



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:53 AM UTC

PDB ID : 6AJ5 / pdb_00006aj5
Title : Crystal structure of ligand-free type DHODH from Eimeria tenella
Authors : Shiba, T.; Inaoka, D.K.; Sato, D.; Hartuti, E.D.; Amalia, E.; Nagahama, M.; Yoshioka, Y.; Matsubayashi, M.; Balogun, E.O.; Tsuji, N.; Kita, K.; Harada, S.
Deposited on : 2018-08-27
Resolution : 3.50 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

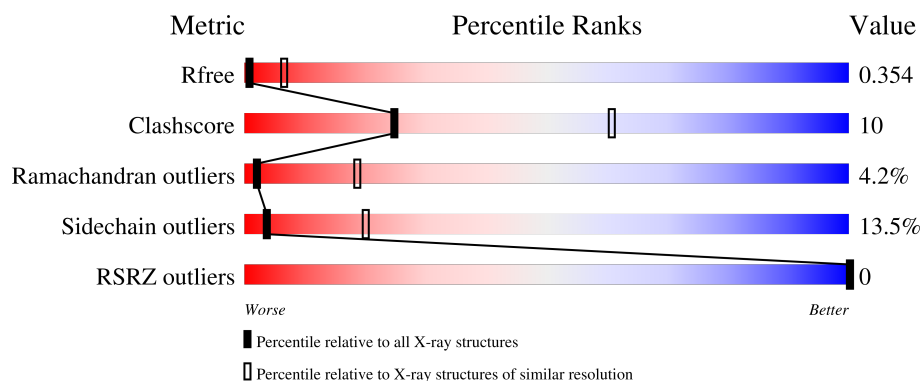
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	436	
1	B	436	
1	C	436	
1	D	436	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11453 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 Dihydroorotate dehydrogenase (quinone), mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	0	0
			2801	1753	509	528	11			
1	B	362	Total	C	N	O	S	0	0	0
			2828	1769	516	532	11			
1	C	362	Total	C	N	O	S	0	0	0
			2828	1769	516	532	11			
1	D	362	Total	C	N	O	S	0	0	0
			2828	1769	516	532	11			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP U6KL66
A	-20	GLY	-	expression tag	UNP U6KL66
A	-19	HIS	-	expression tag	UNP U6KL66
A	-18	HIS	-	expression tag	UNP U6KL66
A	-17	HIS	-	expression tag	UNP U6KL66
A	-16	HIS	-	expression tag	UNP U6KL66
A	-15	HIS	-	expression tag	UNP U6KL66
A	-14	HIS	-	expression tag	UNP U6KL66
A	-13	HIS	-	expression tag	UNP U6KL66
A	-12	HIS	-	expression tag	UNP U6KL66
A	-11	HIS	-	expression tag	UNP U6KL66
A	-10	SER	-	expression tag	UNP U6KL66
A	-9	SER	-	expression tag	UNP U6KL66
A	-8	GLY	-	expression tag	UNP U6KL66
A	-7	HIS	-	expression tag	UNP U6KL66
A	-6	ILE	-	expression tag	UNP U6KL66
A	-5	ASP	-	expression tag	UNP U6KL66
A	-4	ASP	-	expression tag	UNP U6KL66
A	-3	ASP	-	expression tag	UNP U6KL66
A	-2	ASP	-	expression tag	UNP U6KL66
A	-1	LYS	-	expression tag	UNP U6KL66

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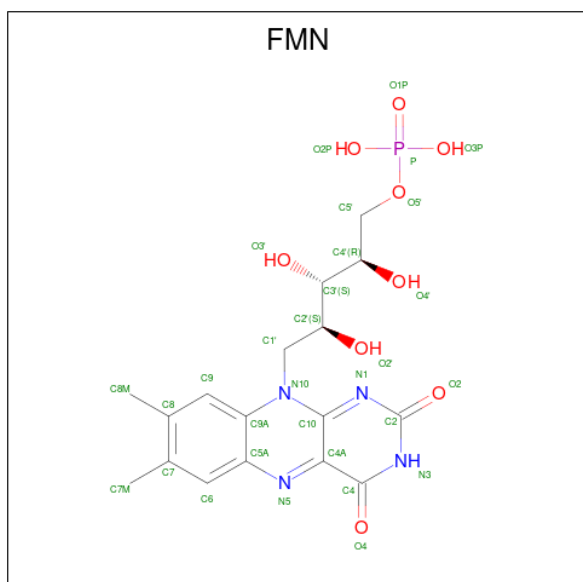
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP U6KL66
B	-21	MET	-	initiating methionine	UNP U6KL66
B	-20	GLY	-	expression tag	UNP U6KL66
B	-19	HIS	-	expression tag	UNP U6KL66
B	-18	HIS	-	expression tag	UNP U6KL66
B	-17	HIS	-	expression tag	UNP U6KL66
B	-16	HIS	-	expression tag	UNP U6KL66
B	-15	HIS	-	expression tag	UNP U6KL66
B	-14	HIS	-	expression tag	UNP U6KL66
B	-13	HIS	-	expression tag	UNP U6KL66
B	-12	HIS	-	expression tag	UNP U6KL66
B	-11	HIS	-	expression tag	UNP U6KL66
B	-10	SER	-	expression tag	UNP U6KL66
B	-9	SER	-	expression tag	UNP U6KL66
B	-8	GLY	-	expression tag	UNP U6KL66
B	-7	HIS	-	expression tag	UNP U6KL66
B	-6	ILE	-	expression tag	UNP U6KL66
B	-5	ASP	-	expression tag	UNP U6KL66
B	-4	ASP	-	expression tag	UNP U6KL66
B	-3	ASP	-	expression tag	UNP U6KL66
B	-2	ASP	-	expression tag	UNP U6KL66
B	-1	LYS	-	expression tag	UNP U6KL66
B	0	HIS	-	expression tag	UNP U6KL66
C	-21	MET	-	initiating methionine	UNP U6KL66
C	-20	GLY	-	expression tag	UNP U6KL66
C	-19	HIS	-	expression tag	UNP U6KL66
C	-18	HIS	-	expression tag	UNP U6KL66
C	-17	HIS	-	expression tag	UNP U6KL66
C	-16	HIS	-	expression tag	UNP U6KL66
C	-15	HIS	-	expression tag	UNP U6KL66
C	-14	HIS	-	expression tag	UNP U6KL66
C	-13	HIS	-	expression tag	UNP U6KL66
C	-12	HIS	-	expression tag	UNP U6KL66
C	-11	HIS	-	expression tag	UNP U6KL66
C	-10	SER	-	expression tag	UNP U6KL66
C	-9	SER	-	expression tag	UNP U6KL66
C	-8	GLY	-	expression tag	UNP U6KL66
C	-7	HIS	-	expression tag	UNP U6KL66
C	-6	ILE	-	expression tag	UNP U6KL66
C	-5	ASP	-	expression tag	UNP U6KL66
C	-4	ASP	-	expression tag	UNP U6KL66
C	-3	ASP	-	expression tag	UNP U6KL66

