



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 09:37 am BST

PDB ID : 4TMC
Title : CRYSTAL STRUCTURE of OLD YELLOW ENZYME from CANDIDA MACEDONIENSIS AKU4588 COMPLEXED with P-HYDROXYBENZALDEHYDE
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Deposited on : 2014-05-31
Resolution : 1.80 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	:	2.11
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)	:	2.11

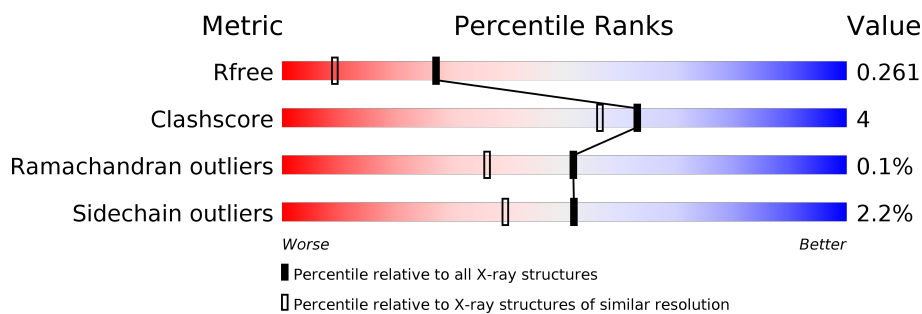
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 on 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	403	
1	B	403	
1	C	403	
1	D	403	

2 Entry composition [i](#)

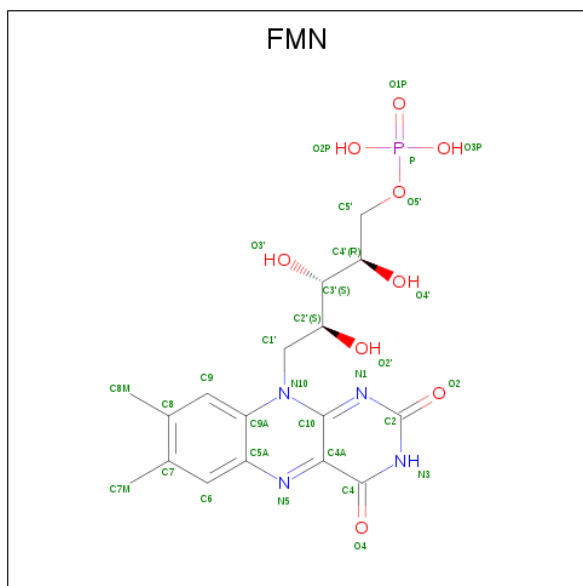
There are 4 unique types of molecules in this entry. The entry contains 14010 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Old yellow enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	0	0
			3209	2055	543	605	6			
1	B	398	Total	C	N	O	S	0	0	0
			3200	2050	542	602	6			
1	C	399	Total	C	N	O	S	0	0	0
			3209	2055	543	605	6			
1	D	396	Total	C	N	O	S	0	0	0
			3182	2038	538	600	6			

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



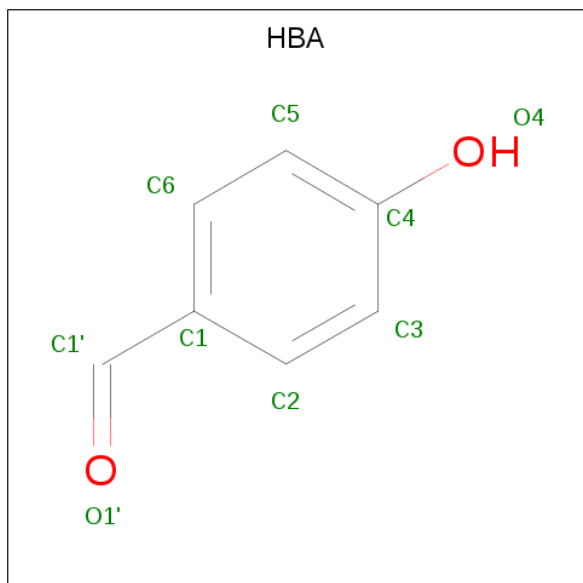
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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		

- Molecule 3 is P-HYDROXYBENZALDEHYDE (three-letter code: HBA) (formula: $C_7H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			9	7	2		
3	B	1	Total	C	O	0	0
			9	7	2		
3	C	1	Total	C	O	0	0
			9	7	2		
3	D	1	Total	C	O	0	0
			9	7	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	310	Total	O	0	0
			310	310		
4	B	254	Total	O	0	0
			254	254		
4	C	280	Total	O	0	0
			280	280		

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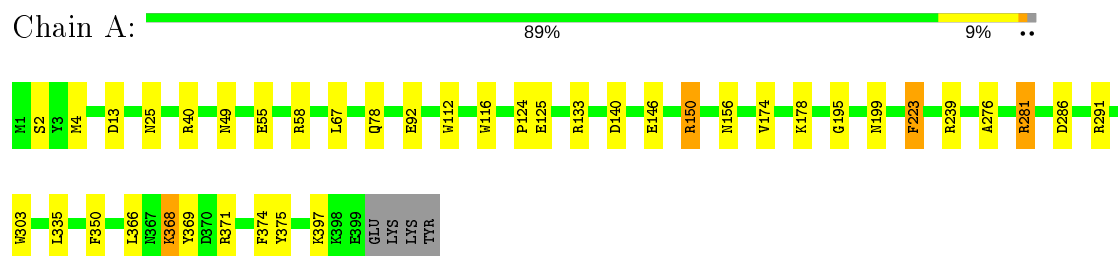
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	206	Total 206	O 206	0	0

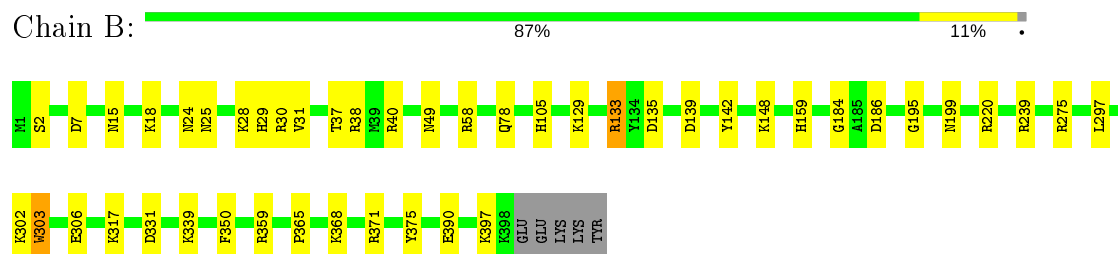
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Old yellow enzyme



- Molecule 1: Old yellow enzyme





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.39Å 151.03Å 199.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 – 1.80 19.95 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (19.95-1.80) 99.8 (19.95-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.167 , 0.205 0.240 , 0.261	Depositor DCC
R_{free} test set	7378 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14010	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: FMN, HBA

