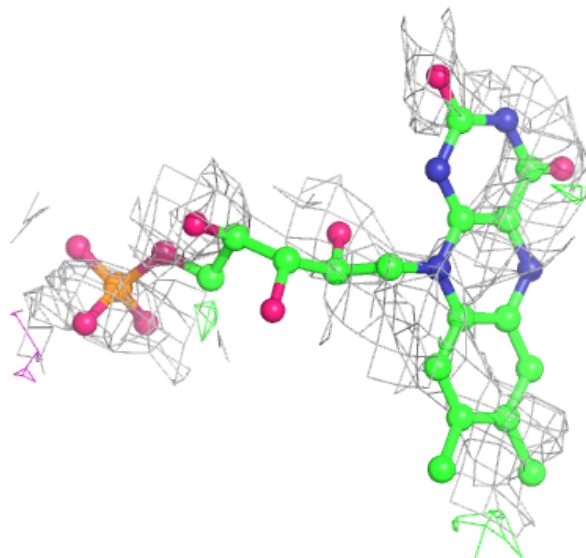
Electron density around FMN E 152:

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



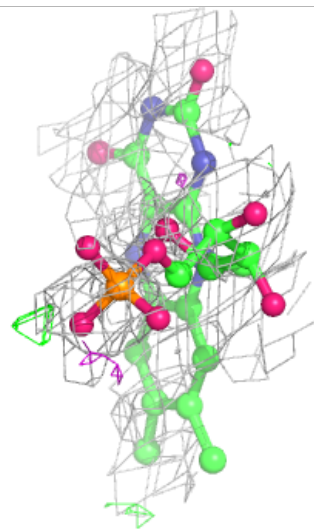
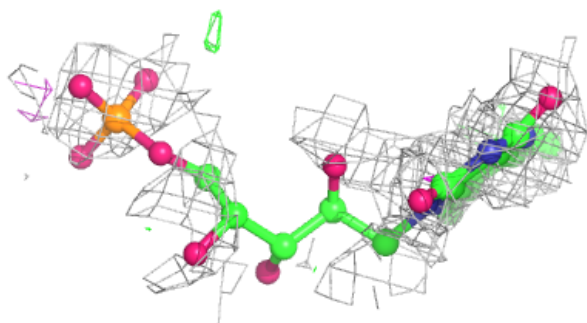
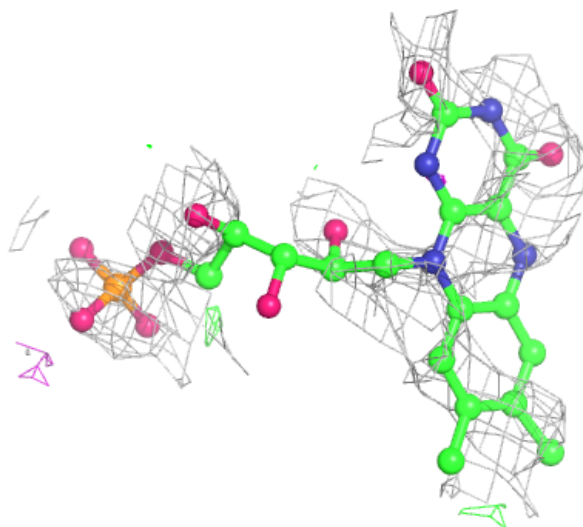
Electron density around FMN F 153:

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



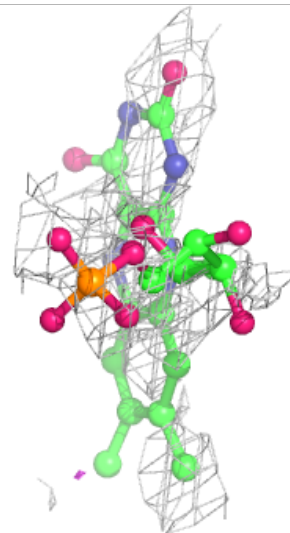
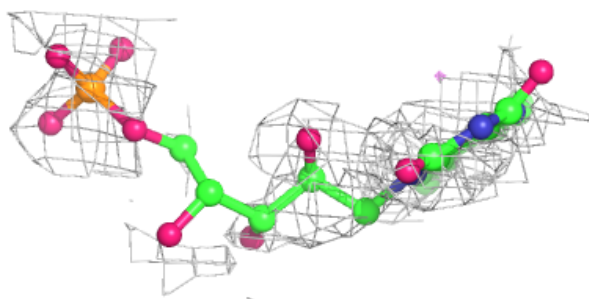
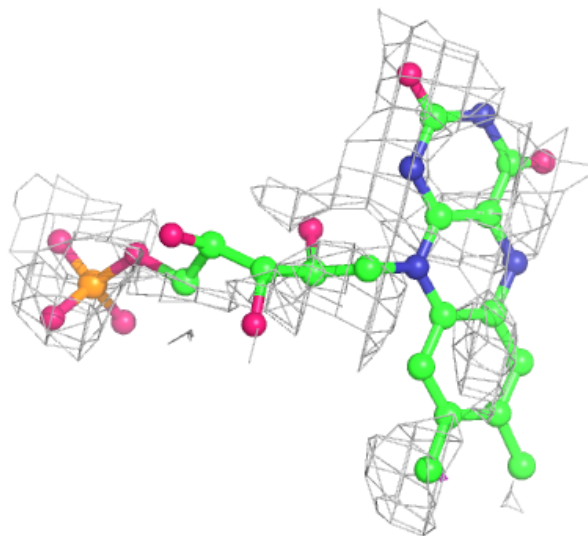
Electron density around FMN H 154:

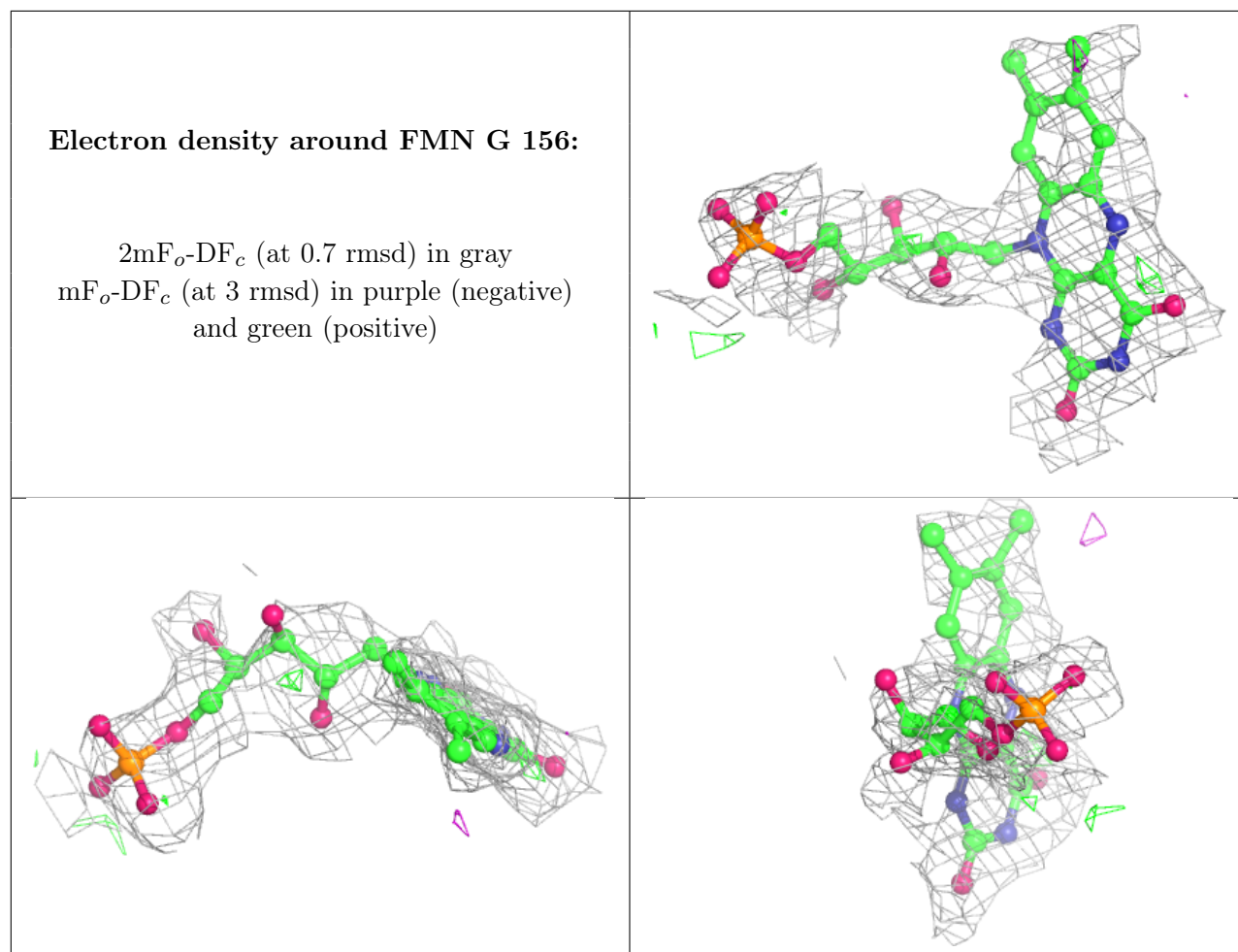
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FMN I 155:

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





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

Unable to reproduce the depositor's R factor - this section is therefore empty.