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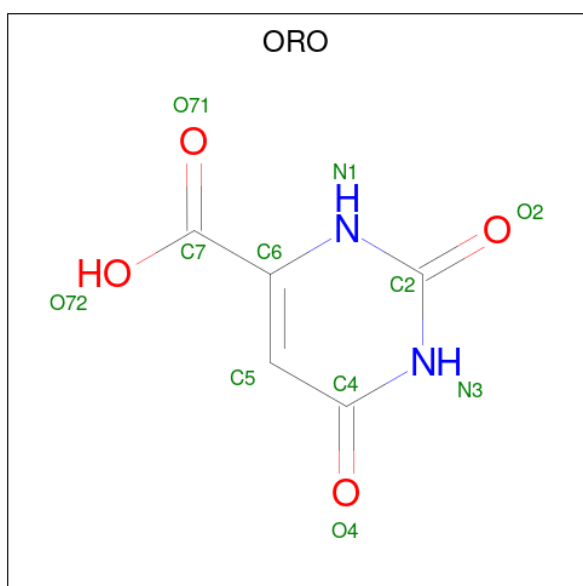
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	ASP	-	expression tag	UNP U6KL66
C	-1	LYS	-	expression tag	UNP U6KL66
C	0	HIS	-	expression tag	UNP U6KL66
D	-21	MET	-	initiating methionine	UNP U6KL66
D	-20	GLY	-	expression tag	UNP U6KL66
D	-19	HIS	-	expression tag	UNP U6KL66
D	-18	HIS	-	expression tag	UNP U6KL66
D	-17	HIS	-	expression tag	UNP U6KL66
D	-16	HIS	-	expression tag	UNP U6KL66
D	-15	HIS	-	expression tag	UNP U6KL66
D	-14	HIS	-	expression tag	UNP U6KL66
D	-13	HIS	-	expression tag	UNP U6KL66
D	-12	HIS	-	expression tag	UNP U6KL66
D	-11	HIS	-	expression tag	UNP U6KL66
D	-10	SER	-	expression tag	UNP U6KL66
D	-9	SER	-	expression tag	UNP U6KL66
D	-8	GLY	-	expression tag	UNP U6KL66
D	-7	HIS	-	expression tag	UNP U6KL66
D	-6	ILE	-	expression tag	UNP U6KL66
D	-5	ASP	-	expression tag	UNP U6KL66
D	-4	ASP	-	expression tag	UNP U6KL66
D	-3	ASP	-	expression tag	UNP U6KL66
D	-2	ASP	-	expression tag	UNP U6KL66
D	-1	LYS	-	expression tag	UNP U6KL66
D	0	HIS	-	expression tag	UNP U6KL66

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



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		

- Molecule 3 is OROTIC ACID (CCD ID: ORO) (formula: $C_5H_4N_2O_4$).

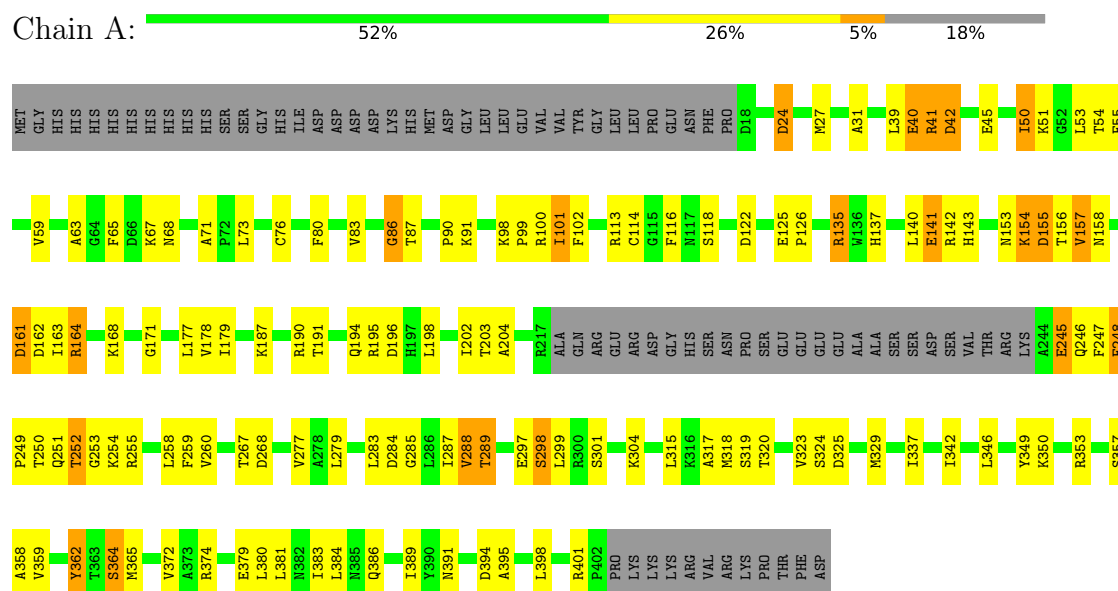


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	5	2	4		
3	B	1	Total	C	N	O	0	0
			11	5	2	4		
3	C	1	Total	C	N	O	0	0
			11	5	2	4		
3	D	1	Total	C	N	O	0	0
			11	5	2	4		

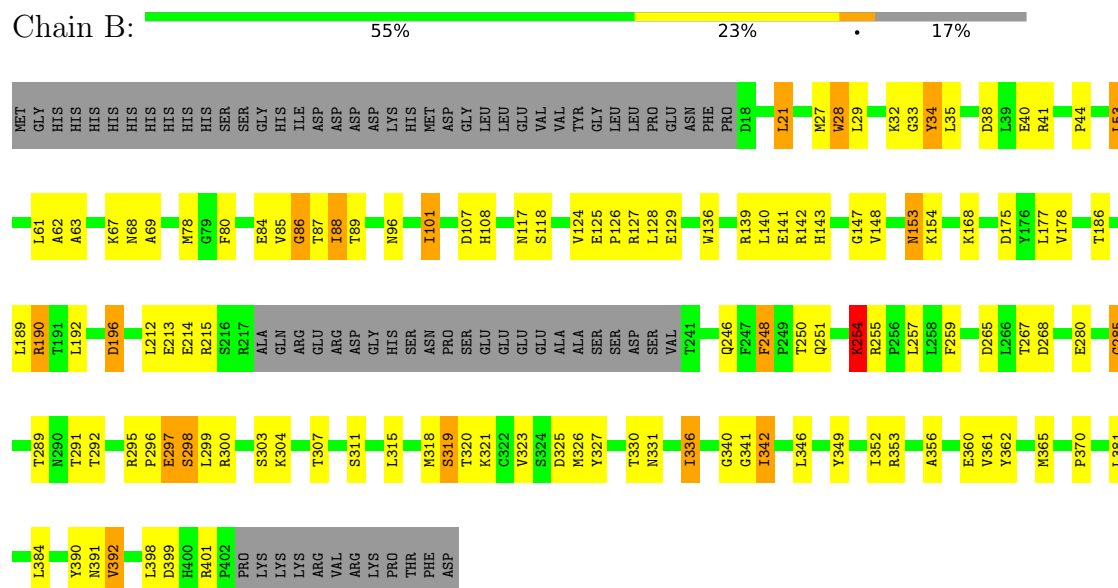
3 Residue-property plots

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: Dihydroorotate dehydrogenase (quinone), mitochondrial

