



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:36 PM UTC

PDB ID : 5EBU / pdb_00005ebu
Title : Aerococcus viridans L-lactate oxidase Y215F mutant
Authors : Rainer, D.; Nidetzky, B.; Wilson, D.K.
Deposited on : 2015-10-19
Resolution : 2.60 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

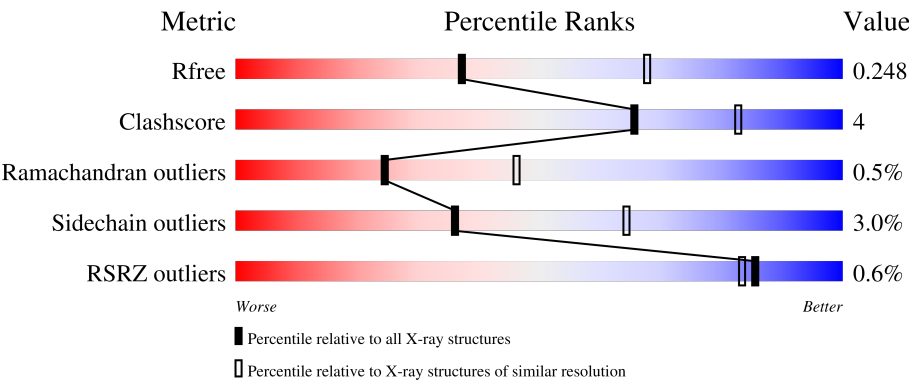
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	374	86%11%..
1	B	374	89%8%..
1	C	374	%88%9%..
1	D	374	%80%14%6%
1	E	374	87%11%.

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Mol	Chain	Length	Quality of chain
1	F	374	2% 83% 13% ..
1	G	374	88% 10% ..
1	H	374	84% 9% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 22897 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 L-lactate oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			2822	1785	490	540	7			
1	B	367	Total	C	N	O	S	0	0	0
			2822	1785	490	540	7			
1	C	367	Total	C	N	O	S	0	0	0
			2822	1785	490	540	7			
1	D	353	Total	C	N	O	S	0	0	0
			2711	1716	468	521	6			
1	E	367	Total	C	N	O	S	0	0	0
			2822	1785	490	540	7			
1	F	367	Total	C	N	O	S	0	0	0
			2822	1785	490	540	7			
1	G	367	Total	C	N	O	S	0	0	0
			2822	1785	490	540	7			
1	H	350	Total	C	N	O	S	0	0	0
			2690	1703	465	516	6			

There are 40 discrepancies between the modelled and reference sequences:

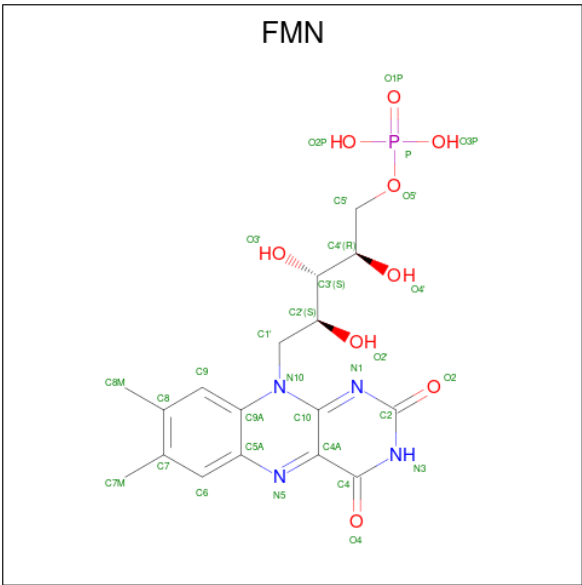
Chain	Residue	Modelled	Actual	Comment	Reference
A	102	ALA	THR	engineered mutation	UNP Q44467
A	163	GLY	SER	engineered mutation	UNP Q44467
A	215	PHE	TYR	engineered mutation	UNP Q44467
A	232	ALA	GLY	engineered mutation	UNP Q44467
A	255	ALA	ARG	engineered mutation	UNP Q44467
B	102	ALA	THR	engineered mutation	UNP Q44467
B	163	GLY	SER	engineered mutation	UNP Q44467
B	215	PHE	TYR	engineered mutation	UNP Q44467
B	232	ALA	GLY	engineered mutation	UNP Q44467
B	255	ALA	ARG	engineered mutation	UNP Q44467
C	102	ALA	THR	engineered mutation	UNP Q44467
C	163	GLY	SER	engineered mutation	UNP Q44467
C	215	PHE	TYR	engineered mutation	UNP Q44467

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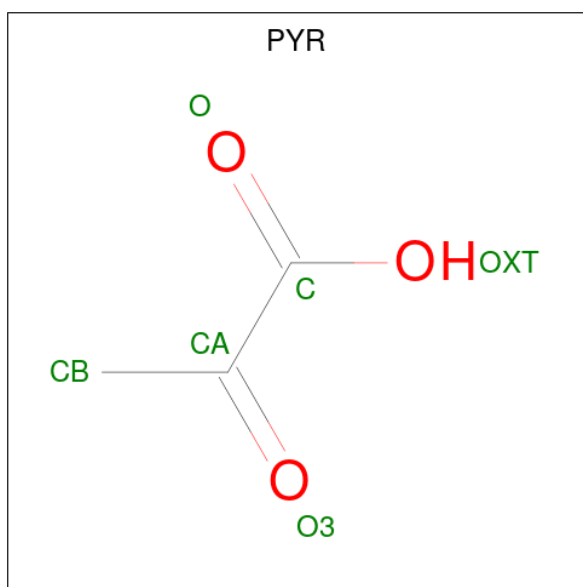
Chain	Residue	Modelled	Actual	Comment	Reference
C	232	ALA	GLY	engineered mutation	UNP Q44467
C	255	ALA	ARG	engineered mutation	UNP Q44467
D	102	ALA	THR	engineered mutation	UNP Q44467
D	163	GLY	SER	engineered mutation	UNP Q44467
D	215	PHE	TYR	engineered mutation	UNP Q44467
D	232	ALA	GLY	engineered mutation	UNP Q44467
D	255	ALA	ARG	engineered mutation	UNP Q44467
E	102	ALA	THR	engineered mutation	UNP Q44467
E	163	GLY	SER	engineered mutation	UNP Q44467
E	215	PHE	TYR	engineered mutation	UNP Q44467
E	232	ALA	GLY	engineered mutation	UNP Q44467
E	255	ALA	ARG	engineered mutation	UNP Q44467
F	102	ALA	THR	engineered mutation	UNP Q44467
F	163	GLY	SER	engineered mutation	UNP Q44467
F	215	PHE	TYR	engineered mutation	UNP Q44467
F	232	ALA	GLY	engineered mutation	UNP Q44467
F	255	ALA	ARG	engineered mutation	UNP Q44467
G	102	ALA	THR	engineered mutation	UNP Q44467
G	163	GLY	SER	engineered mutation	UNP Q44467
G	215	PHE	TYR	engineered mutation	UNP Q44467
G	232	ALA	GLY	engineered mutation	UNP Q44467
G	255	ALA	ARG	engineered mutation	UNP Q44467
H	102	ALA	THR	engineered mutation	UNP Q44467
H	163	GLY	SER	engineered mutation	UNP Q44467
H	215	PHE	TYR	engineered mutation	UNP Q44467
H	232	ALA	GLY	engineered mutation	UNP Q44467
H	255	ALA	ARG	engineered mutation	UNP Q44467

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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	C	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	G	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		

- Molecule 3 is PYRUVIC ACID (CCD ID: PYR) (formula: C₃H₄O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	F	1	Total C O 6 3 3	0	0
3	G	1	Total C O 6 3 3	0	0
3	H	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	32	Total O 32 32	0	0
4	B	47	Total O 47 47	0	0
4	C	25	Total O 25 25	0	0
4	D	23	Total O 23 23	0	0

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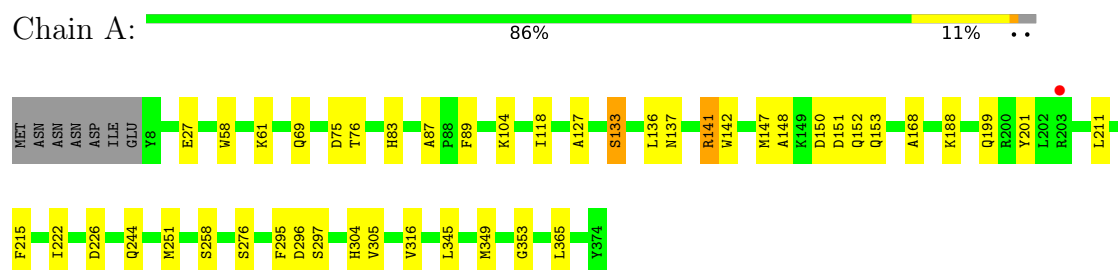
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	36	Total 36	O 36	0	0
4	F	36	Total 36	O 36	0	0
4	G	39	Total 39	O 39	0	0
4	H	30	Total 30	O 30	0	0

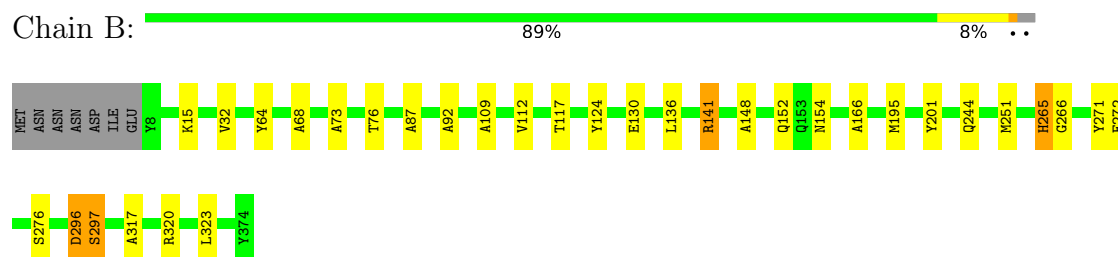
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