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	0.97	2/3293 (0.1%)	1.03	9/4463 (0.2%)
1	B	0.97	2/3284 (0.1%)	1.06	19/4451 (0.4%)
1	C	0.95	2/3293 (0.1%)	1.18	21/4463 (0.5%)
1	D	0.89	3/3266 (0.1%)	1.05	13/4429 (0.3%)
All	All	0.94	9/13136 (0.1%)	1.08	62/17806 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	389	GLU	CD-OE1	9.07	1.35	1.25
1	D	218	GLU	CD-OE1	7.03	1.33	1.25
1	D	218	GLU	CD-OE2	6.57	1.32	1.25
1	B	133	ARG	CD-NE	-6.40	1.35	1.46
1	B	239	ARG	CD-NE	-6.33	1.35	1.46
1	A	116	TRP	CG-CD1	-5.55	1.28	1.36
1	C	239	ARG	CD-NE	-5.29	1.37	1.46
1	D	40	ARG	CD-NE	-5.28	1.37	1.46
1	A	92	GLU	CD-OE1	5.15	1.31	1.25

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	40	ARG	NE-CZ-NH1	24.27	132.43	120.30
1	C	40	ARG	NE-CZ-NH2	-22.28	109.16	120.30
1	B	133	ARG	NE-CZ-NH2	-20.77	109.91	120.30
1	D	40	ARG	NE-CZ-NH2	-18.41	111.10	120.30
1	D	40	ARG	NE-CZ-NH1	17.81	129.21	120.30
1	A	150	ARG	NE-CZ-NH1	17.19	128.90	120.30
1	B	133	ARG	NE-CZ-NH1	14.85	127.72	120.30
1	C	133	ARG	NE-CZ-NH2	-14.63	112.99	120.30
1	A	150	ARG	NE-CZ-NH2	-13.67	113.46	120.30
1	C	133	ARG	NE-CZ-NH1	13.43	127.02	120.30
1	D	133	ARG	NE-CZ-NH2	-13.27	113.67	120.30
1	C	58	ARG	NE-CZ-NH1	12.45	126.52	120.30
1	C	239	ARG	NE-CZ-NH2	-11.72	114.44	120.30
1	D	133	ARG	NE-CZ-NH1	10.88	125.74	120.30
1	C	58	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	D	348	ARG	NE-CZ-NH2	-9.41	115.60	120.30
1	C	239	ARG	NE-CZ-NH1	9.32	124.96	120.30
1	C	40	ARG	CD-NE-CZ	9.13	136.38	123.60
1	D	348	ARG	NE-CZ-NH1	8.46	124.53	120.30
1	D	40	ARG	CD-NE-CZ	8.40	135.37	123.60
1	A	286	ASP	CB-CG-OD1	7.91	125.42	118.30
1	C	108	LYS	CD-CE-NZ	7.87	129.80	111.70
1	B	133	ARG	CD-NE-CZ	7.46	134.05	123.60
1	D	371	ARG	NE-CZ-NH1	7.38	123.99	120.30
1	A	239	ARG	NE-CZ-NH2	-7.36	116.62	120.30
1	C	40	ARG	CB-CG-CD	7.20	130.32	111.60
1	B	275	ARG	NE-CZ-NH1	7.11	123.86	120.30
1	A	58	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	D	58	ARG	NE-CZ-NH2	-6.83	116.89	120.30
1	D	371	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	B	58	ARG	NE-CZ-NH1	6.77	123.68	120.30
1	C	62	GLN	CB-CA-C	-6.70	97.01	110.40
1	C	209	ARG	NE-CZ-NH1	6.69	123.65	120.30
1	B	220	ARG	NE-CZ-NH2	-6.46	117.07	120.30
1	C	39	MET	CG-SD-CE	6.23	110.16	100.20
1	A	239	ARG	NE-CZ-NH1	6.20	123.40	120.30
1	D	141	LEU	CB-CG-CD1	6.12	121.39	111.00
1	C	62	GLN	CA-CB-CG	6.04	126.70	113.40
1	B	139	ASP	CB-CG-OD1	6.02	123.71	118.30
1	B	239	ARG	NE-CZ-NH2	-5.98	117.31	120.30
1	B	133	ARG	CB-CG-CD	-5.96	96.10	111.60
1	D	40	ARG	CG-CD-NE	-5.93	99.34	111.80
1	C	371	ARG	NE-CZ-NH1	5.92	123.26	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	331	ASP	CB-CG-OD1	5.85	123.56	118.30
1	C	222	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	B	275	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	B	28	LYS	CB-CA-C	5.59	121.58	110.40
1	C	359	ARG	NE-CZ-NH1	5.57	123.08	120.30
1	B	133	ARG	CA-CB-CG	5.53	125.56	113.40
1	A	335	LEU	CA-CB-CG	5.53	128.02	115.30
1	D	203	ASP	CB-CG-OD1	5.53	123.28	118.30
1	C	399	GLU	N-CA-CB	-5.50	100.70	110.60
1	C	223	PHE	CB-CG-CD1	5.50	124.65	120.80
1	A	286	ASP	CB-CG-OD2	-5.44	113.40	118.30
1	B	58	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	B	24	ASN	CB-CA-C	-5.27	99.86	110.40
1	A	223	PHE	CB-CG-CD1	5.26	124.48	120.80
1	B	30	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	B	303	TRP	CA-CB-CG	5.07	123.34	113.70
1	B	390	GLU	CA-CB-CG	5.04	124.48	113.40
1	C	370	ASP	CB-CG-OD2	-5.04	113.77	118.30
1	B	139	ASP	CB-CG-OD2	-5.01	113.79	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	1	MET	Peptide