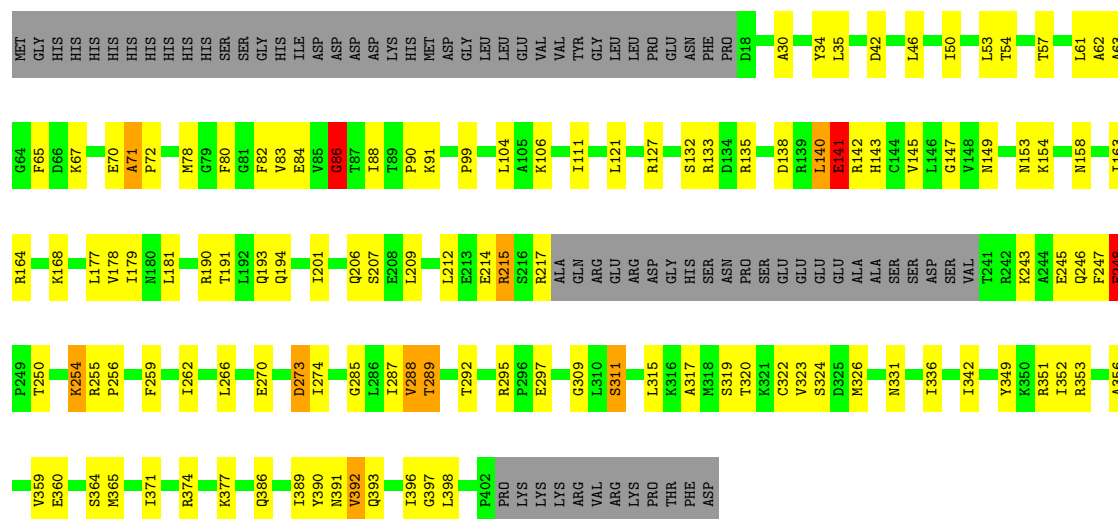


- Molecule 1: Dihydroorotate dehydrogenase (quinone), mitochondrial



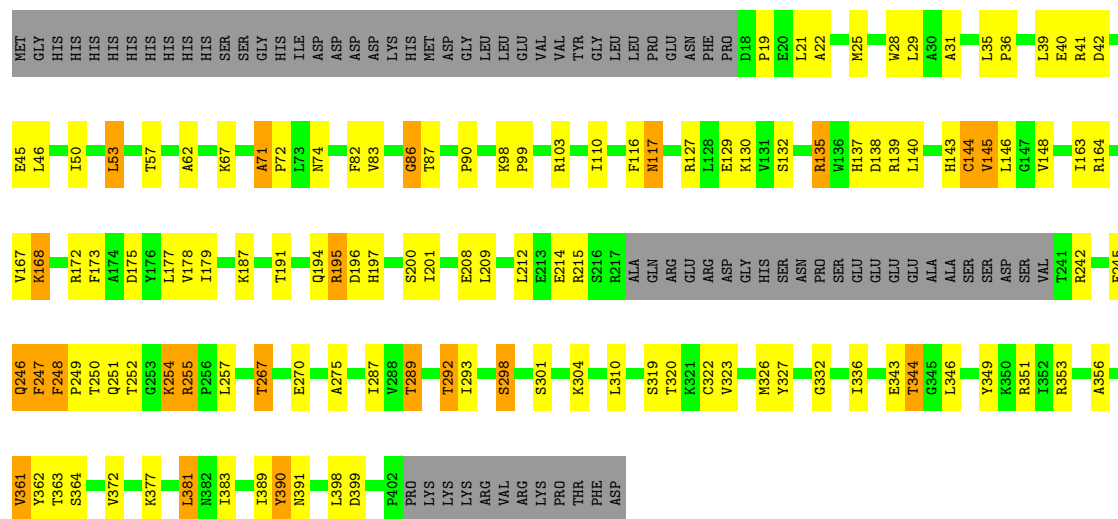
• Molecule 1: Dihydroorotate dehydrogenase (quinone), mitochondrial

Chain C:  55% 25% 17%



• Molecule 1: Dihydroorotate dehydrogenase (quinone), mitochondrial

Chain D:  55% 23% 5% 17%



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	248.81Å 248.81Å 248.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.50 20.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	95.3 (20.00-3.50) 95.9 (20.00-3.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.32 (at 3.52Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.272 , 0.359 0.271 , 0.354	Depositor DCC
R_{free} test set	1493 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	48.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 97.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.147 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11453	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.44% 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, ORO

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	0.88	0/2848	1.11	9/3846 (0.2%)
1	B	0.87	0/2875	1.11	7/3881 (0.2%)
1	C	0.91	0/2875	1.13	6/3881 (0.2%)
1	D	0.90	0/2875	1.16	3/3881 (0.1%)
All	All	0.89	0/11473	1.13	25/15489 (0.2%)

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	A	0	2
1	B	0	2
1	C	0	3
1	D	0	3
All	All	0	10

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	87	THR	N-CA-C	-7.08	97.36	108.90
1	B	300	ARG	N-CA-C	6.82	120.83	112.23
1	A	50	ILE	CB-CA-C	6.52	117.84	110.41
1	D	40	GLU	N-CA-C	6.20	118.04	111.28
1	B	214	GLU	N-CA-C	6.08	119.46	110.46
1	C	248	PHE	CA-C-N	5.86	128.41	120.79
1	C	248	PHE	C-N-CA	5.86	128.41	120.79
1	B	87	THR	N-CA-C	-5.82	100.50	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	96	ASN	CA-C-N	-5.73	114.35	120.03
1	B	96	ASN	C-N-CA	-5.73	114.35	120.03
1	C	141	GLU	N-CA-C	5.69	118.72	108.48
1	B	34	TYR	N-CA-C	5.68	122.89	110.80
1	C	147	GLY	N-CA-C	-5.65	104.45	112.37
1	D	390	TYR	N-CA-C	-5.56	102.66	110.50
1	D	298	SER	N-CA-C	-5.53	103.80	110.88
1	B	285	GLY	N-CA-C	5.34	119.31	110.55
1	A	24	ASP	N-CA-C	5.33	117.17	111.36
1	A	251	GLN	N-CA-C	-5.23	104.22	111.28
1	A	279	LEU	CA-C-N	5.17	127.63	120.29
1	A	279	LEU	C-N-CA	5.17	127.63	120.29
1	A	277	VAL	CB-CA-C	-5.11	105.19	111.94
1	A	142	ARG	N-CA-C	-5.09	101.30	109.39
1	A	141	GLU	N-CA-C	5.03	117.52	110.23
1	C	288	VAL	CA-C-N	5.03	131.15	121.54
1	C	288	VAL	C-N-CA	5.03	131.15	121.54

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	248	PHE	Peptide
1	A	86	GLY	Peptide
1	B	248	PHE	Peptide
1	B	86	GLY	Peptide
1	C	141	GLU	Peptide
1	C	248	PHE	Peptide
1	C	86	GLY	Peptide
1	D	144	CYS	Peptide
1	D	214	GLU	Peptide
1	D	248	PHE	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	2801	0	2828	59	0
1	B	2828	0	2861	59	0
1	C	2828	0	2861	57	0
1	D	2828	0	2861	49	0
2	A	31	0	19	1	0
2	B	31	0	19	1	0
2	C	31	0	19	1	0
2	D	31	0	19	0	0
3	A	11	0	3	1	0
3	B	11	0	3	0	0
3	C	11	0	3	0	0
3	D	11	0	3	0	0
All	All	11453	0	11499	225	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 10.