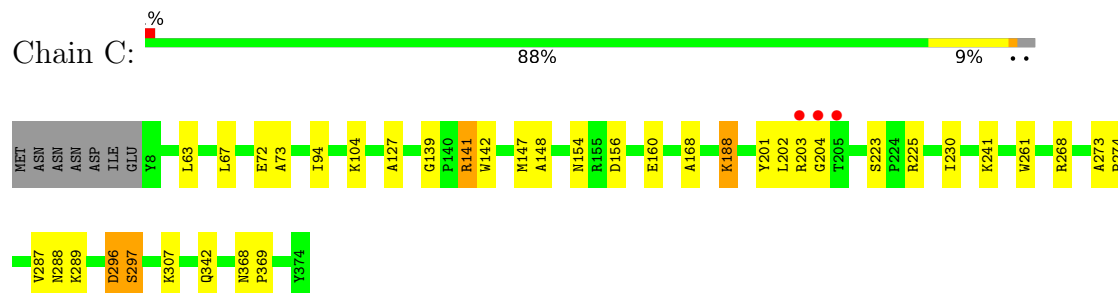
• Molecule 1: L-lactate oxidase



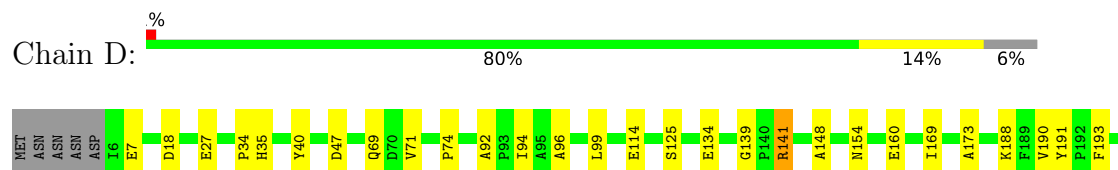
• Molecule 1: L-lactate oxidase

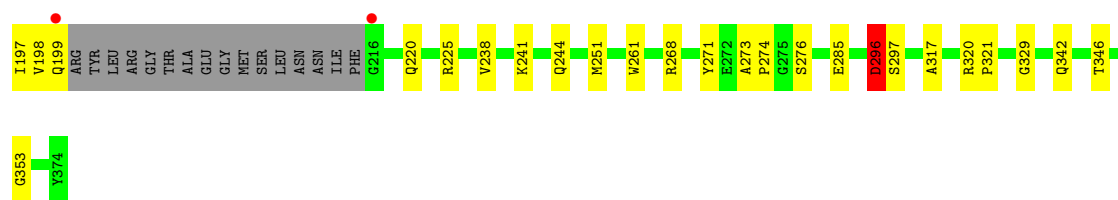


• Molecule 1: L-lactate oxidase



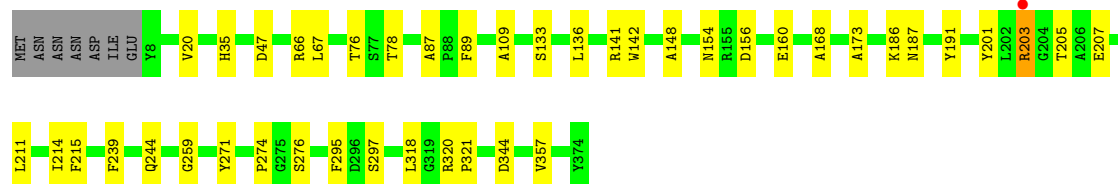
• Molecule 1: L-lactate oxidase





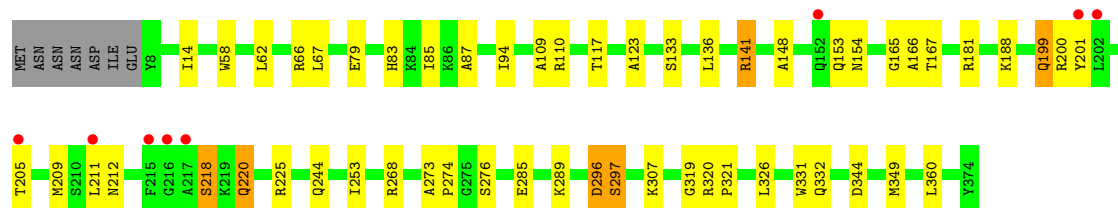
- Molecule 1: L-lactate oxidase

Chain E: 87% 11% .



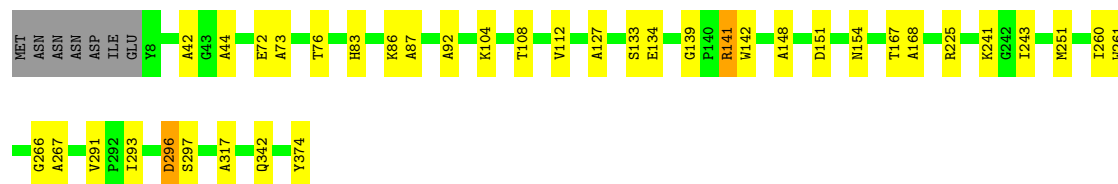
- Molecule 1: L-lactate oxidase

Chain F: 83% 13% . .



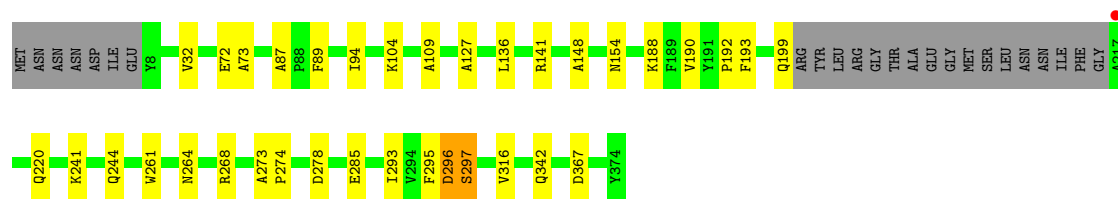
- Molecule 1: L-lactate oxidase

Chain G: 88% 10% . .



- Molecule 1: L-lactate oxidase

Chain H: 84% 9% . 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	107.35Å 119.18Å 119.56Å 90.00° 107.52° 90.00°	Depositor
Resolution (Å)	39.75 – 2.60 39.75 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.75-2.60) 99.3 (39.75-2.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.06 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.182 , 0.246 0.189 , 0.248	Depositor DCC
R_{free} test set	2637 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 18.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22897	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 80.25 % 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 4.6643e-07. 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PYR, 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	0.82	0/2886	0.99	0/3910
1	B	0.85	1/2886 (0.0%)	1.04	5/3910 (0.1%)
1	C	0.82	0/2886	0.98	2/3910 (0.1%)
1	D	0.83	0/2772	0.98	1/3756 (0.0%)
1	E	0.85	0/2886	0.99	2/3910 (0.1%)
1	F	0.86	0/2886	1.01	2/3910 (0.1%)
1	G	0.84	1/2886 (0.0%)	1.00	2/3910 (0.1%)
1	H	0.84	0/2751	0.99	1/3728 (0.0%)
All	All	0.84	2/22839 (0.0%)	1.00	15/30944 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	73	ALA	C-O	-6.21	1.21	1.23
1	G	291	VAL	C-O	-5.11	1.20	1.24

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	64	TYR	CA-C-N	-6.55	113.20	120.14
1	B	64	TYR	C-N-CA	-6.55	113.20	120.14
1	B	320	ARG	CA-C-N	-6.03	112.30	119.84
1	B	320	ARG	C-N-CA	-6.03	112.30	119.84
1	B	32	VAL	N-CA-C	5.90	117.77	112.17
1	C	202	LEU	N-CA-C	-5.79	105.71	112.89
1	G	151	ASP	N-CA-C	5.76	119.12	111.75
1	C	204	GLY	N-CA-C	-5.64	105.97	112.29
1	F	212	ASN	N-CA-C	5.58	117.83	111.02
1	H	32	VAL	CB-CA-C	-5.45	104.93	110.93
1	E	357	VAL	N-CA-C	5.32	116.05	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	296	ASP	N-CA-C	5.30	116.33	108.60
1	F	253	ILE	N-CA-C	-5.19	105.65	110.53
1	E	20	VAL	N-CA-C	-5.04	106.24	111.58
1	G	42	ALA	N-CA-C	5.02	116.83	111.36

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	2822	0	2754	24	0
1	B	2822	0	2754	17	0
1	C	2822	0	2754	20	0
1	D	2711	0	2643	23	0
1	E	2822	0	2754	22	0
1	F	2822	0	2754	32	0
1	G	2822	0	2754	17	0
1	H	2690	0	2623	17	0
2	A	31	0	19	0	0
2	B	31	0	19	2	0
2	C	31	0	19	2	0
2	D	31	0	19	2	0
2	E	31	0	19	0	0
2	F	31	0	19	5	0
2	G	31	0	19	0	0
2	H	31	0	19	2	0
3	A	6	0	0	0	0
3	B	6	0	0	2	0
3	C	6	0	0	0	0
3	D	6	0	0	0	0
3	E	6	0	0	0	0
3	F	6	0	0	1	0
3	G	6	0	0	0	0
3	H	6	0	0	0	0
4	A	32	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	47	0	0	0	0
4	C	25	0	0	0	0
4	D	23	0	0	0	0
4	E	36	0	0	0	0
4	F	36	0	0	0	0
4	G	39	0	0	0	0
4	H	30	0	0	0	0
All	All	22897	0	21942	171	0