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	3209	0	3138	27	0
1	B	3200	0	3132	26	0
1	C	3209	0	3138	24	0
1	D	3182	0	3106	35	0
2	A	31	0	19	2	0
2	B	31	0	19	2	0
2	C	31	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	31	0	19	3	0
3	A	9	0	5	0	0
3	B	9	0	5	0	0
3	C	9	0	5	0	0
3	D	9	0	5	0	0
4	A	310	0	0	1	0
4	B	254	0	0	3	0
4	C	280	0	0	1	0
4	D	206	0	0	5	0
All	All	14010	0	12610	111	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 (111) 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:A:4:MET:HE3	1:A:366:LEU:HB2	1.37	1.07
1:B:368:LYS:HG3	4:B:823:HOH:O	1.52	1.07
1:D:371:ARG:NH2	4:D:641:HOH:O	2.01	0.93
1:A:55:GLU:HG2	4:A:673:HOH:O	1.75	0.87
1:A:4:MET:CE	1:A:366:LEU:HB2	2.06	0.85
1:A:4:MET:HE3	1:A:366:LEU:CB	2.09	0.82
1:B:133:ARG:HD2	1:B:135:ASP:OD1	1.80	0.82
1:A:4:MET:CE	1:A:366:LEU:CB	2.58	0.81
1:C:78:GLN:HE22	1:C:133:ARG:H	1.31	0.79
1:A:78:GLN:HE22	1:A:133:ARG:H	1.32	0.77
1:D:78:GLN:HE22	1:D:133:ARG:H	1.33	0.76
1:B:195:GLY:H	1:B:199:ASN:HD22	1.36	0.74
1:A:124:PRO:HD2	1:A:150:ARG:HD2	1.70	0.73
1:A:125:GLU:OE1	1:A:150:ARG:HD3	1.88	0.73
1:A:146:GLU:H	1:A:146:GLU:CD	1.92	0.72
1:D:195:GLY:H	1:D:199:ASN:HD22	1.38	0.72
1:C:67:LEU:HD11	1:C:112:TRP:CD1	2.27	0.69
1:B:29:HIS:HD2	1:B:31:VAL:H	1.40	0.68
1:C:40:ARG:HD3	1:C:378:THR:O	1.95	0.67
1:C:25:ASN:HD21	1:C:186:ASP:HB3	1.58	0.66
1:D:18:LYS:HG3	1:D:19:PRO:HD2	1.78	0.66
1:C:195:GLY:H	1:C:199:ASN:HD22	1.44	0.66
1:C:108:LYS:HE3	4:C:759:HOH:O	1.96	0.65
1:D:175:ASP:OD2	1:D:179:LYS:HE2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:VAL:O	1:C:239:ARG:HD3	1.96	0.64
1:C:133:ARG:HD2	1:C:135:ASP:OD1	1.98	0.64
1:D:102:ASN:HB3	4:D:744:HOH:O	1.97	0.64
1:D:49:ASN:OD1	1:D:51:GLU:HG3	1.97	0.64
1:A:195:GLY:H	1:A:199:ASN:HD22	1.44	0.64
1:B:40:ARG:O	1:B:49:ASN:HB2	1.98	0.64
1:B:375:TYR:CE1	2:B:501:FMN:HM72	2.32	0.63
1:B:2:SER:HB2	1:B:397:LYS:O	1.99	0.62
1:C:235:VAL:O	1:C:239:ARG:CD	2.49	0.61
1:A:375:TYR:CE1	2:A:501:FMN:HM72	2.35	0.61
1:B:78:GLN:HE22	1:B:133:ARG:H	1.48	0.61
1:D:195:GLY:H	1:D:199:ASN:ND2	1.99	0.60
1:A:4:MET:CE	1:A:366:LEU:HB3	2.31	0.60
1:B:15:ASN:HD22	1:B:18:LYS:HD2	1.67	0.60
1:B:148:LYS:HE2	4:B:604:HOH:O	2.02	0.60
1:D:299:GLU:OE1	1:D:369:TYR:OH	2.15	0.59
1:A:375:TYR:CZ	2:A:501:FMN:HM72	2.39	0.58
1:B:375:TYR:CZ	2:B:501:FMN:HM72	2.40	0.56
1:C:258:ASN:HB3	1:C:261:ILE:HD13	1.87	0.56
1:C:195:GLY:H	1:C:199:ASN:ND2	2.03	0.56
1:D:133:ARG:HD2	1:D:135:ASP:OD1	2.06	0.56
1:D:348:ARG:HD3	2:D:501:FMN:O1P	2.05	0.56
1:D:280:LYS:CE	4:D:696:HOH:O	2.54	0.56
1:A:40:ARG:O	1:A:49:ASN:HB2	2.06	0.55
1:D:323:VAL:HG22	1:D:345:GLY:HA3	1.88	0.55
1:D:50:THR:OG1	1:D:96:GLU:HB3	2.06	0.55
1:D:40:ARG:O	1:D:49:ASN:HB2	2.07	0.55
1:B:148:LYS:CE	4:B:604:HOH:O	2.56	0.54
1:D:52:TRP:CE2	1:D:379:LYS:HG2	2.43	0.54
1:B:29:HIS:CD2	1:B:31:VAL:H	2.23	0.54
1:A:276:ALA:HB1	1:A:281:ARG:HB2	1.90	0.52
1:B:133:ARG:CD	1:B:135:ASP:OD1	2.56	0.51
1:B:317:LYS:HE2	1:D:306:GLU:HB3	1.92	0.51
1:D:102:ASN:CB	4:D:744:HOH:O	2.54	0.51
1:A:371:ARG:HD2	1:A:374:PHE:CD2	2.46	0.51
1:B:195:GLY:H	1:B:199:ASN:ND2	2.06	0.49
1:B:105:HIS:HE1	1:B:184:GLY:O	1.95	0.49
1:D:375:TYR:CZ	2:D:501:FMN:HM72	2.48	0.49
1:A:276:ALA:CB	1:A:281:ARG:HB2	2.43	0.49
1:C:39:MET:CE	1:C:375:TYR:HB3	2.43	0.48
1:C:261:ILE:HG22	1:C:262:VAL:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:50:THR:HG21	1:D:99:LYS:HD3	1.95	0.48
1:D:280:LYS:HE2	4:D:696:HOH:O	2.11	0.48
1:C:39:MET:HE3	1:C:375:TYR:HB3	1.94	0.48
1:C:40:ARG:HD2	1:C:382:TYR:CD1	2.49	0.48
1:D:67:LEU:HD11	1:D:112:TRP:CD1	2.48	0.48
1:B:297:LEU:HD13	1:B:302:LYS:HG2	1.96	0.47
1:A:140:ASP:OD1	1:A:140:ASP:N	2.47	0.47
1:B:297:LEU:HD13	1:B:302:LYS:CG	2.45	0.46
1:D:296:PHE:HA	1:D:371:ARG:NH2	2.30	0.46
1:D:20:ILE:CD1	1:D:341:ASN:HD22	2.28	0.46
1:A:125:GLU:CD	1:A:150:ARG:HD3	2.36	0.46
1:A:25:ASN:ND2	1:A:112:TRP:HE1	2.13	0.46
1:A:291:ARG:HA	1:A:303:TRP:CD1	2.51	0.46
1:B:15:ASN:ND2	1:B:18:LYS:HD2	2.31	0.46
1:C:133:ARG:HD3	1:C:159:HIS:CD2	2.52	0.45
1:C:67:LEU:CD1	1:C:112:TRP:CD1	2.98	0.45
1:A:195:GLY:H	1:A:199:ASN:ND2	2.12	0.45
1:A:2:SER:HB2	1:A:397:LYS:O	2.17	0.45
1:C:125:GLU:O	1:C:129:LYS:HD3	2.17	0.44
1:C:235:VAL:O	1:C:239:ARG:HD2	2.18	0.44
1:D:387:SER:OG	1:D:390:GLU:HG3	2.18	0.44
1:C:105:HIS:HE1	1:C:184:GLY:O	2.01	0.43
1:C:291:ARG:HA	1:C:303:TRP:CD1	2.53	0.43
1:D:47:ILE:HD12	1:D:92:GLU:HB3	2.00	0.43
1:D:348:ARG:CD	2:D:501:FMN:O1P	2.67	0.43
1:B:133:ARG:HD3	1:B:159:HIS:CD2	2.53	0.43
1:B:15:ASN:HA	1:B:18:LYS:HG3	2.00	0.43
1:A:368:LYS:HD2	1:A:369:TYR:H	1.84	0.43
1:C:39:MET:HA	1:C:84:ASN:O	2.19	0.43
1:D:6:PHE:CG	1:D:7:ASP:N	2.87	0.43
1:D:305:LYS:HB2	1:D:305:LYS:HE2	1.88	0.42
1:B:25:ASN:HD21	1:B:186:ASP:HB3	1.84	0.42
1:A:67:LEU:HD11	1:A:112:TRP:CD1	2.55	0.42
1:C:40:ARG:HD2	1:C:382:TYR:CG	2.55	0.42
1:B:142:TYR:CE2	1:B:148:LYS:HA	2.55	0.41
1:B:37:THR:O	1:B:38:ARG:HD2	2.20	0.41
1:D:39:MET:HA	1:D:84:ASN:O	2.20	0.41
1:A:174:VAL:CG1	1:A:178:LYS:HE3	2.51	0.41
1:A:4:MET:HE2	1:A:366:LEU:HB3	2.01	0.41
1:D:28:LYS:HG3	1:D:65:GLY:HA3	2.02	0.41
1:B:359:ARG:HD3	1:B:365:PRO:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:346:TYR:O	1:C:350:PHE:HB2	2.21	0.41
1:D:156:ASN:HA	1:D:156:ASN:HD22	1.72	0.41
1:D:25:ASN:HD21	1:D:186:ASP:HB3	1.86	0.41
1:D:346:TYR:HB3	1:D:349:SER:OG	2.21	0.40
1:D:50:THR:HG1	1:D:96:GLU:HB3	1.85	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	397/403 (98%)	386 (97%)	11 (3%)	0	100	100
1	B	396/403 (98%)	382 (96%)	14 (4%)	0	100	100
1	C	397/403 (98%)	385 (97%)	12 (3%)	0	100	100
1	D	394/403 (98%)	379 (96%)	14 (4%)	1 (0%)	41	27
All	All	1584/1612 (98%)	1532 (97%)	51 (3%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	6	PHE