All (225) 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:178:VAL:HG11	1:A:287:ILE:HD12	1.71	0.71
1:C:181:LEU:HD11	1:C:201:ILE:HG21	1.71	0.71
1:C:193:GLN:HE22	1:C:266:LEU:HD11	1.57	0.68
1:D:209:LEU:HD13	1:D:255:ARG:HE	1.62	0.65
1:C:215:ARG:O	1:C:217:ARG:NH1	2.31	0.64
1:D:323:VAL:HG13	1:D:336:ILE:HG21	1.80	0.63
1:D:194:GLN:O	1:D:195:ARG:C	2.41	0.63
1:D:110:ILE:HD12	1:D:363:THR:HG23	1.80	0.63
1:A:178:VAL:CG1	1:A:287:ILE:HD12	2.29	0.62
1:D:53:LEU:HD11	1:D:175:ASP:HB3	1.81	0.62
1:B:323:VAL:HG13	1:B:336:ILE:HG21	1.81	0.61
1:A:153:ASN:O	1:A:155:ASP:N	2.35	0.60
1:B:67:LYS:HA	1:B:86:GLY:CA	2.31	0.60
1:C:262:ILE:HD11	1:C:288:VAL:HG22	1.83	0.60
1:A:288:VAL:O	1:A:288:VAL:HG13	2.03	0.59
1:B:296:PRO:HD2	1:B:299:LEU:HD11	1.84	0.59
1:B:315:LEU:HD23	1:B:340:GLY:HA2	1.84	0.59
1:A:67:LYS:HA	1:A:86:GLY:CA	2.33	0.58
1:C:292:THR:HG22	1:C:315:LEU:HD13	1.85	0.58
1:D:163:ILE:HD12	1:D:179:ILE:HG23	1.87	0.57
1:D:135:ARG:HD3	1:D:143:HIS:CE1	2.40	0.57
1:A:346:LEU:O	1:A:350:LYS:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:311:SER:HA	1:C:315:LEU:HD22	1.87	0.56
1:D:57:THR:HG21	1:D:377:LYS:HD3	1.87	0.56
1:B:248:PHE:O	1:B:254:LYS:HB3	2.06	0.56
1:D:163:ILE:HG21	1:D:201:ILE:HG23	1.87	0.56
1:B:340:GLY:N	1:B:342:ILE:HD11	2.20	0.56
1:A:353:ARG:HA	1:A:395:ALA:O	2.07	0.55
1:A:337:ILE:HG12	1:A:358:ALA:HB3	1.88	0.55
1:A:364:SER:HB2	1:A:372:VAL:HG21	1.88	0.55
1:B:67:LYS:HA	1:B:86:GLY:HA3	1.88	0.55
1:C:46:LEU:HA	1:C:392:VAL:CG1	2.36	0.55
1:C:289:THR:HG21	1:C:319:SER:HA	1.89	0.55
1:A:125:GLU:HB3	1:A:126:PRO:HD3	1.90	0.54
1:B:175:ASP:HA	1:B:250:THR:HG23	1.89	0.54
1:C:178:VAL:HG11	1:C:287:ILE:HD12	1.89	0.54
1:A:288:VAL:CG1	1:A:323:VAL:HG22	2.38	0.54
1:C:62:ALA:HB2	1:C:360:GLU:HB3	1.88	0.54
1:A:50:ILE:HD12	1:A:357:SER:HB2	1.88	0.54
1:A:287:ILE:HA	1:A:337:ILE:O	2.08	0.54
1:D:42:ASP:OD2	1:D:377:LYS:HD2	2.08	0.54
1:C:70:GLU:O	1:C:71:ALA:HB2	2.08	0.53
1:C:259:PHE:CE1	1:C:285:GLY:HA3	2.42	0.53
1:A:349:TYR:CZ	1:A:353:ARG:HD2	2.44	0.53
1:D:250:THR:O	1:D:251:GLN:HB3	2.08	0.53
1:B:349:TYR:CZ	1:B:353:ARG:HD2	2.44	0.52
1:D:135:ARG:HD3	1:D:143:HIS:ND1	2.24	0.52
1:B:88:ILE:HD13	1:B:124:VAL:HG11	1.91	0.52
1:C:254:LYS:O	1:C:255:ARG:C	2.52	0.52
1:B:67:LYS:HE2	1:B:117:ASN:C	2.35	0.52
1:B:384:LEU:HD11	1:B:392:VAL:HG22	1.91	0.52
1:A:156:THR:HG21	1:A:162:ASP:CG	2.35	0.52
1:A:163:ILE:HD12	1:A:179:ILE:HG23	1.93	0.52
1:C:349:TYR:CZ	1:C:353:ARG:HD2	2.46	0.51
1:A:289:THR:HG21	1:A:319:SER:CB	2.40	0.51
1:B:295:ARG:HD2	1:B:304:LYS:O	2.10	0.51
1:B:384:LEU:CD1	1:B:392:VAL:HG22	2.40	0.51
1:A:384:LEU:HD13	1:A:391:ASN:O	2.09	0.51
1:D:349:TYR:OH	1:D:353:ARG:NH1	2.43	0.51
1:D:98:LYS:HA	1:D:99:PRO:C	2.35	0.51
1:D:289:THR:HG21	1:D:319:SER:HA	1.93	0.51
1:C:342:ILE:HD11	1:C:351:ARG:HD2	1.93	0.51
1:D:361:VAL:HG11	1:D:372:VAL:HG11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:374:ARG:HA	1:C:377:LYS:HE2	1.93	0.50
1:B:186:THR:O	1:B:190:ARG:NH2	2.44	0.50
1:D:87:THR:HG21	1:D:116:PHE:CE1	2.47	0.50
1:B:289:THR:HG21	1:B:319:SER:HA	1.93	0.50
2:C:501:FMN:O3P	2:C:501:FMN:O4'	2.28	0.50
1:C:88:ILE:HG22	1:C:121:LEU:HD23	1.94	0.50
1:D:194:GLN:O	1:D:196:ASP:N	2.45	0.50
1:C:61:LEU:HB3	1:C:83:VAL:HG12	1.94	0.50
1:A:59:VAL:HA	1:A:359:VAL:HG23	1.93	0.50
1:D:82:PHE:HB3	1:D:145:VAL:HB	1.94	0.50
1:B:67:LYS:HA	1:B:86:GLY:HA2	1.93	0.49
1:C:179:ILE:HG22	1:C:181:LEU:HG	1.92	0.49
1:C:288:VAL:HG12	1:C:289:THR:HG23	1.95	0.49
1:B:142:ARG:O	1:B:143:HIS:C	2.55	0.49
1:B:189:LEU:HD12	1:B:192:LEU:CD1	2.43	0.49
1:C:178:VAL:CG1	1:C:287:ILE:HD12	2.43	0.49
1:C:209:LEU:HD22	1:C:256:PRO:HD2	1.95	0.49
1:B:319:SER:O	1:B:323:VAL:HG23	2.12	0.49
1:A:380:LEU:O	1:A:384:LEU:HG	2.13	0.49
1:D:67:LYS:HA	1:D:86:GLY:HA3	1.94	0.49
1:D:31:ALA:HA	1:D:71:ALA:HB2	1.94	0.49
1:C:212:LEU:HD11	1:C:255:ARG:NH1	2.28	0.48
1:D:135:ARG:NH2	1:D:249:PRO:O	2.35	0.48
1:C:30:ALA:CA	1:C:35:LEU:HD12	2.43	0.48
1:B:89:THR:HG1	1:B:118:SER:HG	1.60	0.48
1:C:248:PHE:CB	1:C:254:LYS:HD2	2.44	0.48
1:A:68:ASN:HD21	1:A:118:SER:HA	1.79	0.48
1:C:61:LEU:HD13	1:C:80:PHE:CE2	2.49	0.48
1:A:67:LYS:HA	1:A:86:GLY:HA2	1.95	0.48
1:A:289:THR:HG21	1:A:319:SER:OG	2.14	0.48
1:D:129:GLU:HG2	1:D:173:PHE:CZ	2.49	0.48
1:A:27:MET:HE3	1:A:65:PHE:O	2.14	0.48
1:B:189:LEU:HD12	1:B:192:LEU:HD11	1.96	0.48
1:B:33:GLY:O	1:B:35:LEU:N	2.39	0.47
1:D:250:THR:O	1:D:250:THR:HG22	2.13	0.47
1:A:153:ASN:O	1:A:154:LYS:C	2.57	0.47
1:B:53:LEU:HD23	1:B:257:LEU:HD13	1.96	0.47
1:B:142:ARG:HA	1:B:142:ARG:NE	2.29	0.47
1:C:111:ILE:HA	1:C:309:GLY:O	2.13	0.47
1:A:260:VAL:HG23	1:A:283:LEU:HD11	1.96	0.47
1:B:136:TRP:O	1:B:140:LEU:HD23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:CYS:N	3:A:502:ORO:O71	2.47	0.47
1:B:28:TRP:CZ3	1:B:32:LYS:HG3	2.49	0.47
1:C:352:ILE:HA	1:C:356:ALA:O	2.15	0.47
1:D:361:VAL:HG13	1:D:364:SER:HB2	1.95	0.47
1:C:153:ASN:O	1:C:154:LYS:C	2.57	0.47
1:D:327:TYR:CZ	1:D:332:GLY:HA2	2.49	0.47
1:B:125:GLU:HB3	1:B:126:PRO:HD3	1.97	0.47
1:C:82:PHE:HB3	1:C:145:VAL:HB	1.97	0.47
1:D:45:GLU:OE1	1:D:45:GLU:N	2.48	0.47
1:A:164:ARG:CZ	1:A:204:ALA:HB1	2.45	0.46