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

All (171) 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:B:148:ALA:H	1:B:154:ASN:HD21	1.15	0.94
1:C:147:MET:HE3	1:C:230:ILE:HD11	1.62	0.81
1:H:94:ILE:HG23	2:H:400:FMN:C6	2.18	0.73
1:F:199:GLN:HE21	1:F:199:GLN:HA	1.56	0.70
1:C:148:ALA:H	1:C:154:ASN:HD21	1.40	0.69
1:A:148:ALA:HB2	1:A:201:TYR:CD2	2.29	0.67
1:F:148:ALA:H	1:F:154:ASN:HD21	1.42	0.67
1:E:148:ALA:H	1:E:154:ASN:HD21	1.42	0.67
1:E:148:ALA:HB2	1:E:201:TYR:CD2	2.32	0.64
1:G:148:ALA:H	1:G:154:ASN:HD21	1.44	0.63
1:G:241:LYS:HA	1:G:261:TRP:HB3	1.81	0.63
1:C:241:LYS:HA	1:C:261:TRP:HB3	1.82	0.60
1:G:296:ASP:C	1:G:296:ASP:OD1	2.44	0.60
1:E:142:TRP:CD1	1:E:168:ALA:HB3	2.36	0.60
1:F:94:ILE:HG23	2:F:400:FMN:C6	2.32	0.60
1:A:76:THR:O	1:A:87:ALA:HA	2.01	0.60
1:D:273:ALA:HB1	1:D:274:PRO:HD2	1.82	0.60
1:B:148:ALA:N	1:B:154:ASN:HD21	1.94	0.59
1:A:142:TRP:CD1	1:A:168:ALA:HB3	2.38	0.59
1:D:40:TYR:O	1:D:268:ARG:NH2	2.35	0.58
1:A:104:LYS:HE2	1:A:127:ALA:HB2	1.83	0.58
1:D:139:GLY:O	1:D:141:ARG:NH2	2.34	0.58
1:C:142:TRP:CG	1:C:168:ALA:HB3	2.39	0.58
1:H:296:ASP:O	1:H:297:SER:HB2	2.04	0.57
1:F:14:ILE:HG22	1:F:332:GLN:OE1	2.04	0.57
1:B:148:ALA:H	1:B:154:ASN:ND2	1.96	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:THR:O	1:B:87:ALA:HA	2.05	0.56
1:H:241:LYS:HA	1:H:261:TRP:HB3	1.88	0.55
1:G:83:HIS:NE2	1:G:167:THR:OG1	2.36	0.55
1:F:218:SER:O	1:F:220:GLN:NE2	2.40	0.55
1:F:148:ALA:N	1:F:154:ASN:HD21	2.05	0.54
1:C:268:ARG:HD2	2:C:400:FMN:HM82	1.88	0.54
1:D:94:ILE:HG23	2:D:400:FMN:C6	2.36	0.54
1:A:142:TRP:CG	1:A:168:ALA:HB3	2.43	0.54
1:F:148:ALA:HB2	1:F:201:TYR:CG	2.42	0.54
1:D:241:LYS:HA	1:D:261:TRP:HB3	1.91	0.53
1:E:173:ALA:HB3	1:F:67:LEU:HD23	1.90	0.53
1:C:296:ASP:OD1	1:C:296:ASP:C	2.52	0.52
1:E:205:THR:HG23	1:E:207:GLU:H	1.74	0.52
1:G:142:TRP:CD1	1:G:168:ALA:HB3	2.45	0.52
1:E:142:TRP:CG	1:E:168:ALA:HB3	2.45	0.52
1:D:244:GLN:HE22	1:D:276:SER:HA	1.76	0.51
1:F:181:ARG:CZ	1:F:211:LEU:HD21	2.41	0.51
1:C:142:TRP:CD1	1:C:168:ALA:HB3	2.45	0.51
1:B:296:ASP:O	1:B:297:SER:HB2	2.11	0.51
1:E:76:THR:O	1:E:87:ALA:HA	2.10	0.51
1:C:296:ASP:O	1:C:297:SER:HB2	2.11	0.51
1:B:141:ARG:HG2	1:B:166:ALA:HA	1.93	0.50
2:B:400:FMN:C4A	3:B:401:PYR:O3	2.60	0.50
1:E:156:ASP:O	1:E:160:GLU:HG3	2.11	0.50
1:F:148:ALA:HB2	1:F:201:TYR:CD2	2.45	0.50
1:B:296:ASP:OD1	1:B:296:ASP:C	2.53	0.50
1:B:92:ALA:HB2	1:B:317:ALA:HB1	1.94	0.50
1:F:268:ARG:HD2	2:F:400:FMN:HM83	1.94	0.49
1:G:108:THR:O	1:G:112:VAL:HG23	2.12	0.49
1:G:251:MET:C	1:G:251:MET:SD	2.95	0.49
1:D:148:ALA:H	1:D:154:ASN:HD21	1.59	0.49
1:E:191:TYR:CE2	1:E:214:ILE:HD12	2.48	0.49
1:A:136:LEU:O	1:A:137:ASN:C	2.56	0.49
1:E:203:ARG:HD3	1:E:203:ARG:H	1.77	0.49
1:B:148:ALA:HB2	1:B:201:TYR:CD2	2.47	0.49
1:C:94:ILE:HG23	2:C:400:FMN:C6	2.43	0.49
1:B:112:VAL:HG13	1:B:117:THR:HG23	1.95	0.48
1:G:76:THR:O	1:G:87:ALA:HA	2.13	0.48
1:D:47:ASP:OD1	1:D:271:TYR:OH	2.30	0.48
1:H:148:ALA:H	1:H:154:ASN:HD21	1.60	0.48
1:F:109:ALA:HB1	1:F:136:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:296:ASP:O	1:F:297:SER:HB2	2.14	0.48
1:D:96:ALA:HB1	1:D:99:LEU:HG	1.96	0.47
1:E:47:ASP:OD1	1:E:271:TYR:OH	2.32	0.47
1:G:44:ALA:HB1	1:G:267:ALA:O	2.14	0.47
1:E:244:GLN:HE22	1:E:276:SER:HA	1.78	0.47
1:H:296:ASP:OD1	1:H:296:ASP:C	2.56	0.47
1:A:147:MET:HE1	1:A:226:ASP:OD1	2.14	0.47
1:B:124:TYR:HB3	1:B:195:MET:CE	2.44	0.47
1:E:89:PHE:CD1	1:E:318:LEU:HD11	2.49	0.47
1:H:192:PRO:HG2	1:H:193:PHE:CE2	2.49	0.47
1:C:67:LEU:HD23	1:D:173:ALA:HB3	1.96	0.47
1:A:199:GLN:HB3	4:A:503:HOH:O	2.14	0.47
1:F:273:ALA:HB1	1:F:274:PRO:HD2	1.97	0.47
1:A:305:VAL:HG11	1:A:345:LEU:HD22	1.97	0.47
1:A:150:ASP:OD2	1:A:153:GLN:HG3	2.14	0.47
1:A:61:LYS:HB3	1:A:365:LEU:HD13	1.96	0.46
1:H:72:GLU:O	1:H:73:ALA:C	2.58	0.46
1:D:268:ARG:HD2	2:D:400:FMN:C8M	2.45	0.46
1:D:197:ILE:HG22	1:D:197:ILE:O	2.14	0.46
1:F:244:GLN:HE22	1:F:276:SER:HA	1.80	0.46
1:G:139:GLY:O	1:G:141:ARG:NH2	2.49	0.46
1:F:79:GLU:HA	1:F:83:HIS:O	2.14	0.46
1:H:148:ALA:N	1:H:154:ASN:HD21	2.14	0.46
1:G:374:TYR:OH	1:H:278:ASP:OD2	2.26	0.46
1:D:198:VAL:O	1:D:199:GLN:CG	2.64	0.45
1:F:165:GLY:O	1:F:166:ALA:C	2.59	0.45
1:C:139:GLY:O	1:C:141:ARG:NH2	2.49	0.45
1:H:295:PHE:O	1:H:316:VAL:HA	2.17	0.45
1:E:320:ARG:N	1:E:321:PRO:CD	2.80	0.45
1:E:211:LEU:HD11	1:E:215:PHE:CE2	2.51	0.45
1:D:296:ASP:C	1:D:296:ASP:OD1	2.59	0.45
1:H:244:GLN:NE2	1:H:264:ASN:HB3	2.31	0.45
1:A:89:PHE:HA	1:A:316:VAL:O	2.17	0.45
1:D:96:ALA:HB2	1:D:191:TYR:OH	2.17	0.45
1:A:58:TRP:CZ2	1:A:304:HIS:HB3	2.52	0.45
1:F:296:ASP:OD1	1:F:296:ASP:C	2.59	0.44
1:C:223:SER:OG	1:C:225:ARG:NH2	2.50	0.44
1:E:148:ALA:N	1:E:154:ASN:HD21	2.11	0.44
1:G:104:LYS:HE2	1:G:127:ALA:HB2	2.00	0.44
1:H:192:PRO:HG2	1:H:193:PHE:CD2	2.52	0.44
1:B:244:GLN:HE22	1:B:276:SER:HA	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:69:GLN:O	1:D:71:VAL:HG23	2.18	0.44
1:E:35:HIS:HE1	1:E:187:ASN:OD1	2.00	0.44
1:F:349:MET:HG2	1:F:360:LEU:HD21	1.98	0.44
1:D:251:MET:C	1:D:251:MET:SD	3.01	0.44
1:A:75:ASP:O	1:A:349:MET:HE1	2.17	0.44
1:F:66:ARG:C	1:F:67:LEU:HD12	2.43	0.44
1:F:268:ARG:HD2	2:F:400:FMN:C8M	2.48	0.44
1:G:142:TRP:CG	1:G:168:ALA:HB3	2.53	0.44
1:F:133:SER:OG	1:F:141:ARG:NH1	2.50	0.44
1:F:85:ILE:HG22	1:F:117:THR:HA	2.00	0.43
1:F:85:ILE:HD12	1:F:87:ALA:O	2.17	0.43
1:G:243:ILE:HD12	1:G:260:ILE:HG23	2.00	0.43
1:H:109:ALA:HB1	1:H:136:LEU:HG	2.00	0.43
1:A:69:GLN:HG3	1:A:353:GLY:HA3	2.00	0.43
1:A:244:GLN:HE22	1:A:276:SER:HA	1.83	0.43
1:C:72:GLU:O	1:C:73:ALA:C	2.60	0.43
1:H:104:LYS:HE2	1:H:127:ALA:HB2	2.01	0.43
1:F:319:GLY:O	1:F:320:ARG:C	2.61	0.43
1:C:104:LYS:HE2	1:C:127:ALA:HB2	1.99	0.43
1:B:265:HIS:O	1:B:266:GLY:C	2.59	0.43
1:E:274:PRO:HA	1:F:62:LEU:HD13	2.00	0.43
1:G:266:GLY:O	1:G:267:ALA:HB3	2.20	0.42
1:C:148:ALA:HB2	1:C:201:TYR:CD2	2.54	0.42
1:C:273:ALA:HB1	1:C:274:PRO:HD2	2.00	0.42
1:D:34:PRO:O	1:D:35:HIS:C	2.62	0.42
1:D:92:ALA:HB2	1:D:317:ALA:HB1	2.02	0.42
1:F:205:THR:O	1:F:209:MET:SD	2.78	0.42
1:F:109:ALA:HB1	1:F:136:LEU:CD2	2.49	0.42
1:F:153:GLN:CD	1:F:201:TYR:HB3	2.45	0.42
2:B:400:FMN:C4	3:B:401:PYR:O3	2.68	0.41
1:E:66:ARG:C	1:E:67:LEU:HD12	2.45	0.41
1:E:239:PHE:HA	1:E:259:GLY:O	2.21	0.41
1:G:92:ALA:HB2	1:G:317:ALA:HB1	2.01	0.41
1:H:268:ARG:HD2	2:H:400:FMN:HM83	2.01	0.41
1:C:63:LEU:HG	1:C:307:LYS:HE2	2.03	0.41
1:F:58:TRP:O	1:F:307:LYS:NZ	2.54	0.41
1:H:273:ALA:HB1	1:H:274:PRO:HD2	2.02	0.41
1:B:251:MET:SD	1:B:251:MET:C	3.03	0.41
1:F:320:ARG:N	1:F:321:PRO:HD2	2.36	0.41
1:B:271:TYR:CD2	1:B:272:GLU:HB2	2.55	0.41
1:A:211:LEU:HD11	1:A:215:PHE:CZ	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:74:PRO:HG2	1:D:346:THR:HG23	2.03	0.41
2:F:400:FMN:HM81	2:F:400:FMN:HM73	1.88	0.41
1:A:83:HIS:HB2	1:A:118:ILE:HD11	2.02	0.41
1:A:151:ASP:O	1:A:152:GLN:C	2.64	0.41
1:A:296:ASP:OD1	1:A:296:ASP:C	2.64	0.41
1:C:156:ASP:O	1:C:160:GLU:HG3	2.20	0.41
1:E:109:ALA:HB1	1:E:136:LEU:HG	2.02	0.41
1:E:295:PHE:CD1	1:E:295:PHE:C	2.99	0.41
1:F:110:ARG:HB3	1:F:331:TRP:HB2	2.03	0.41
1:G:72:GLU:O	1:G:73:ALA:C	2.64	0.41
1:A:222:ILE:O	1:B:68:ALA:HA	2.21	0.41
1:D:69:GLN:HG3	1:D:353:GLY:HA3	2.02	0.40
1:D:169:ILE:O	1:D:238:VAL:HA	2.20	0.40
1:A:295:PHE:CD2	1:A:295:PHE:C	3.00	0.40
2:F:400:FMN:C4A	3:F:401:PYR:O3	2.69	0.40
1:A:133:SER:OG	1:A:141:ARG:NH1	2.54	0.40
1:B:109:ALA:HB1	1:B:136:LEU:CD2	2.50	0.40
1:D:320:ARG:N	1:D:321:PRO:HD2	2.37	0.40
1:C:368:ASN:HA	1:C:369:PRO:HD2	1.91	0.40
1:A:251:MET:C	1:A:251:MET:SD	3.04	0.40
1:C:287:VAL:O	1:C:288:ASN:C	2.65	0.40
1:H:87:ALA:C	1:H:89:PHE:H	2.29	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	365/374 (98%)	350 (96%)	14 (4%)	1 (0%)	36 58
1	B	365/374 (98%)	349 (96%)	15 (4%)	1 (0%)	36 58
1	C	365/374 (98%)	346 (95%)	16 (4%)	3 (1%)	16 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	349/374 (93%)	331 (95%)	16 (5%)	2 (1%)	21	42
1	E	365/374 (98%)	349 (96%)	15 (4%)	1 (0%)	36	58
1	F	365/374 (98%)	338 (93%)	24 (7%)	3 (1%)	16	34
1	G	365/374 (98%)	352 (96%)	12 (3%)	1 (0%)	36	58
1	H	346/374 (92%)	328 (95%)	17 (5%)	1 (0%)	36	58
All	All	2885/2992 (96%)	2743 (95%)	129 (4%)	13 (0%)	24	46

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	297	SER
1	B	297	SER
1	C	297	SER
1	E	297	SER
1	F	297	SER
1	G	297	SER
1	C	203	ARG
1	D	297	SER
1	H	297	SER
1	F	200	ARG
1	C	188	LYS
1	F	123	ALA
1	D	329	GLY

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	288/295 (98%)	283 (98%)	5 (2%)	53	78
1	B	288/295 (98%)	281 (98%)	7 (2%)	43	70
1	C	288/295 (98%)	283 (98%)	5 (2%)	53	78
1	D	277/295 (94%)	261 (94%)	16 (6%)	18	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	E	288/295 (98%)	282 (98%)	6 (2%)	47 73
1	F	288/295 (98%)	276 (96%)	12 (4%)	26 52
1	G	288/295 (98%)	280 (97%)	8 (3%)	38 66
1	H	275/295 (93%)	265 (96%)	10 (4%)	31 58
All	All	2280/2360 (97%)	2211 (97%)	69 (3%)	36 64

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	GLU
1	A	133	SER
1	A	141	ARG
1	A	188	LYS
1	A	258	SER
1	B	15	LYS
1	B	130	GLU
1	B	141	ARG
1	B	152	GLN
1	B	265	HIS
1	B	296	ASP
1	B	323	LEU
1	C	141	ARG
1	C	188	LYS
1	C	289	LYS
1	C	296	ASP
1	C	342	GLN
1	D	7	GLU
1	D	18	ASP
1	D	27	GLU
1	D	114	GLU
1	D	125	SER
1	D	134	GLU
1	D	141	ARG
1	D	160	GLU
1	D	188	LYS
1	D	190	VAL
1	D	193	PHE
1	D	220	GLN
1	D	225	ARG
1	D	285	GLU
1	D	296	ASP

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Mol	Chain	Res	Type
1	D	342	GLN
1	E	78	THR
1	E	133	SER
1	E	141	ARG
1	E	186	LYS
1	E	203	ARG
1	E	344	ASP
1	F	141	ARG
1	F	167	THR
1	F	188	LYS
1	F	199	GLN
1	F	218	SER
1	F	220	GLN
1	F	225	ARG
1	F	285	GLU
1	F	289	LYS
1	F	296	ASP
1	F	326	LEU
1	F	344	ASP
1	G	86	LYS
1	G	133	SER
1	G	134	GLU
1	G	141	ARG
1	G	225	ARG
1	G	293	ILE
1	G	296	ASP
1	G	342	GLN
1	H	141	ARG
1	H	188	LYS
1	H	190	VAL
1	H	199	GLN
1	H	220	GLN
1	H	285	GLU
1	H	293	ILE
1	H	296	ASP
1	H	342	GLN
1	H	367	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	ASN