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	336/340 (99%)	330 (98%)	6 (2%)	59	48
1	B	335/340 (98%)	328 (98%)	7 (2%)	53	42
1	C	336/340 (99%)	332 (99%)	4 (1%)	71	65
1	D	333/340 (98%)	320 (96%)	13 (4%)	32	17
All	All	1340/1360 (98%)	1310 (98%)	30 (2%)	52	39

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASP
1	A	156	ASN
1	A	223	PHE
1	A	281	ARG
1	A	350	PHE
1	A	368	LYS
1	B	7	ASP
1	B	129	LYS
1	B	303	TRP
1	B	306	GLU
1	B	339	LYS
1	B	350	PHE
1	B	371	ARG
1	C	118	LEU
1	C	121	GLN
1	C	239	ARG
1	C	350	PHE
1	D	2	SER
1	D	7	ASP
1	D	8	PRO
1	D	40	ARG
1	D	91	LYS
1	D	141	LEU
1	D	146	GLU
1	D	156	ASN
1	D	299	GLU
1	D	305	LYS
1	D	350	PHE
1	D	379	LYS
1	D	396	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	46	ASN
1	A	62	GLN
1	A	78	GLN
1	A	107	ASN
1	A	156	ASN
1	A	199	ASN
1	B	15	ASN
1	B	25	ASN
1	B	29	HIS
1	B	46	ASN
1	B	62	GLN
1	B	78	GLN
1	B	199	ASN
1	C	25	ASN
1	C	62	GLN
1	C	78	GLN
1	C	155	ASN
1	C	199	ASN
1	D	15	ASN
1	D	25	ASN
1	D	78	GLN
1	D	156	ASN
1	D	199	ASN
1	D	332	GLN
1	D	341	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

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
3	HBA	B	502	-	9,9,9	0.97	0	11,11,11	1.05	0
2	FMN	C	501	-	31,33,33	2.32	3 (9%)	40,50,50	2.71	15 (37%)
2	FMN	A	501	-	31,33,33	2.89	10 (32%)	40,50,50	2.64	13 (32%)
3	HBA	C	502	-	9,9,9	0.95	0	11,11,11	0.99	0
3	HBA	A	502	-	9,9,9	0.69	0	11,11,11	1.42	1 (9%)
2	FMN	D	501	-	31,33,33	2.30	10 (32%)	40,50,50	2.65	11 (27%)
3	HBA	D	502	-	9,9,9	0.86	0	11,11,11	1.11	1 (9%)
2	FMN	B	501	-	31,33,33	2.55	7 (22%)	40,50,50	2.18	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
3	HBA	B	502	-	-	0/2/2/2	0/1/1/1
2	FMN	C	501	-	-	2/18/18/18	0/3/3/3
2	FMN	A	501	-	-	1/18/18/18	0/3/3/3
3	HBA	C	502	-	-	0/2/2/2	0/1/1/1
3	HBA	A	502	-	-	0/2/2/2	0/1/1/1
2	FMN	D	501	-	-	1/18/18/18	0/3/3/3
3	HBA	D	502	-	-	0/2/2/2	0/1/1/1
2	FMN	B	501	-	-	1/18/18/18	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FMN	C4A-C10	11.61	1.50	1.38
2	C	501	FMN	C4A-C10	10.86	1.49	1.38
2	B	501	FMN	C4A-C10	10.53	1.49	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	FMN	C4A-C10	8.27	1.47	1.38
2	A	501	FMN	C4-C4A	4.98	1.49	1.41
2	B	501	FMN	C4-C4A	4.80	1.49	1.41
2	A	501	FMN	C5'-C4'	4.38	1.58	1.51
2	D	501	FMN	C4-C4A	4.19	1.48	1.41
2	A	501	FMN	C9A-N10	4.19	1.44	1.38
2	D	501	FMN	C10-N1	3.96	1.38	1.33
2	B	501	FMN	C9A-C5A	3.73	1.50	1.42
2	C	501	FMN	C4-C4A	3.64	1.47	1.41
2	B	501	FMN	C8-C7	3.56	1.49	1.40
2	A	501	FMN	C4A-N5	3.48	1.38	1.33
2	D	501	FMN	C5'-C4'	3.06	1.56	1.51
2	A	501	FMN	O3'-C3'	3.01	1.50	1.43
2	B	501	FMN	C5'-C4'	2.96	1.56	1.51
2	A	501	FMN	C6-C5A	-2.61	1.37	1.41
2	A	501	FMN	C4-N3	2.57	1.37	1.33
2	D	501	FMN	C4-N3	2.56	1.37	1.33
2	D	501	FMN	P-O5'	2.52	1.68	1.60
2	D	501	FMN	C9A-N10	2.33	1.41	1.38
2	B	501	FMN	O3'-C3'	2.29	1.48	1.43
2	D	501	FMN	C8-C7	2.26	1.46	1.40
2	B	501	FMN	C6-C5A	-2.21	1.38	1.41
2	D	501	FMN	C9A-C5A	2.21	1.47	1.42
2	A	501	FMN	O2'-C2'	2.17	1.47	1.43
2	A	501	FMN	C10-N1	2.15	1.36	1.33
2	D	501	FMN	O4-C4	2.10	1.29	1.24
2	C	501	FMN	C4-N3	2.10	1.36	1.33