1:B:342:ILE:HD13	1:B:360:GLU:O	2.15	0.46
1:A:288:VAL:HG11	1:A:323:VAL:HG22	1.97	0.46
1:A:63:ALA:O	2:A:501:FMN:C4	2.63	0.46
1:C:135:ARG:NH1	1:C:143:HIS:CE1	2.84	0.46
1:C:273:ASP:OD2	1:C:273:ASP:N	2.49	0.46
1:C:323:VAL:HG13	1:C:336:ILE:HG21	1.96	0.46
1:D:148:VAL:O	1:D:177:LEU:HD23	2.15	0.46
1:B:84:GLU:HA	1:B:147:GLY:O	2.15	0.46
1:C:67:LYS:HA	1:C:86:GLY:CA	2.45	0.46
1:C:46:LEU:HA	1:C:392:VAL:HG12	1.97	0.46
1:A:156:THR:HG21	1:A:162:ASP:OD1	2.16	0.46
1:B:61:LEU:HD13	1:B:80:PHE:CZ	2.51	0.46
1:D:19:PRO:HA	1:D:22:ALA:HB3	1.98	0.45
1:A:258:LEU:O	1:A:284:ASP:HB2	2.16	0.45
1:D:72:PRO:HA	1:D:83:VAL:HG21	1.98	0.45
1:C:135:ARG:CZ	1:C:143:HIS:CE1	2.99	0.45
1:C:270:GLU:O	1:C:274:ILE:HD12	2.16	0.45
1:A:31:ALA:HA	1:A:71:ALA:HB2	1.99	0.45
1:A:67:LYS:HA	1:A:86:GLY:HA3	1.99	0.45
1:C:30:ALA:HB2	1:C:35:LEU:HD12	1.99	0.45
1:B:53:LEU:HD23	1:B:257:LEU:CD1	2.47	0.45
1:B:89:THR:HB	1:B:153:ASN:ND2	2.32	0.45
1:C:35:LEU:HD13	1:C:78:MET:SD	2.57	0.45
1:A:259:PHE:CD1	1:A:285:GLY:C	2.95	0.45
1:C:63:ALA:HB2	1:C:84:GLU:CD	2.42	0.45
1:A:259:PHE:HA	1:A:285:GLY:O	2.17	0.44
1:D:62:ALA:HB3	1:D:362:TYR:HB2	1.98	0.44
1:C:352:ILE:O	1:C:396:ILE:HA	2.16	0.44
1:D:19:PRO:HD3	1:D:103:ARG:HB2	1.99	0.44
1:D:275:ALA:HB2	1:D:326:MET:HE1	1.99	0.44
1:A:362:TYR:CD1	1:A:362:TYR:C	2.95	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:139:ARG:O	1:D:140:LEU:C	2.60	0.44
1:B:362:TYR:N	2:B:501:FMN:O3P	2.44	0.44
1:C:67:LYS:HA	1:C:86:GLY:HA2	2.00	0.44
1:A:383:ILE:HG22	1:A:383:ILE:O	2.18	0.44
1:B:107:ASP:O	1:B:108:HIS:C	2.60	0.44
1:A:98:LYS:CG	1:A:99:PRO:HA	2.47	0.44
1:A:325:ASP:O	1:A:329:MET:HB2	2.18	0.44
1:A:362:TYR:C	1:A:362:TYR:HD1	2.26	0.44
1:D:267:THR:HB	1:D:270:GLU:H	1.82	0.44
1:D:292:THR:HG23	1:D:310:LEU:HB3	2.00	0.44
1:C:104:LEU:HD11	1:C:111:ILE:HD12	1.99	0.44
1:B:62:ALA:HB2	1:B:360:GLU:CB	2.48	0.44
1:D:167:VAL:HG11	1:D:208:GLU:HB2	1.99	0.44
1:B:315:LEU:HD23	1:B:340:GLY:CA	2.48	0.43
1:D:117:ASN:OD1	1:D:117:ASN:N	2.50	0.43
1:A:297:GLU:O	1:A:298:SER:OG	2.28	0.43
1:B:326:MET:O	1:B:330:THR:HG23	2.18	0.43
1:C:86:GLY:O	1:C:149:ASN:HB3	2.18	0.43
1:B:292:THR:OG1	1:B:318:MET:HE1	2.18	0.43
1:B:68:ASN:O	1:B:69:ALA:HB3	2.18	0.43
1:C:191:THR:HG22	1:C:191:THR:O	2.17	0.43
1:A:194:GLN:O	1:A:195:ARG:C	2.60	0.43
1:A:379:GLU:O	1:A:383:ILE:HG12	2.17	0.43
1:B:352:ILE:HA	1:B:356:ALA:O	2.19	0.43
1:C:138:ASP:O	1:C:140:LEU:N	2.49	0.43
1:C:163:ILE:HD12	1:C:179:ILE:HG23	2.00	0.43
1:A:158:ASN:HB2	1:A:161:ASP:CG	2.44	0.43
1:B:175:ASP:HA	1:B:250:THR:CG2	2.49	0.43
1:A:289:THR:HG21	1:A:319:SER:HB3	2.00	0.43
1:C:88:ILE:CG2	1:C:121:LEU:HD23	2.49	0.43
1:A:91:LYS:HB2	1:A:153:ASN:OD1	2.19	0.42
1:D:390:TYR:O	1:D:391:ASN:HB2	2.19	0.42
1:A:198:LEU:HG	1:A:202:ILE:HD11	2.01	0.42
1:B:297:GLU:O	1:B:298:SER:CB	2.67	0.42
1:D:246:GLN:C	1:D:247:PHE:O	2.62	0.42
1:A:73:LEU:HA	1:A:76:CYS:HB2	2.01	0.42
1:D:191:THR:O	1:D:191:THR:HG22	2.19	0.42
1:D:346:LEU:HD13	1:D:383:ILE:HD12	2.01	0.42
1:A:317:ALA:HA	1:A:320:THR:HG22	2.02	0.42
1:D:46:LEU:HD11	1:D:381:LEU:HD23	2.02	0.42
1:B:63:ALA:HB2	1:B:84:GLU:OE1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:SER:O	1:B:320:THR:C	2.63	0.42
1:D:127:ARG:O	1:D:130:LYS:HB3	2.20	0.42
1:A:102:PHE:CD2	1:A:102:PHE:N	2.88	0.42
1:B:27:MET:HE3	1:B:27:MET:O	2.20	0.42
1:B:175:ASP:OD1	1:B:251:GLN:HB2	2.20	0.42
1:B:327:TYR:HD1	1:B:336:ILE:HD12	1.84	0.42
1:A:250:THR:CG2	1:A:254:LYS:HA	2.50	0.41
1:C:30:ALA:HA	1:C:35:LEU:HD12	2.01	0.41
1:A:135:ARG:NH1	1:A:143:HIS:CE1	2.87	0.41
1:C:72:PRO:HA	1:C:83:VAL:HG21	2.02	0.41
1:B:89:THR:OG1	1:B:118:SER:OG	2.29	0.41
1:A:80:PHE:HZ	1:A:365:MET:HE2	1.85	0.41
1:B:21:LEU:HD13	1:B:21:LEU:O	2.19	0.41
1:A:50:ILE:CG2	1:A:55:PHE:CD1	3.03	0.41
1:D:29:LEU:HD22	1:D:35:LEU:CD2	2.51	0.41
1:A:41:ARG:O	1:A:42:ASP:O	2.38	0.41
1:A:349:TYR:CD2	1:A:383:ILE:HG21	2.55	0.41
1:B:291:THR:HG22	1:B:311:SER:HB3	2.01	0.41
1:C:317:ALA:HA	1:C:320:THR:HG22	2.02	0.41
1:C:61:LEU:HB2	1:C:80:PHE:CD2	2.54	0.41
1:D:25:MET:O	1:D:28:TRP:HB3	2.21	0.41
1:B:259:PHE:CE1	1:B:285:GLY:HA3	2.56	0.41
1:A:315:LEU:O	1:A:319:SER:OG	2.28	0.41
1:B:28:TRP:CD1	1:B:29:LEU:N	2.89	0.41
1:B:365:MET:HE3	1:B:370:PRO:HA	2.02	0.41
1:C:396:ILE:HG22	1:C:397:GLY:N	2.36	0.41
1:D:336:ILE:O	1:D:356:ALA:HA	2.21	0.41
1:C:322:CYS:O	1:C:326:MET:HG2	2.21	0.41
1:B:101:ILE:HG23	1:B:101:ILE:O	2.21	0.40
1:B:342:ILE:HD12	1:B:342:ILE:N	2.36	0.40
1:C:70:GLU:OE1	1:C:127:ARG:NH1	2.53	0.40
1:B:254:LYS:O	1:B:255:ARG:C	2.64	0.40
1:D:208:GLU:OE2	1:D:208:GLU:HA	2.20	0.40
1:C:72:PRO:CA	1:C:83:VAL:HG21	2.51	0.40
1:A:171:GLY:HA3	1:A:177:LEU:HD11	2.04	0.40
1:B:84:GLU:OE2	1:B:178:VAL:HG21	2.21	0.40
1:D:248:PHE:O	1:D:254:LYS:HB3	2.21	0.40
1:B:128:LEU:HD13	1:B:148:VAL:HG21	2.04	0.40
1:C:342:ILE:HD13	1:C:359:VAL:HB	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	355/436 (81%)	284 (80%)	52 (15%)	19 (5%)	1	14
1	B	358/436 (82%)	288 (80%)	58 (16%)	12 (3%)	3	23
1	C	358/436 (82%)	297 (83%)	51 (14%)	10 (3%)	4	26
1	D	358/436 (82%)	291 (81%)	48 (13%)	19 (5%)	1	14
All	All	1429/1744 (82%)	1160 (81%)	209 (15%)	60 (4%)	2	19