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Mol	Chain	Res	Type
1	A	199	GLN
1	A	244	GLN
1	A	332	GLN
1	B	154	ASN
1	B	244	GLN
1	B	332	GLN
1	C	144	GLN
1	C	154	ASN
1	C	199	GLN
1	C	342	GLN
1	C	350	GLN
1	D	35	HIS
1	D	69	GLN
1	D	153	GLN
1	D	154	ASN
1	D	220	GLN
1	D	244	GLN
1	E	35	HIS
1	E	154	ASN
1	E	244	GLN
1	F	154	ASN
1	F	244	GLN
1	G	35	HIS
1	G	154	ASN
1	H	154	ASN
1	H	244	GLN

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

16 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	C	400	-	33,33,33	1.43	5 (15%)	48,50,50	1.17	4 (8%)
2	FMN	G	400	-	33,33,33	1.42	4 (12%)	48,50,50	1.19	3 (6%)
2	FMN	B	400	-	33,33,33	1.61	5 (15%)	48,50,50	1.21	5 (10%)
2	FMN	A	400	-	33,33,33	1.34	3 (9%)	48,50,50	1.20	4 (8%)
3	PYR	F	401	-	5,5,5	1.42	1 (20%)	3,6,6	1.50	1 (33%)
3	PYR	B	401	-	5,5,5	1.74	2 (40%)	3,6,6	2.13	1 (33%)
3	PYR	D	401	-	5,5,5	1.21	0	3,6,6	1.71	1 (33%)
3	PYR	H	401	-	5,5,5	1.25	0	3,6,6	1.88	1 (33%)
2	FMN	F	400	-	33,33,33	1.57	4 (12%)	48,50,50	1.49	8 (16%)
2	FMN	H	400	-	33,33,33	1.39	2 (6%)	48,50,50	1.45	10 (20%)
3	PYR	A	401	-	5,5,5	1.76	1 (20%)	3,6,6	1.20	0
3	PYR	E	401	-	5,5,5	1.79	1 (20%)	3,6,6	0.86	0
2	FMN	E	400	-	33,33,33	1.46	4 (12%)	48,50,50	1.28	7 (14%)
3	PYR	G	401	-	5,5,5	1.68	2 (40%)	3,6,6	1.15	0
2	FMN	D	400	-	33,33,33	1.55	3 (9%)	48,50,50	1.32	7 (14%)
3	PYR	C	401	-	5,5,5	1.78	2 (40%)	3,6,6	0.78	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FMN	C	400	-	-	1/18/18/18	0/3/3/3
2	FMN	G	400	-	-	1/18/18/18	0/3/3/3
2	FMN	B	400	-	-	2/18/18/18	0/3/3/3
2	FMN	A	400	-	-	4/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PYR	F	401	-	-	0/4/4/4	-
3	PYR	B	401	-	-	1/4/4/4	-
3	PYR	D	401	-	-	4/4/4/4	-
3	PYR	H	401	-	-	4/4/4/4	-
2	FMN	F	400	-	-	1/18/18/18	0/3/3/3
2	FMN	H	400	-	-	1/18/18/18	0/3/3/3
3	PYR	A	401	-	-	2/4/4/4	-
3	PYR	E	401	-	-	3/4/4/4	-
2	FMN	E	400	-	-	1/18/18/18	0/3/3/3
3	PYR	G	401	-	-	0/4/4/4	-
2	FMN	D	400	-	-	1/18/18/18	0/3/3/3
3	PYR	C	401	-	-	0/4/4/4	-

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	400	FMN	C9A-C5A	6.02	1.50	1.41
2	F	400	FMN	C9A-C5A	5.35	1.49	1.41
2	B	400	FMN	C9A-C5A	5.22	1.49	1.41
2	C	400	FMN	C9A-C5A	5.14	1.49	1.41
2	H	400	FMN	C9A-C5A	4.99	1.49	1.41
2	G	400	FMN	C9A-C5A	4.93	1.49	1.41
2	E	400	FMN	C9A-C5A	4.74	1.48	1.41
2	A	400	FMN	C9A-C5A	4.03	1.47	1.41
2	B	400	FMN	C8-C7	3.96	1.50	1.40
2	D	400	FMN	C8-C7	3.72	1.49	1.40
2	F	400	FMN	C4-N3	-3.71	1.31	1.38
2	B	400	FMN	C4-N3	-3.34	1.32	1.38
2	E	400	FMN	C4-N3	-3.33	1.32	1.38
2	H	400	FMN	C8-C7	3.30	1.48	1.40
3	A	401	PYR	CA-C	-3.14	1.43	1.54
3	E	401	PYR	CA-C	-3.10	1.44	1.54
2	C	400	FMN	C8-C7	3.08	1.48	1.40
2	G	400	FMN	C4-N3	-3.06	1.33	1.38
2	F	400	FMN	C8-C7	3.03	1.48	1.40
3	B	401	PYR	CA-C	-2.96	1.44	1.54
3	G	401	PYR	CA-C	-2.95	1.44	1.54
2	A	400	FMN	C4-N3	-2.88	1.33	1.38
3	C	401	PYR	CA-C	-2.81	1.45	1.54
2	G	400	FMN	C5A-N5	-2.55	1.34	1.39
2	C	400	FMN	C4-N3	-2.54	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	400	FMN	C4A-N5	2.48	1.36	1.30
2	E	400	FMN	C8-C7	2.44	1.46	1.40
3	B	401	PYR	OXT-C	-2.43	1.23	1.30
2	A	400	FMN	C8-C7	2.37	1.46	1.40
2	G	400	FMN	C8-C7	2.34	1.46	1.40
2	B	400	FMN	C2-N3	-2.27	1.34	1.39
3	F	401	PYR	CA-C	-2.26	1.46	1.54
3	C	401	PYR	OXT-C	-2.22	1.24	1.30
2	D	400	FMN	C5A-N5	-2.15	1.35	1.39
2	C	400	FMN	C4A-N5	2.10	1.35	1.30
2	C	400	FMN	C5A-N5	-2.08	1.35	1.39
2	E	400	FMN	C5A-N5	-2.08	1.35	1.39
2	B	400	FMN	C5A-N5	-2.06	1.35	1.39
3	G	401	PYR	OXT-C	-2.05	1.25	1.30

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	400	FMN	C4-C4A-N5	4.54	124.48	118.21
2	H	400	FMN	C4-C4A-N5	4.12	123.90	118.21
2	F	400	FMN	O3P-P-O2P	3.72	121.74	107.80
3	B	401	PYR	OXT-C-CA	3.50	123.29	113.59
2	C	400	FMN	C4-C4A-N5	3.36	122.84	118.21
2	F	400	FMN	C4A-C10-N1	-2.96	117.32	124.59
2	D	400	FMN	C4A-C10-N10	2.92	120.66	116.48
2	F	400	FMN	C10-N1-C2	2.86	123.03	116.85
2	C	400	FMN	O2-C2-N1	-2.85	117.06	121.80
2	D	400	FMN	O2-C2-N1	-2.85	117.07	121.80
3	D	401	PYR	OXT-C-CA	2.81	121.38	113.59
2	F	400	FMN	C4A-C4-N3	2.72	120.18	113.25
2	B	400	FMN	C4A-C10-N1	-2.69	117.99	124.59
2	E	400	FMN	C4A-C10-N1	-2.68	118.01	124.59
2	H	400	FMN	C10-N1-C2	2.66	122.62	116.85
2	A	400	FMN	C4-C4A-N5	2.65	121.88	118.21
2	C	400	FMN	C4A-C10-N10	2.60	120.21	116.48
3	H	401	PYR	OXT-C-CA	2.60	120.79	113.59
2	G	400	FMN	O4-C4-C4A	-2.58	119.72	126.53
2	D	400	FMN	O4-C4-C4A	-2.57	119.75	126.53
2	H	400	FMN	O2-C2-N1	-2.55	117.56	121.80
2	H	400	FMN	C4A-C4-N3	2.49	119.60	113.25
2	F	400	FMN	C10-C4A-N5	-2.48	119.75	124.81
2	H	400	FMN	C4A-C10-N10	2.46	120.01	116.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	400	FMN	C4-C4A-N5	2.44	121.58	118.21
2	D	400	FMN	C10-N1-C2	2.43	122.11	116.85
2	H	400	FMN	C4A-C10-N1	-2.43	118.63	124.59
2	H	400	FMN	C4-N3-C2	-2.43	121.33	125.64
2	G	400	FMN	C4A-C10-N1	-2.42	118.66	124.59
2	E	400	FMN	C10-N1-C2	2.38	122.01	116.85
2	B	400	FMN	C5A-N5-C4A	2.37	121.93	118.09
2	E	400	FMN	O3P-P-O2P	2.37	116.68	107.80
2	E	400	FMN	C4-C4A-N5	2.35	121.46	118.21
2	B	400	FMN	C9A-C5A-N5	-2.33	119.98	122.45
2	E	400	FMN	O4-C4-C4A	-2.32	120.41	126.53
2	D	400	FMN	O3'-C3'-C4'	2.31	114.18	108.93
2	H	400	FMN	C10-C4A-N5	-2.30	120.11	124.81
2	A	400	FMN	O3P-P-O1P	2.27	119.68	110.83
2	E	400	FMN	C4A-C4-N3	2.26	119.01	113.25
2	B	400	FMN	O3P-P-O2P	2.26	116.26	107.80
2	A	400	FMN	C4A-C10-N10	2.25	119.70	116.48
3	F	401	PYR	OXT-C-CA	2.23	119.78	113.59
2	F	400	FMN	C4A-C10-N10	2.20	119.63	116.48
2	A	400	FMN	O2-C2-N1	-2.18	118.17	121.80
2	H	400	FMN	O4-C4-C4A	-2.18	120.79	126.53
2	C	400	FMN	C10-C4A-N5	-2.18	120.36	124.81
2	B	400	FMN	C4-C4A-N5	2.18	121.21	118.21
2	G	400	FMN	O3P-P-O2P	2.17	115.95	107.80
2	H	400	FMN	O3P-P-O5'	2.12	112.20	106.67
2	E	400	FMN	C4-N3-C2	-2.06	121.99	125.64
2	F	400	FMN	C5A-N5-C4A	2.04	121.38	118.09
2	D	400	FMN	C4A-C10-N1	-2.03	119.62	124.59

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	401	PYR	O-C-CA-O3
3	D	401	PYR	OXT-C-CA-O3
3	E	401	PYR	O-C-CA-CB
3	E	401	PYR	OXT-C-CA-CB
3	H	401	PYR	O-C-CA-O3
3	H	401	PYR	OXT-C-CA-O3
3	D	401	PYR	O-C-CA-CB
3	H	401	PYR	O-C-CA-CB
2	E	400	FMN	C4'-C5'-O5'-P