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	FMN	C4-N3-C2	9.89	123.49	115.14
2	C	501	FMN	C4-N3-C2	9.39	123.07	115.14
2	A	501	FMN	C4-N3-C2	8.33	122.17	115.14
2	B	501	FMN	C4-N3-C2	7.64	121.59	115.14
2	D	501	FMN	C1'-N10-C9A	7.61	124.28	118.29
2	C	501	FMN	C4A-N5-C5A	6.34	123.11	116.77
2	A	501	FMN	C4A-N5-C5A	5.89	122.66	116.77
2	C	501	FMN	C1'-N10-C9A	5.72	122.79	118.29
2	D	501	FMN	C4-C4A-C10	-5.56	116.27	119.95
2	A	501	FMN	C1'-N10-C9A	5.46	122.59	118.29
2	C	501	FMN	C4A-C4-N3	-5.27	116.23	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	FMN	C4-C4A-C10	-5.14	116.55	119.95
2	B	501	FMN	C4A-C4-N3	-4.92	116.70	123.43
2	B	501	FMN	C4A-N5-C5A	4.67	121.44	116.77
2	D	501	FMN	C4A-C4-N3	-4.61	117.13	123.43
2	A	501	FMN	C5A-C9A-N10	4.56	121.02	117.72
2	A	501	FMN	C4A-C4-N3	-4.30	117.55	123.43
2	A	501	FMN	O2'-C2'-C1'	4.12	119.52	109.59
2	A	501	FMN	C4-C4A-N5	3.95	123.12	118.60
2	B	501	FMN	C4-C4A-N5	3.88	123.03	118.60
2	C	501	FMN	C4-C4A-N5	3.85	123.00	118.60
2	D	501	FMN	C9A-N10-C10	-3.61	117.18	121.91
2	B	501	FMN	C4-C4A-C10	-3.50	117.64	119.95
3	A	502	HBA	O1'-C1'-C1	-3.45	113.40	124.59
2	C	501	FMN	C4-C4A-C10	-3.42	117.69	119.95
2	B	501	FMN	C1'-N10-C9A	3.39	120.96	118.29
2	D	501	FMN	C5A-C9A-N10	3.15	120.00	117.72
2	A	501	FMN	O3'-C3'-C4'	3.09	116.28	108.81
2	D	501	FMN	C4-C4A-N5	3.02	122.05	118.60
2	D	501	FMN	C4A-N5-C5A	2.86	119.63	116.77
2	C	501	FMN	C10-C4A-N5	-2.83	119.30	121.26
2	C	501	FMN	P-O5'-C5'	-2.79	110.61	118.30
2	B	501	FMN	C10-C4A-N5	-2.78	119.33	121.26
2	D	501	FMN	O3P-P-O2P	2.70	117.97	107.64
2	C	501	FMN	C5A-C9A-N10	2.70	119.67	117.72
3	D	502	HBA	O1'-C1'-C1	-2.63	116.07	124.59
2	C	501	FMN	C7M-C7-C8	-2.56	115.49	120.74
2	A	501	FMN	C9A-C5A-N5	-2.49	118.46	122.36
2	A	501	FMN	C4A-C10-N10	-2.49	117.75	120.30
2	D	501	FMN	O5'-P-O1P	-2.47	99.54	106.47
2	C	501	FMN	C7M-C7-C6	2.35	125.96	120.34
2	C	501	FMN	O2P-P-O5'	-2.26	100.72	106.73
2	B	501	FMN	O3P-P-O1P	2.22	119.38	110.68
2	A	501	FMN	C6-C5A-N5	2.21	121.49	119.05
2	A	501	FMN	O4'-C4'-C3'	2.21	114.47	109.10
2	C	501	FMN	O2'-C2'-C1'	2.18	114.84	109.59
2	C	501	FMN	O3P-P-O2P	2.16	115.90	107.64
2	D	501	FMN	O2P-P-O5'	-2.10	101.14	106.73
2	C	501	FMN	C9A-N10-C10	-2.05	119.23	121.91

There are no chirality outliers.

All (5) torsion outliers are listed below:

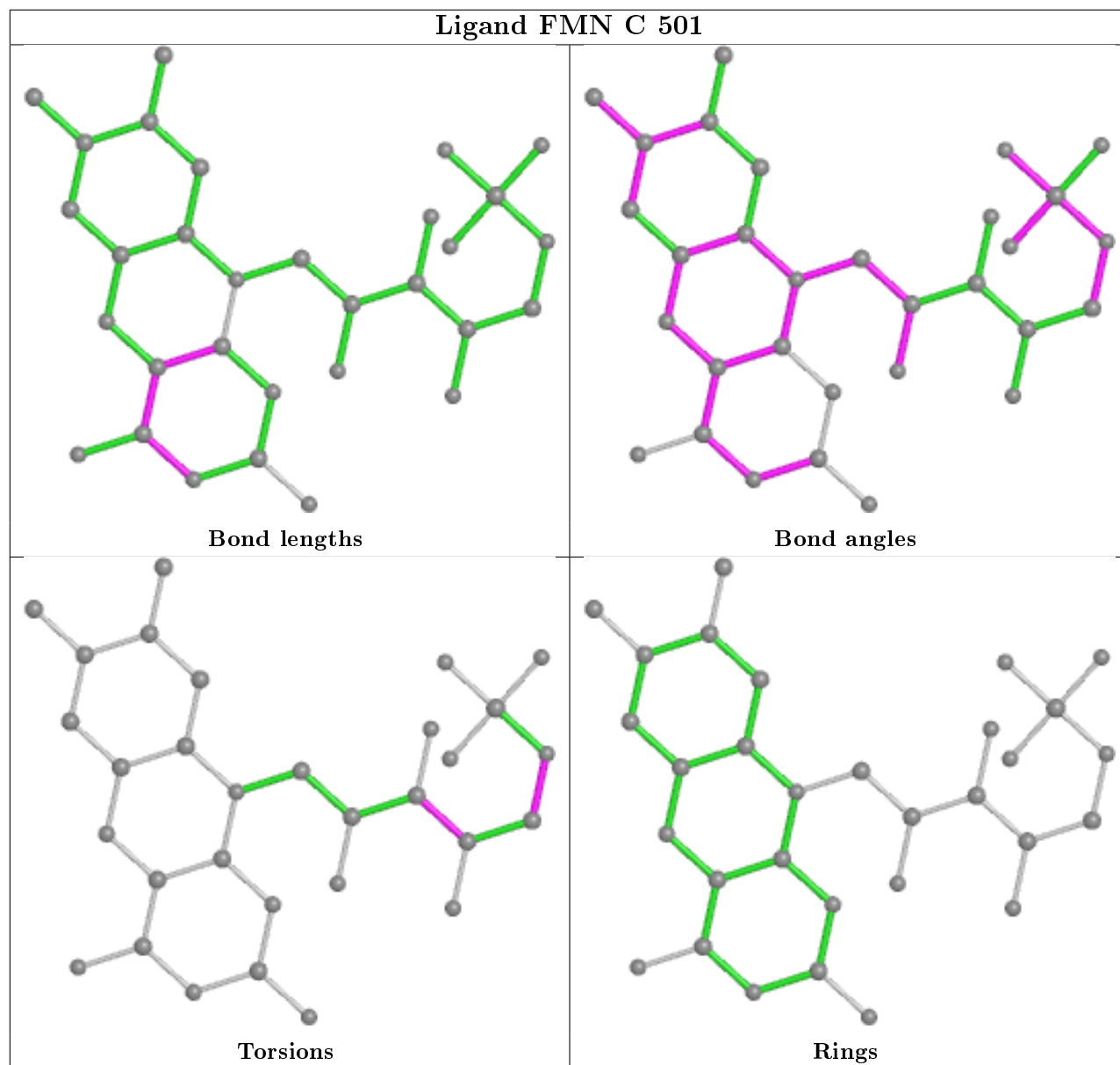
Mol	Chain	Res	Type	Atoms
2	A	501	FMN	C4'-C5'-O5'-P
2	D	501	FMN	C4'-C5'-O5'-P
2	C	501	FMN	C2'-C3'-C4'-O4'
2	C	501	FMN	C4'-C5'-O5'-P
2	B	501	FMN	C4'-C5'-O5'-P