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	ASP
1	A	116	PHE
1	A	137	HIS
1	A	154	LYS
1	A	157	VAL
1	A	252	THR
1	B	34	TYR
1	B	101	ILE
1	C	86	GLY
1	D	86	GLY
1	D	138	ASP
1	D	195	ARG
1	D	247	PHE
1	D	254	LYS
1	A	40	GLU
1	A	51	LYS
1	A	245	GLU
1	A	247	PHE
1	A	253	GLY
1	A	304	LYS
1	B	153	ASN
1	B	298	SER

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Mol	Chain	Res	Type
1	C	34	TYR
1	C	71	ALA
1	C	289	THR
1	C	386	GLN
1	D	172	ARG
1	D	399	ASP
1	A	248	PHE
1	A	298	SER
1	B	196	ASP
1	B	254	LYS
1	C	42	ASP
1	D	36	PRO
1	D	41	ARG
1	D	242	ARG
1	D	304	LYS
1	A	101	ILE
1	B	341	GLY
1	C	65	PHE
1	C	295	ARG
1	D	289	THR
1	D	344	THR
1	A	90	PRO
1	B	139	ARG
1	B	391	ASN
1	C	90	PRO
1	D	90	PRO
1	D	146	LEU
1	D	168	LYS
1	D	255	ARG
1	A	187	LYS
1	B	392	VAL
1	C	393	GLN
1	A	249	PRO
1	B	336	ILE
1	A	255	ARG
1	B	44	PRO
1	D	71	ALA
1	D	145	VAL

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	302/371 (81%)	257 (85%)	45 (15%)	3	17
1	B	305/371 (82%)	264 (87%)	41 (13%)	4	20
1	C	305/371 (82%)	264 (87%)	41 (13%)	4	20
1	D	305/371 (82%)	268 (88%)	37 (12%)	5	22
All	All	1217/1484 (82%)	1053 (86%)	164 (14%)	4	20

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASP
1	A	39	LEU
1	A	40	GLU
1	A	41	ARG
1	A	45	GLU
1	A	53	LEU
1	A	54	THR
1	A	83	VAL
1	A	100	ARG
1	A	101	ILE
1	A	113	ARG
1	A	122	ASP
1	A	135	ARG
1	A	140	LEU
1	A	141	GLU
1	A	155	ASP
1	A	157	VAL
1	A	161	ASP
1	A	164	ARG
1	A	168	LYS
1	A	190	ARG
1	A	191	THR
1	A	196	ASP
1	A	203	THR

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Mol	Chain	Res	Type
1	A	245	GLU
1	A	246	GLN
1	A	252	THR
1	A	267	THR
1	A	268	ASP
1	A	288	VAL
1	A	289	THR
1	A	299	LEU
1	A	301	SER
1	A	318	MET
1	A	324	SER
1	A	342	ILE
1	A	362	TYR
1	A	364	SER
1	A	374	ARG
1	A	381	LEU
1	A	386	GLN
1	A	389	ILE
1	A	394	ASP
1	A	398	LEU
1	A	401	ARG
1	B	21	LEU
1	B	28	TRP
1	B	38	ASP
1	B	40	GLU
1	B	41	ARG
1	B	53	LEU
1	B	78	MET
1	B	85	VAL
1	B	88	ILE
1	B	127	ARG
1	B	129	GLU
1	B	141	GLU
1	B	154	LYS
1	B	168	LYS
1	B	177	LEU
1	B	190	ARG
1	B	196	ASP
1	B	212	LEU
1	B	213	GLU
1	B	215	ARG
1	B	246	GLN

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Mol	Chain	Res	Type
1	B	254	LYS
1	B	265	ASP
1	B	267	THR
1	B	268	ASP
1	B	280	GLU
1	B	297	GLU
1	B	303	SER
1	B	307	THR
1	B	319	SER
1	B	321	LYS
1	B	325	ASP
1	B	331	ASN
1	B	342	ILE
1	B	346	LEU
1	B	361	VAL
1	B	381	LEU
1	B	390	TYR
1	B	398	LEU
1	B	399	ASP
1	B	401	ARG
1	C	50	ILE
1	C	53	LEU
1	C	54	THR
1	C	57	THR
1	C	91	LYS
1	C	99	PRO
1	C	106	LYS
1	C	132	SER
1	C	133	ARG
1	C	140	LEU
1	C	141	GLU
1	C	142	ARG
1	C	158	ASN
1	C	164	ARG
1	C	168	LYS
1	C	177	LEU
1	C	190	ARG
1	C	194	GLN
1	C	206	GLN
1	C	207	SER
1	C	214	GLU
1	C	215	ARG