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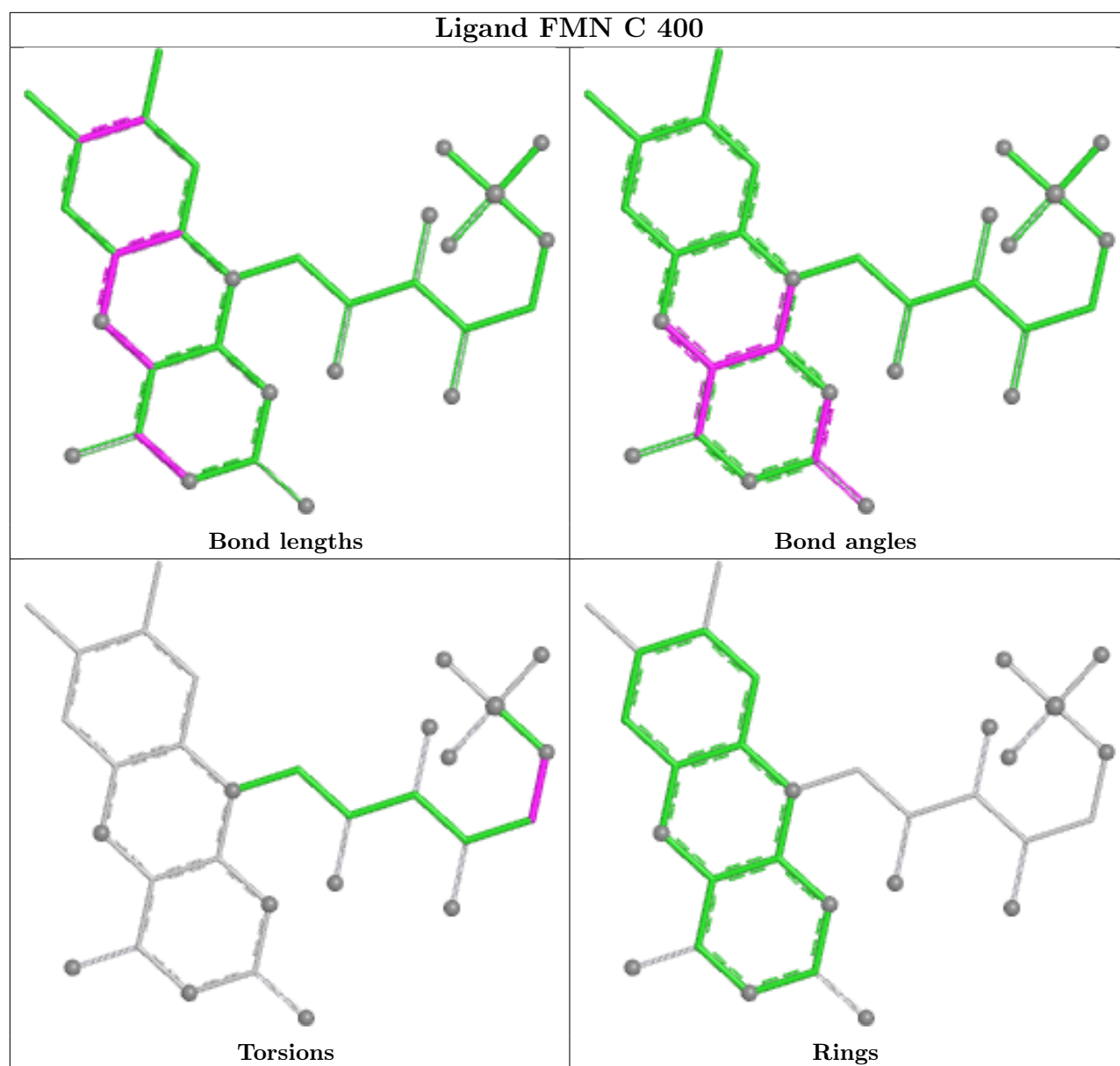
Mol	Chain	Res	Type	Atoms
2	G	400	FMN	C4'-C5'-O5'-P
3	A	401	PYR	OXT-C-CA-O3
3	B	401	PYR	OXT-C-CA-O3
3	D	401	PYR	OXT-C-CA-CB
3	E	401	PYR	OXT-C-CA-O3
3	H	401	PYR	OXT-C-CA-CB
2	A	400	FMN	C4'-C5'-O5'-P
2	H	400	FMN	C4'-C5'-O5'-P
2	C	400	FMN	C4'-C5'-O5'-P
2	F	400	FMN	C4'-C5'-O5'-P
2	A	400	FMN	C2'-C3'-C4'-O4'
2	A	400	FMN	O3'-C3'-C4'-O4'
2	D	400	FMN	C4'-C5'-O5'-P
2	B	400	FMN	C4'-C5'-O5'-P
3	A	401	PYR	O-C-CA-CB
2	A	400	FMN	O3'-C3'-C4'-C5'
2	B	400	FMN	O3'-C3'-C4'-C5'

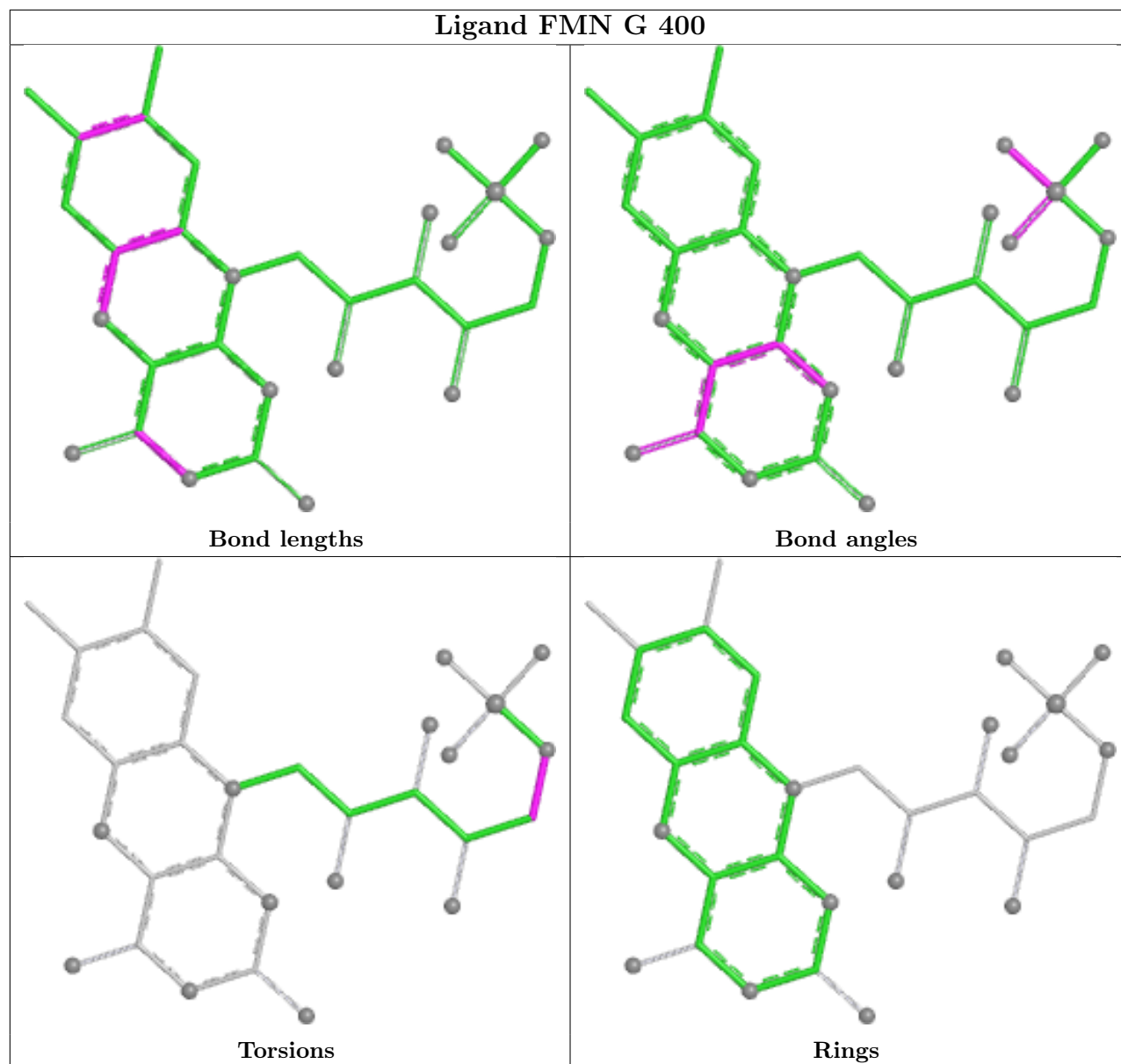
There are no ring outliers.

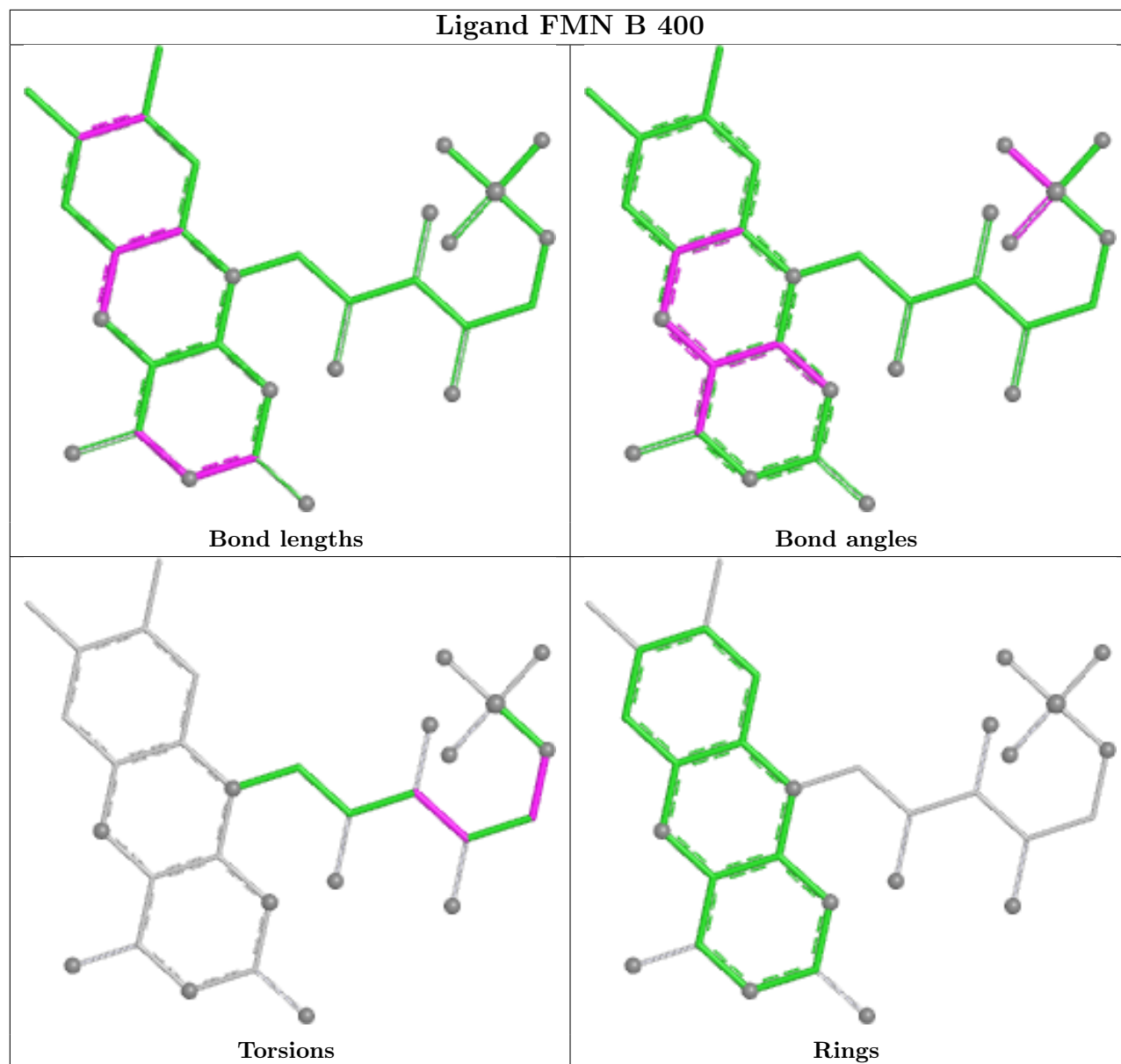
7 monomers are involved in 13 short contacts:

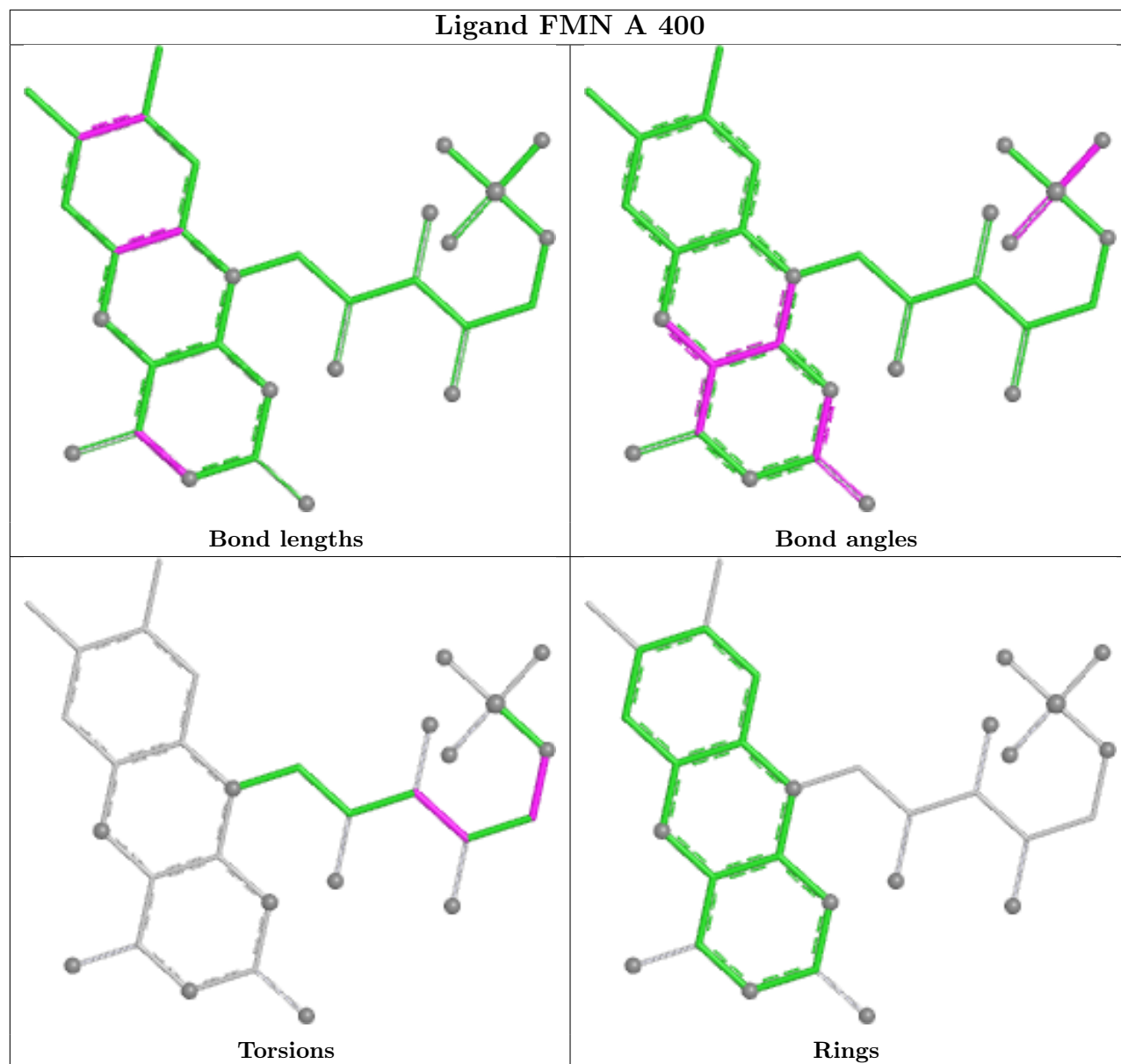
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	400	FMN	2	0
2	B	400	FMN	2	0
3	F	401	PYR	1	0
3	B	401	PYR	2	0
2	F	400	FMN	5	0
2	H	400	FMN	2	0
2	D	400	FMN	2	0

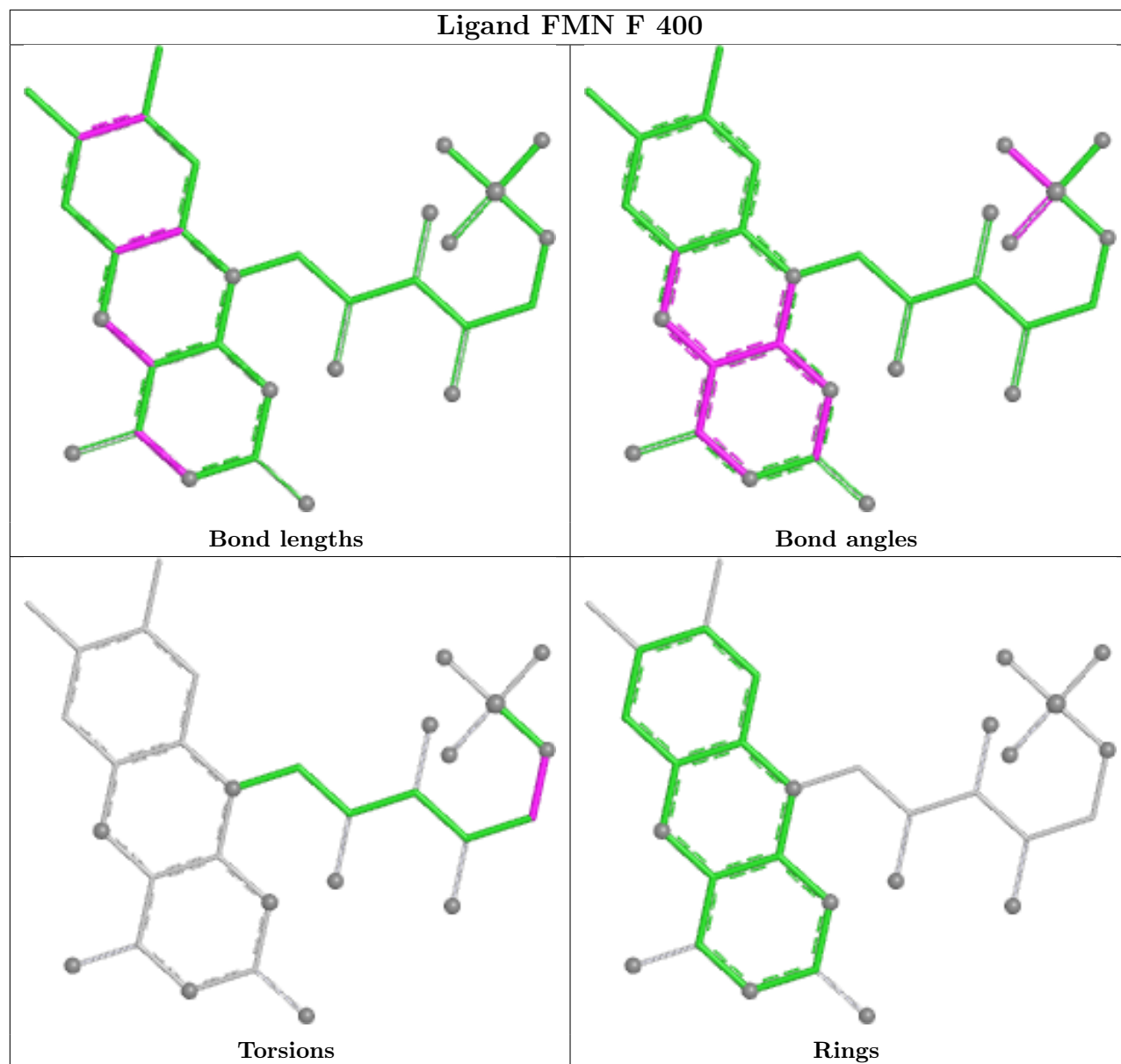
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