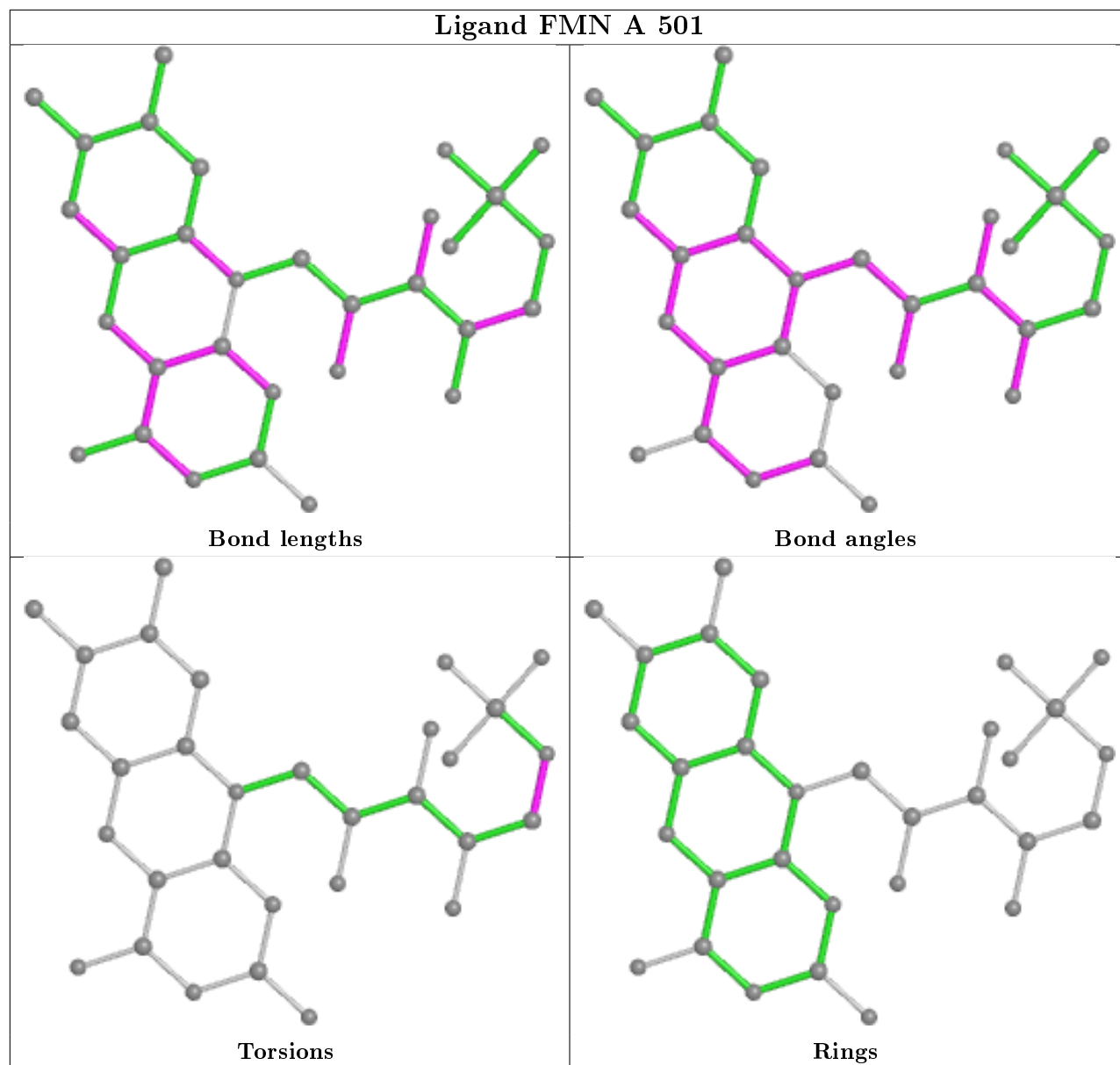
There are no ring outliers.

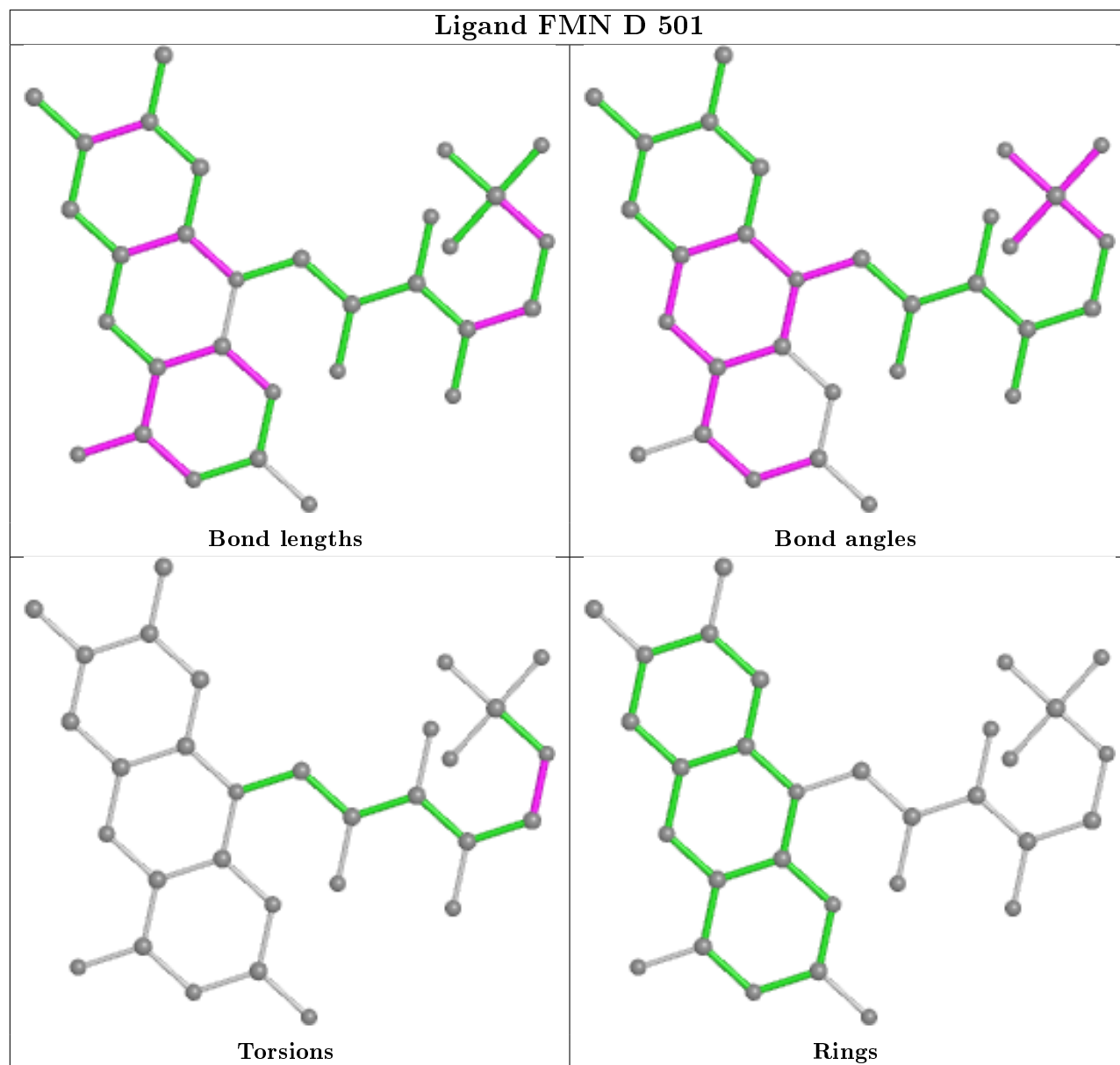
3 monomers are involved in 7 short contacts:

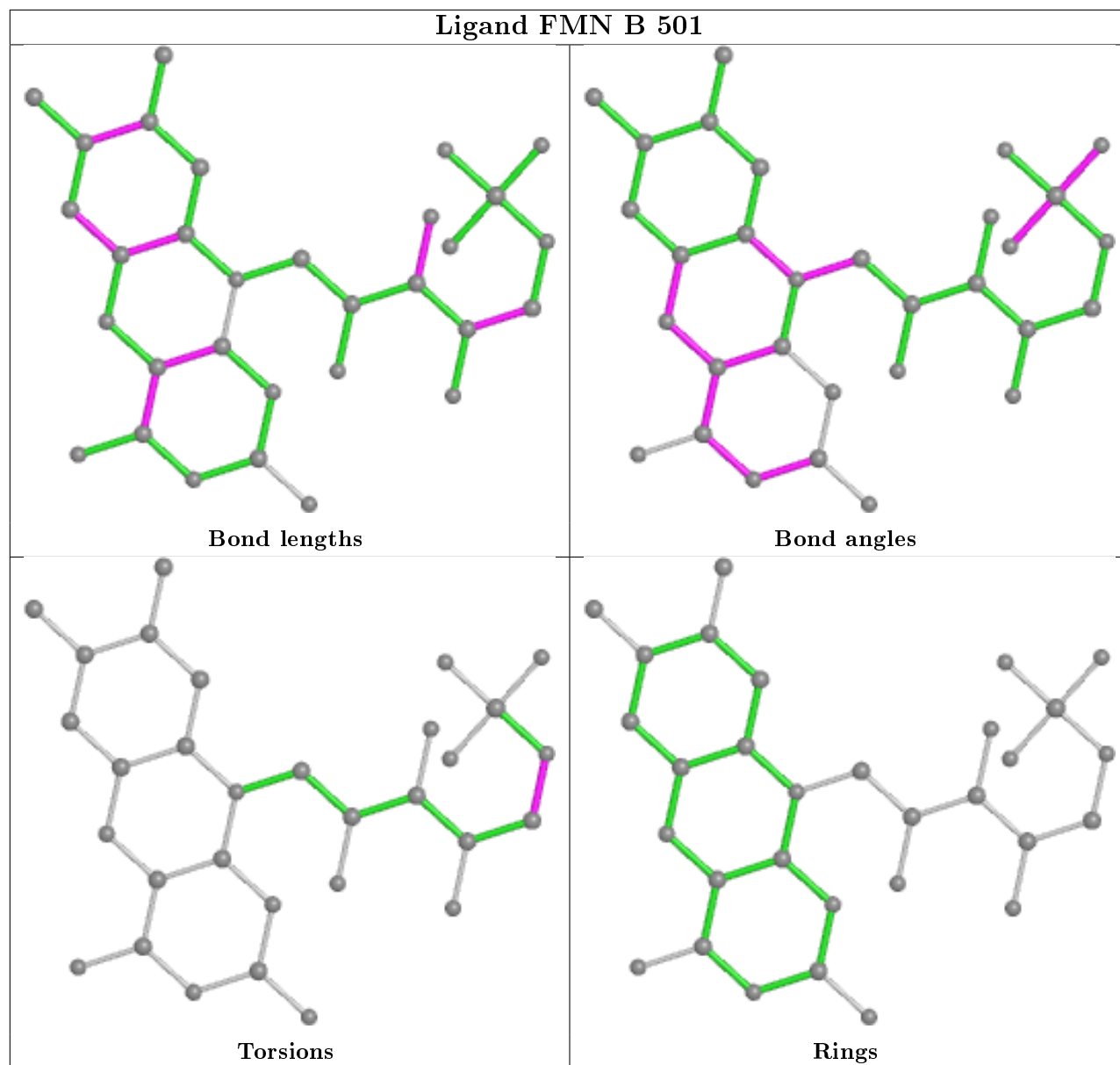
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	FMN	2	0
2	D	501	FMN	3	0
2	B	501	FMN	2	0

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.

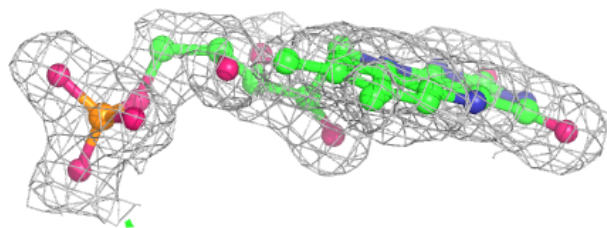
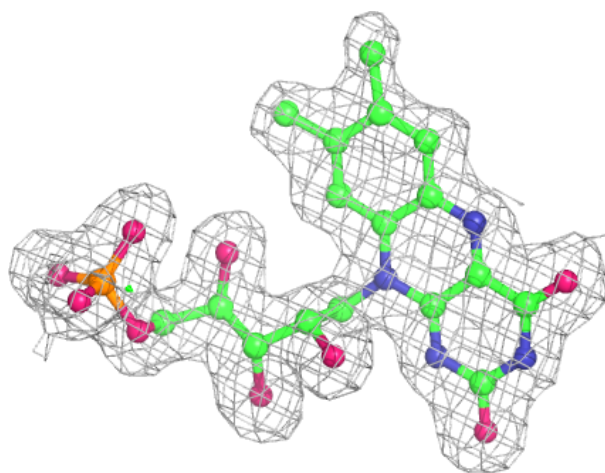
6.4 Ligands ⓘ

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.