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Mol	Chain	Res	Type
1	C	243	LYS
1	C	245	GLU
1	C	246	GLN
1	C	247	PHE
1	C	250	THR
1	C	254	LYS
1	C	273	ASP
1	C	297	GLU
1	C	311	SER
1	C	324	SER
1	C	331	ASN
1	C	364	SER
1	C	365	MET
1	C	371	ILE
1	C	389	ILE
1	C	390	TYR
1	C	391	ASN
1	C	392	VAL
1	C	398	LEU
1	D	21	LEU
1	D	39	LEU
1	D	50	ILE
1	D	53	LEU
1	D	74	ASN
1	D	117	ASN
1	D	132	SER
1	D	135	ARG
1	D	137	HIS
1	D	144	CYS
1	D	164	ARG
1	D	168	LYS
1	D	178	VAL
1	D	187	LYS
1	D	197	HIS
1	D	200	SER
1	D	212	LEU
1	D	215	ARG
1	D	245	GLU
1	D	246	GLN
1	D	252	THR
1	D	257	LEU
1	D	267	THR

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Mol	Chain	Res	Type
1	D	287	ILE
1	D	292	THR
1	D	293	ILE
1	D	298	SER
1	D	301	SER
1	D	320	THR
1	D	322	CYS
1	D	343	GLU
1	D	344	THR
1	D	351	ARG
1	D	361	VAL
1	D	381	LEU
1	D	389	ILE
1	D	398	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	68	ASN
1	A	112	ASN
1	A	143	HIS
1	A	193	GLN
1	A	194	GLN
1	A	206	GLN
1	A	251	GLN
1	A	294	GLN
1	A	333	GLN
1	A	385	ASN
1	A	386	GLN
1	A	393	GLN
1	B	96	ASN
1	B	112	ASN
1	B	158	ASN
1	B	206	GLN
1	B	251	GLN
1	B	393	GLN
1	C	74	ASN
1	C	143	HIS
1	C	193	GLN
1	C	206	GLN
1	C	251	GLN

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Mol	Chain	Res	Type
1	C	331	ASN
1	C	382	ASN
1	C	385	ASN
1	D	68	ASN
1	D	74	ASN
1	D	185	ASN
1	D	206	GLN
1	D	251	GLN
1	D	294	GLN
1	D	393	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	C	501	-	33,33,33	1.46	5 (15%)	48,50,50	1.64	10 (20%)
2	FMN	D	501	-	33,33,33	1.60	4 (12%)	48,50,50	1.24	6 (12%)
2	FMN	B	501	-	33,33,33	1.41	4 (12%)	48,50,50	1.46	7 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ORO	B	502	-	11,11,11	1.52	3 (27%)	14,15,15	2.86	5 (35%)
3	ORO	D	502	-	11,11,11	1.58	1 (9%)	14,15,15	2.48	7 (50%)
2	FMN	A	501	-	33,33,33	1.48	4 (12%)	48,50,50	1.39	10 (20%)
3	ORO	A	502	-	11,11,11	1.76	5 (45%)	14,15,15	2.74	6 (42%)
3	ORO	C	502	-	11,11,11	1.54	1 (9%)	14,15,15	2.61	6 (42%)

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	501	-	-	1/18/18/18	0/3/3/3
2	FMN	D	501	-	-	2/18/18/18	0/3/3/3
2	FMN	B	501	-	-	4/18/18/18	0/3/3/3
3	ORO	B	502	-	-	2/4/4/4	0/1/1/1
3	ORO	D	502	-	-	0/4/4/4	0/1/1/1
2	FMN	A	501	-	-	4/18/18/18	0/3/3/3
3	ORO	A	502	-	-	0/4/4/4	0/1/1/1
3	ORO	C	502	-	-	2/4/4/4	0/1/1/1

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FMN	C9A-C5A	5.60	1.50	1.41
2	D	501	FMN	C9A-C5A	5.51	1.50	1.41
2	C	501	FMN	C9A-C5A	4.33	1.48	1.41
2	B	501	FMN	C9A-C5A	4.26	1.48	1.41
2	D	501	FMN	C8-C7	3.71	1.49	1.40
2	B	501	FMN	C8-C7	3.28	1.48	1.40
2	C	501	FMN	C5A-N5	-3.03	1.33	1.39
2	D	501	FMN	C4-N3	-2.84	1.33	1.38
2	C	501	FMN	C4-N3	-2.60	1.34	1.38
2	C	501	FMN	C8-C7	2.60	1.47	1.40
3	A	502	ORO	C6-N1	-2.54	1.33	1.38
2	A	501	FMN	C8-C7	2.52	1.47	1.40
3	A	502	ORO	C2-N1	-2.49	1.33	1.37
2	D	501	FMN	C5A-N5	-2.48	1.34	1.39
3	A	502	ORO	C4-N3	-2.45	1.34	1.38
2	B	501	FMN	C4A-N5	2.43	1.36	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	ORO	C5-C4	-2.33	1.37	1.42
3	A	502	ORO	C2-N3	-2.28	1.33	1.37
3	D	502	ORO	C4-N3	-2.28	1.34	1.38
3	B	502	ORO	C2-N3	-2.21	1.33	1.37
2	A	501	FMN	C4A-N5	2.18	1.35	1.30
2	A	501	FMN	C4-N3	-2.15	1.34	1.38
3	B	502	ORO	C4-N3	-2.14	1.35	1.38
2	B	501	FMN	C5A-N5	-2.11	1.35	1.39
3	B	502	ORO	C6-N1	-2.10	1.34	1.38
2	C	501	FMN	C2-N3	-2.08	1.34	1.39
3	C	502	ORO	C2-N1	-2.07	1.34	1.37