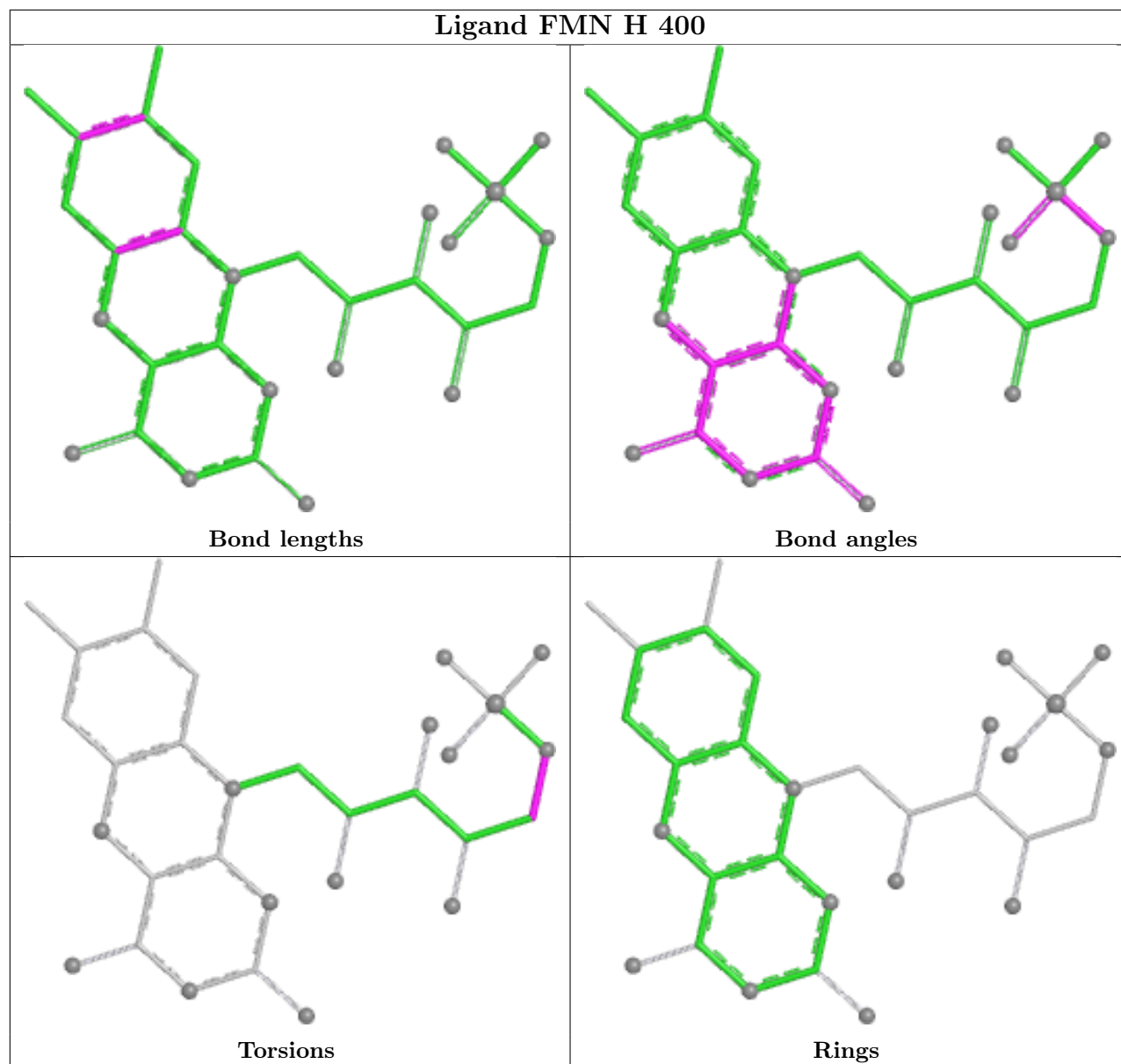


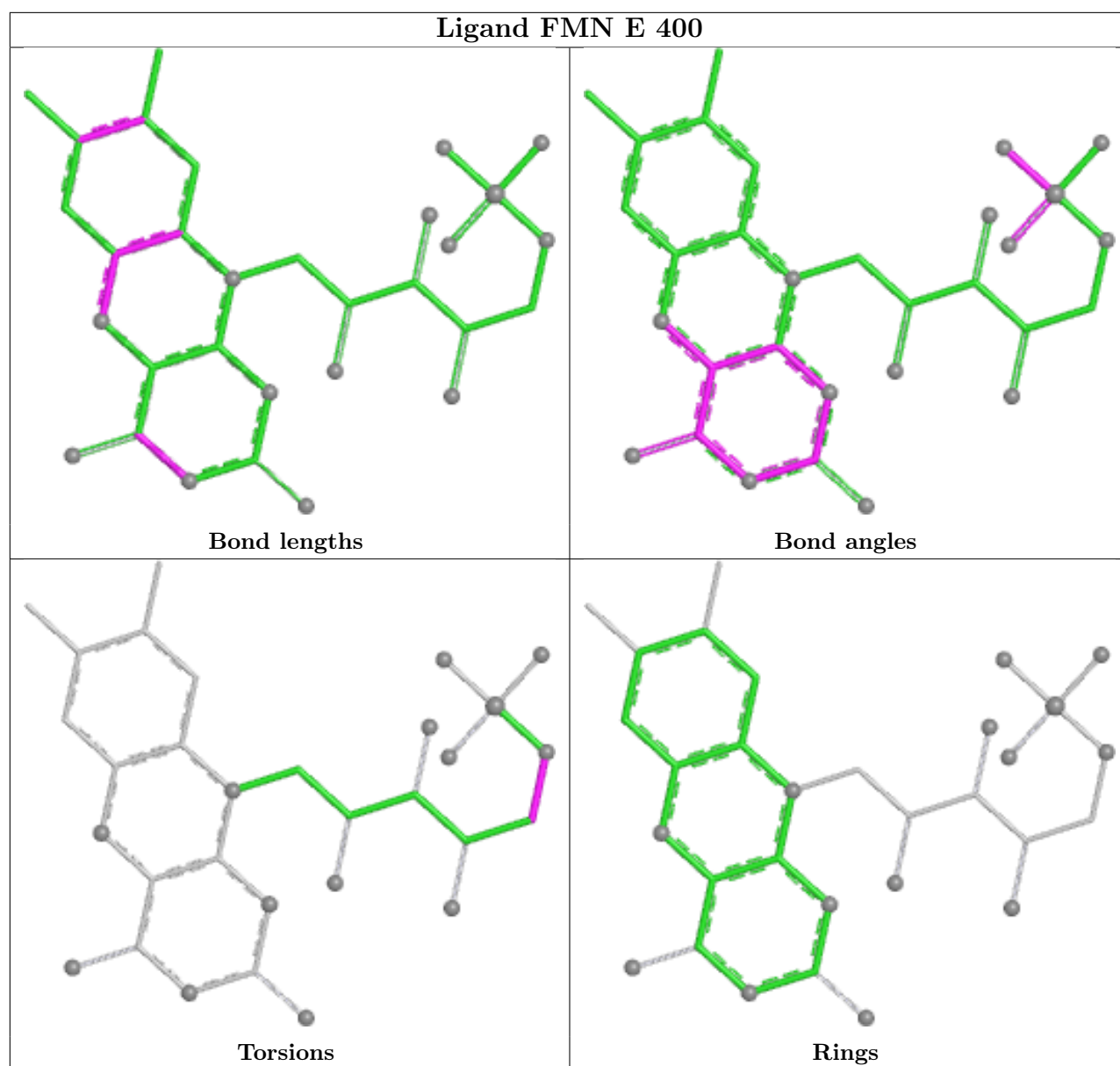


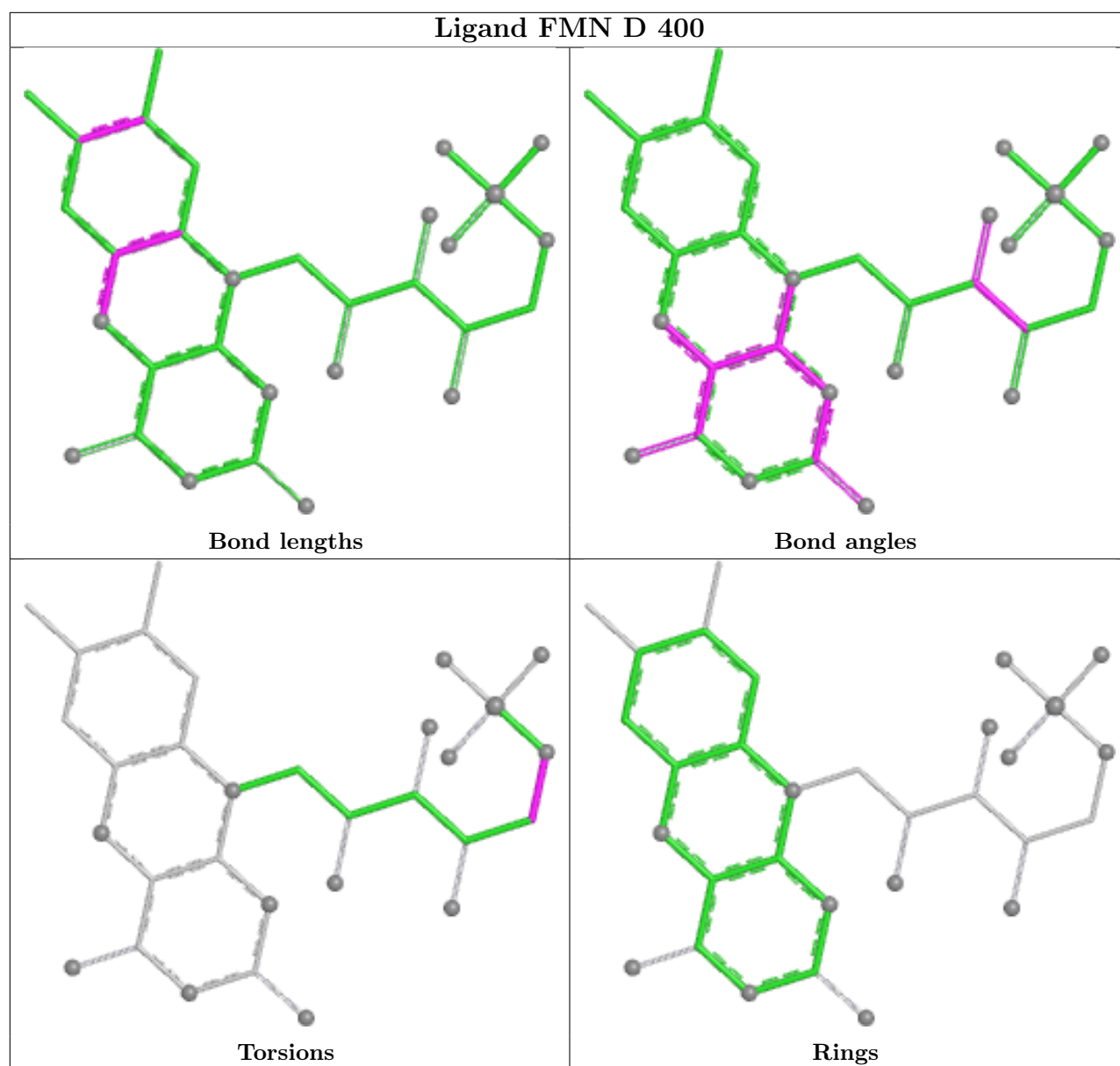












5.7 Other polymers [i](#)

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 ⓘ

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	367/374 (98%)	-0.54	1 (0%) 90 88	11, 22, 35, 72	0
1	B	367/374 (98%)	-0.58	0 100 100	10, 21, 35, 49	0
1	C	367/374 (98%)	-0.39	3 (0%) 82 80	14, 26, 44, 102	0
1	D	353/374 (94%)	-0.46	2 (0%) 85 83	12, 23, 40, 72	0
1	E	367/374 (98%)	-0.56	1 (0%) 90 88	10, 21, 36, 88	0
1	F	367/374 (98%)	-0.25	8 (2%) 62 57	13, 25, 56, 83	0
1	G	367/374 (98%)	-0.55	0 100 100	14, 24, 36, 54	0
1	H	350/374 (93%)	-0.43	1 (0%) 90 88	12, 25, 40, 59	0
All	All	2905/2992 (97%)	-0.47	16 (0%) 85 83	10, 23, 41, 102	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	201	TYR	5.4
1	H	217	ALA	4.7
1	F	202	LEU	4.5
1	F	216	GLY	3.5
1	C	203	ARG	3.5
1	E	203	ARG	3.3
1	F	217	ALA	3.0
1	F	211	LEU	3.0
1	D	199	GLN	2.9
1	A	203	ARG	2.9
1	F	215	PHE	2.6
1	F	152	GLN	2.5
1	D	216	GLY	2.5
1	F	205	THR	2.4
1	C	205	THR	2.1
1	C	204	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

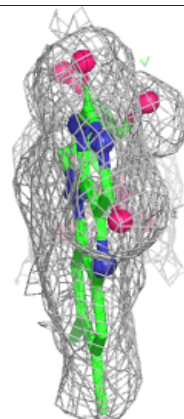
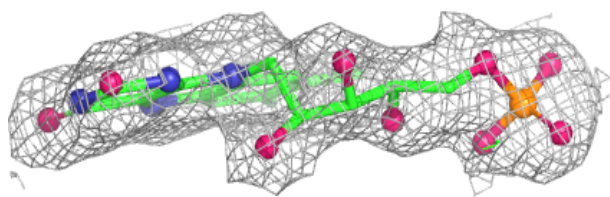
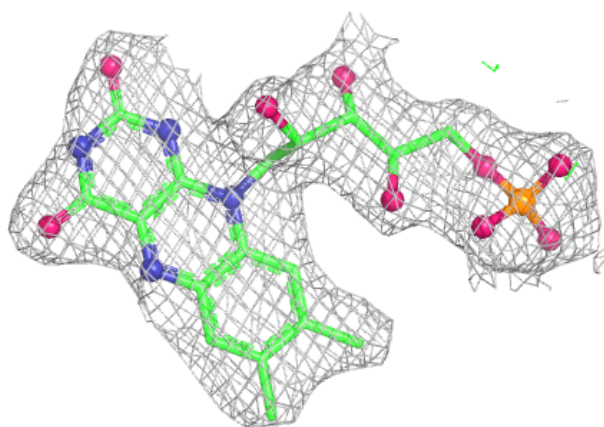
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PYR	D	401	6/6	0.70	0.24	48,55,59,60	0
3	PYR	H	401	6/6	0.83	0.17	55,59,61,62	0
3	PYR	F	401	6/6	0.93	0.12	47,51,52,54	0
3	PYR	B	401	6/6	0.94	0.11	30,32,34,38	0
3	PYR	C	401	6/6	0.95	0.09	36,38,39,43	0
3	PYR	A	401	6/6	0.95	0.07	22,23,24,25	0
2	FMN	C	400	31/31	0.96	0.07	17,23,25,26	0
3	PYR	G	401	6/6	0.96	0.07	25,29,29,32	0
2	FMN	F	400	31/31	0.96	0.07	15,22,28,30	0
2	FMN	H	400	31/31	0.97	0.07	17,22,24,25	0
3	PYR	E	401	6/6	0.97	0.06	25,26,26,28	0
2	FMN	A	400	31/31	0.97	0.06	12,16,17,17	0
2	FMN	B	400	31/31	0.97	0.07	13,21,22,23	0
2	FMN	G	400	31/31	0.97	0.06	14,21,23,24	0
2	FMN	E	400	31/31	0.98	0.06	13,16,17,18	0
2	FMN	D	400	31/31	0.98	0.06	18,23,27,29	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.

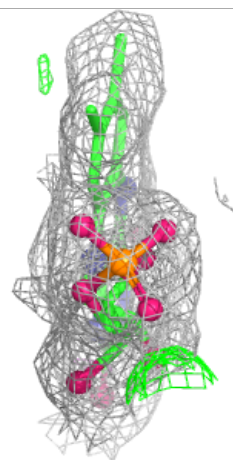
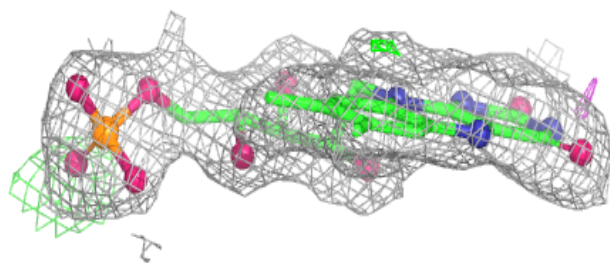
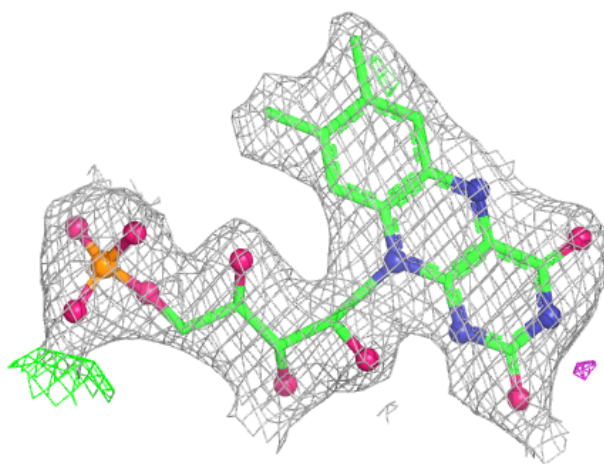
Electron density around FMN C 400:

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



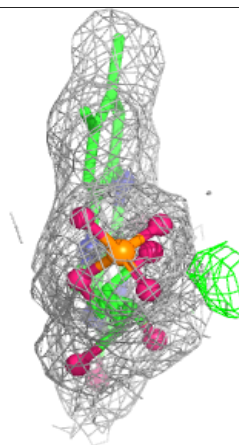
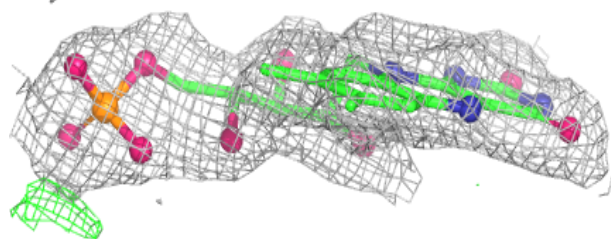
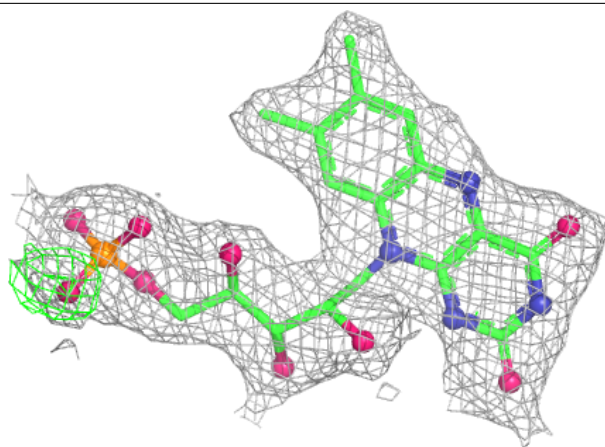
Electron density around FMN F 400:

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



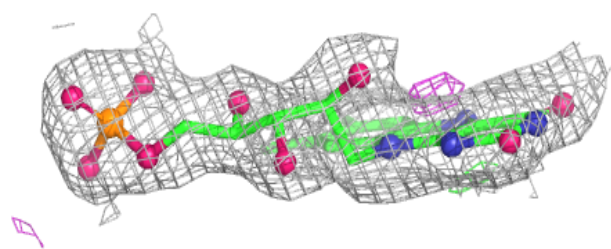
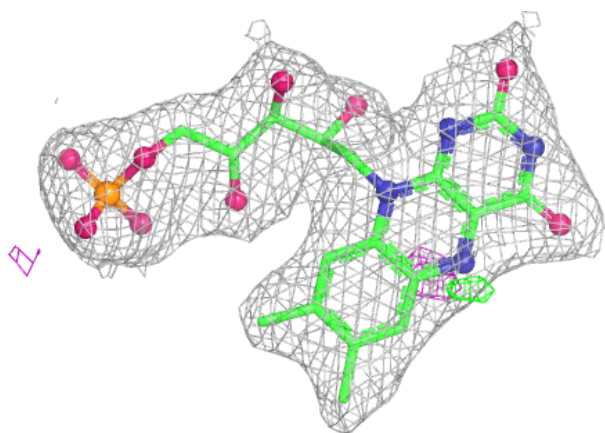
Electron density around FMN H 400:

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



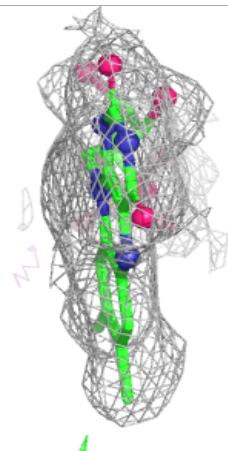
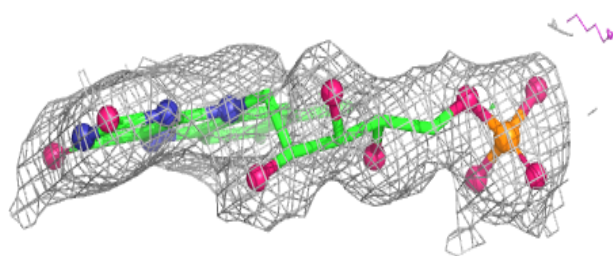
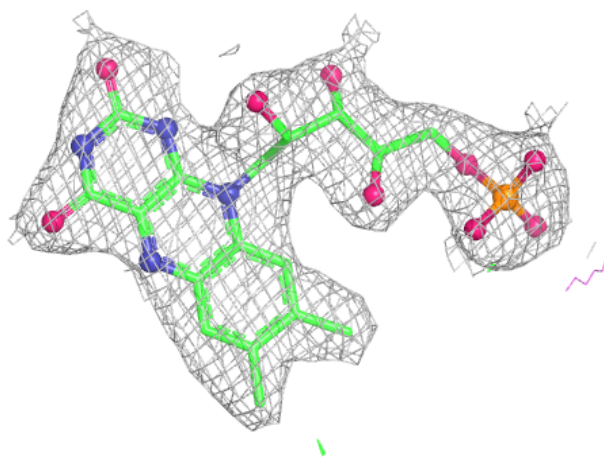
Electron density around FMN A 400:

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



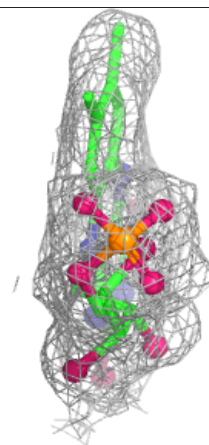
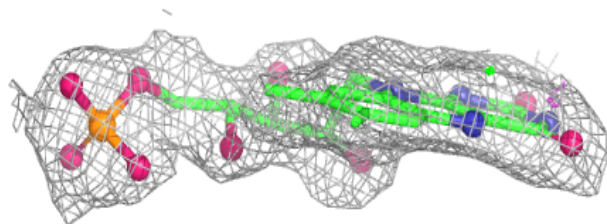
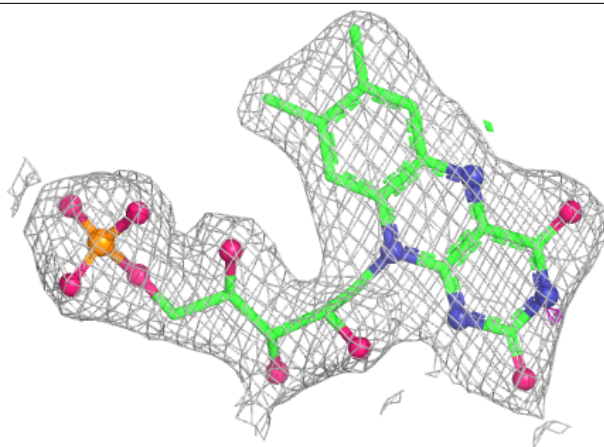
Electron density around FMN B 400:

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



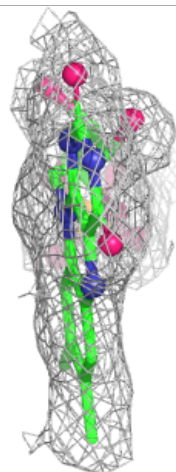
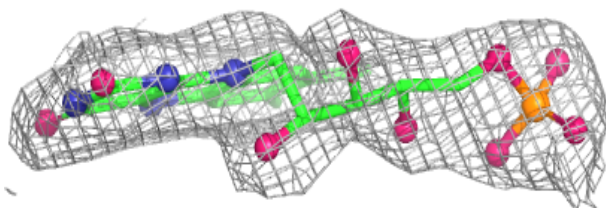
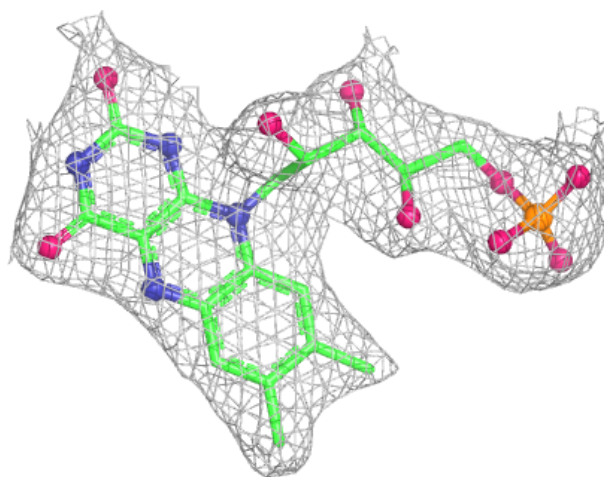
Electron density around FMN G 400:

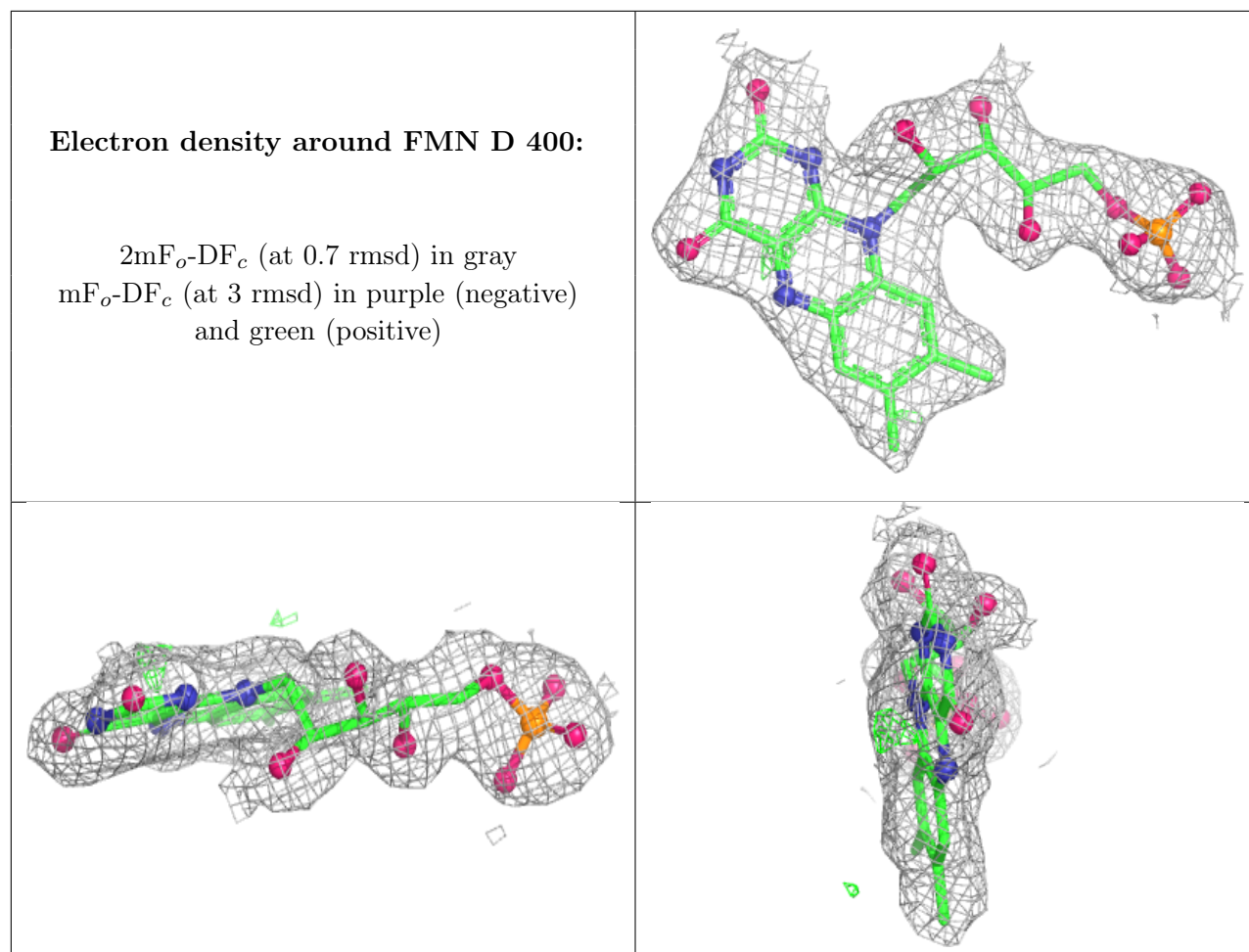
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FMN E 400:

$2mF_o-DF_c$ (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.