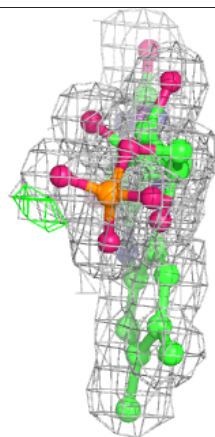
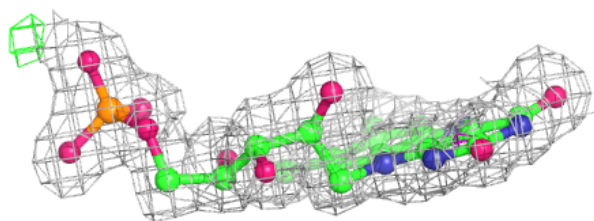
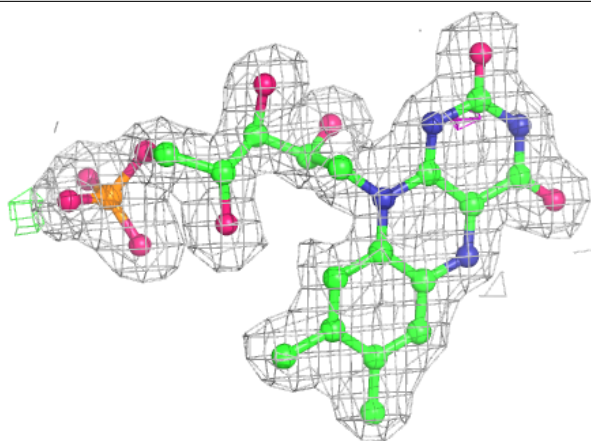
Electron density around FMN C 501:

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



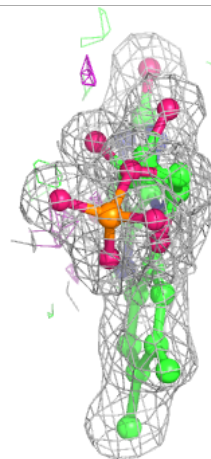
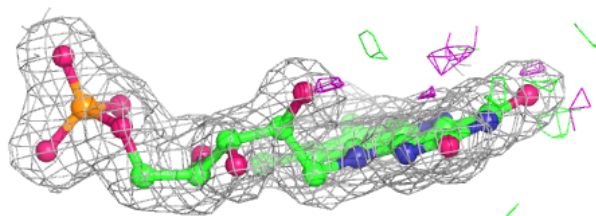
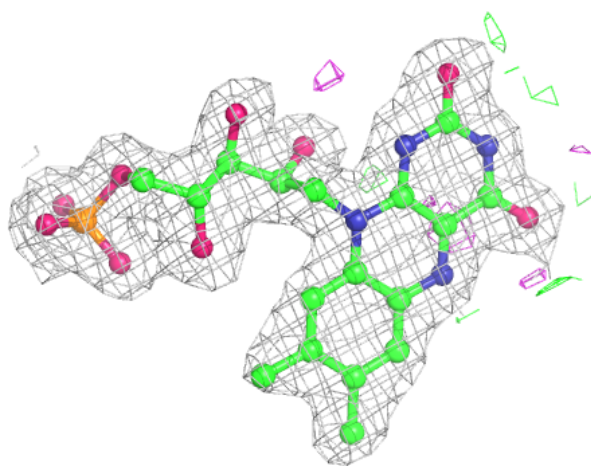
Electron density around FMN A 501:

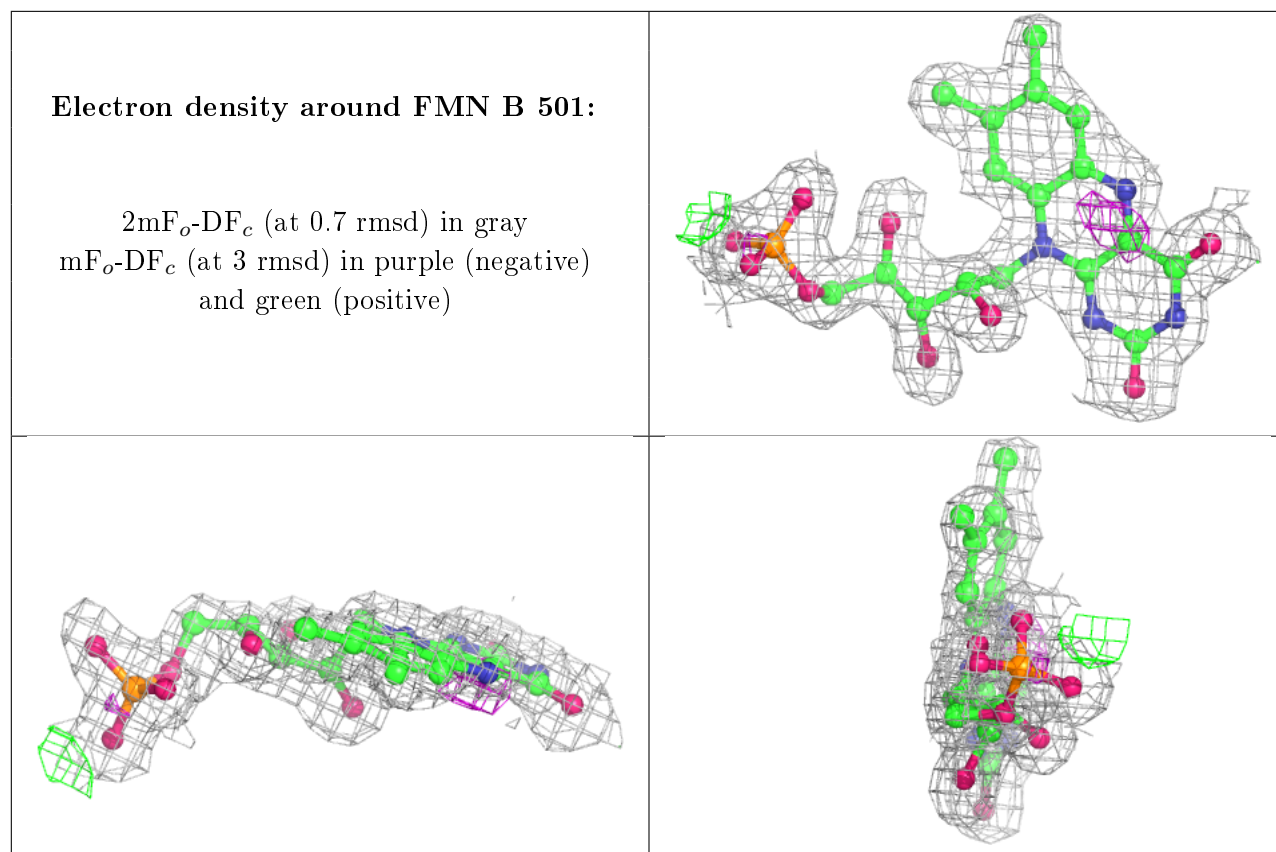
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FMN D 501:

$2mF_o-DF_c$ (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.