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	ORO	C4-N3-C2	-6.00	119.74	125.55
3	A	502	ORO	O4-C4-C5	-5.44	117.95	125.46
3	B	502	ORO	O4-C4-C5	-5.28	118.17	125.46
3	A	502	ORO	C4-N3-C2	-5.27	120.44	125.55
3	C	502	ORO	C4-N3-C2	-5.20	120.51	125.55
3	C	502	ORO	O4-C4-C5	-4.67	119.01	125.46
3	B	502	ORO	C5-C4-N3	4.51	120.84	115.24
3	D	502	ORO	C4-N3-C2	-4.31	121.37	125.55
3	D	502	ORO	O4-C4-C5	-4.26	119.57	125.46
3	A	502	ORO	C5-C4-N3	4.05	120.27	115.24
2	B	501	FMN	C4-C4A-N5	3.99	123.72	118.21
2	B	501	FMN	O3P-P-O5'	-3.74	96.91	106.67
2	C	501	FMN	C5'-C4'-C3'	3.41	118.66	112.22
2	C	501	FMN	O4'-C4'-C5'	-3.32	102.67	109.99
3	C	502	ORO	N3-C2-N1	3.30	120.92	115.74
3	C	502	ORO	C5-C4-N3	3.27	119.31	115.24
3	D	502	ORO	N3-C2-N1	3.25	120.85	115.74
2	A	501	FMN	C4-C4A-N5	3.23	122.66	118.21
3	D	502	ORO	C7-C6-N1	3.19	121.30	115.47
2	C	501	FMN	C4A-C10-N1	-3.06	117.10	124.59
2	B	501	FMN	O2-C2-N1	-3.00	116.81	121.80
2	C	501	FMN	O3'-C3'-C4'	2.97	115.68	108.93
3	B	502	ORO	N3-C2-N1	2.95	120.37	115.74
2	A	501	FMN	O2P-P-O5'	-2.79	99.40	106.67
3	A	502	ORO	N3-C2-N1	2.79	120.12	115.74
2	C	501	FMN	O3'-C3'-C2'	-2.77	102.63	108.93
3	D	502	ORO	C5-C4-N3	2.73	118.63	115.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	FMN	C4-C4A-N5	2.72	121.97	118.21
3	B	502	ORO	C7-C6-N1	2.65	120.30	115.47
2	A	501	FMN	C10-N1-C2	2.61	122.49	116.85
2	A	501	FMN	C4A-C10-N1	-2.56	118.30	124.59
2	D	501	FMN	C4A-C10-N10	2.48	120.03	116.48
3	C	502	ORO	O72-C7-C6	2.47	119.60	114.27
3	D	502	ORO	O72-C7-C6	2.43	119.50	114.27
2	C	501	FMN	C10-N1-C2	2.43	122.11	116.85
2	A	501	FMN	C4A-C4-N3	2.37	119.28	113.25
2	A	501	FMN	O4'-C4'-C5'	-2.35	104.80	109.99
2	B	501	FMN	C10-C4A-N5	-2.33	120.05	124.81
2	C	501	FMN	C4-N3-C2	-2.31	121.54	125.64
2	C	501	FMN	C4A-C10-N10	2.28	119.75	116.48
2	D	501	FMN	O4-C4-C4A	-2.26	120.57	126.53
3	A	502	ORO	O71-C7-C6	-2.25	116.45	121.01
2	B	501	FMN	C4A-C10-N1	-2.25	119.09	124.59
2	B	501	FMN	C5A-N5-C4A	2.23	121.70	118.09
2	C	501	FMN	C4-C4A-N5	2.22	121.28	118.21
2	D	501	FMN	C4A-C10-N1	-2.20	119.19	124.59
2	D	501	FMN	O2-C2-N1	-2.20	118.14	121.80
2	A	501	FMN	C5A-N5-C4A	2.18	121.61	118.09
2	A	501	FMN	O4-C4-C4A	-2.14	120.88	126.53
3	D	502	ORO	C6-N1-C2	-2.14	120.36	122.65
2	B	501	FMN	C10-N1-C2	2.13	121.46	116.85
2	A	501	FMN	O2'-C2'-C3'	2.11	114.18	109.25
3	A	502	ORO	O72-C7-C6	2.09	118.77	114.27
3	C	502	ORO	O2-C2-N1	-2.07	118.18	121.86
2	A	501	FMN	C9A-C5A-N5	-2.04	120.29	122.45
2	C	501	FMN	O4-C4-C4A	-2.01	121.22	126.53
2	D	501	FMN	C4A-C4-N3	2.01	118.37	113.25

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	FMN	C5'-O5'-P-O2P
2	A	501	FMN	C5'-O5'-P-O3P
2	B	501	FMN	C5'-O5'-P-O2P
2	B	501	FMN	C5'-O5'-P-O3P
3	C	502	ORO	N1-C6-C7-O71
3	C	502	ORO	N1-C6-C7-O72
2	B	501	FMN	C4'-C5'-O5'-P

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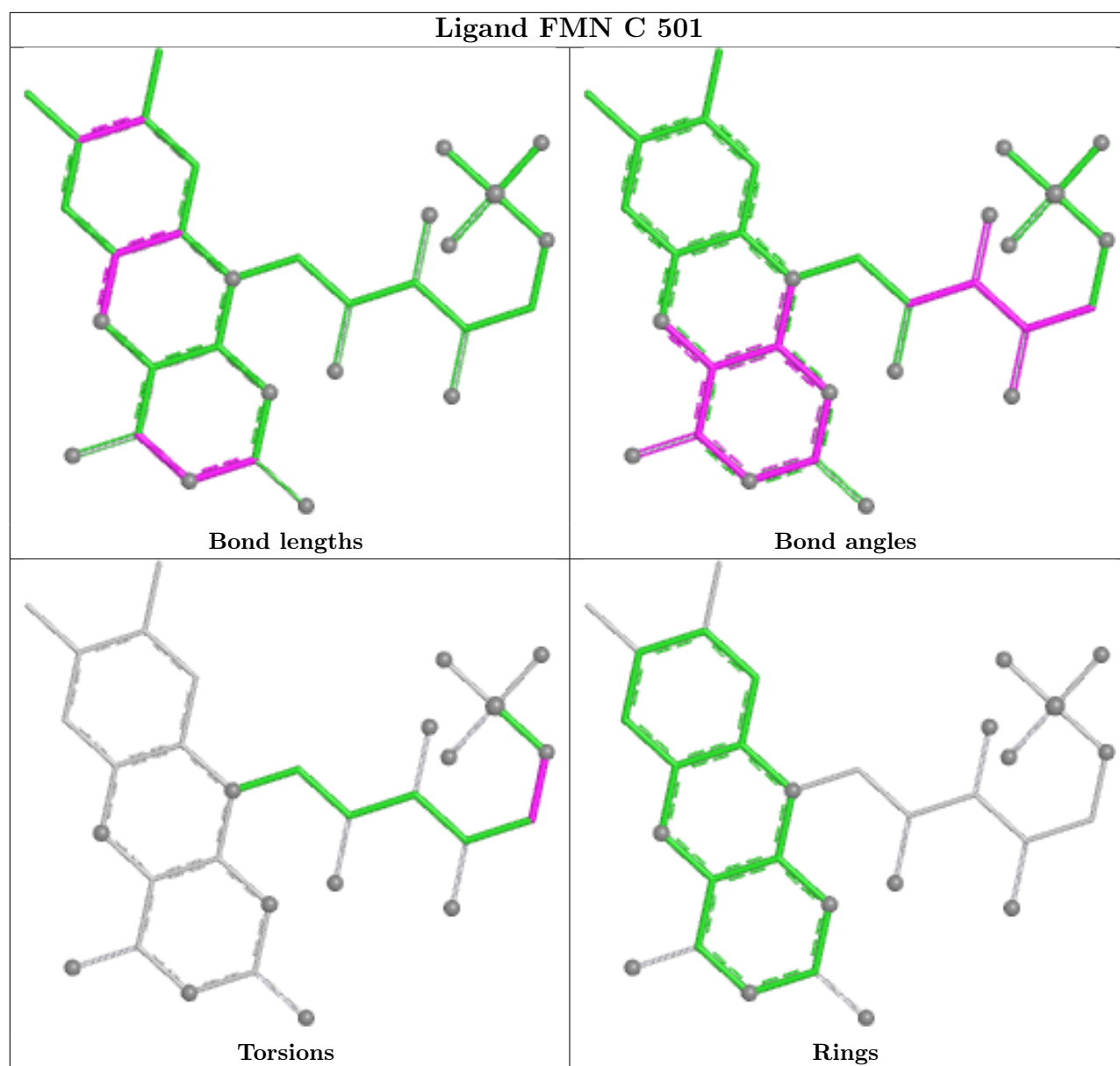
Mol	Chain	Res	Type	Atoms
2	A	501	FMN	C5'-O5'-P-O1P
2	B	501	FMN	C5'-O5'-P-O1P
2	A	501	FMN	C4'-C5'-O5'-P
2	C	501	FMN	C4'-C5'-O5'-P
3	B	502	ORO	N1-C6-C7-O72
2	D	501	FMN	C4'-C5'-O5'-P
3	B	502	ORO	N1-C6-C7-O71
2	D	501	FMN	C5'-O5'-P-O2P

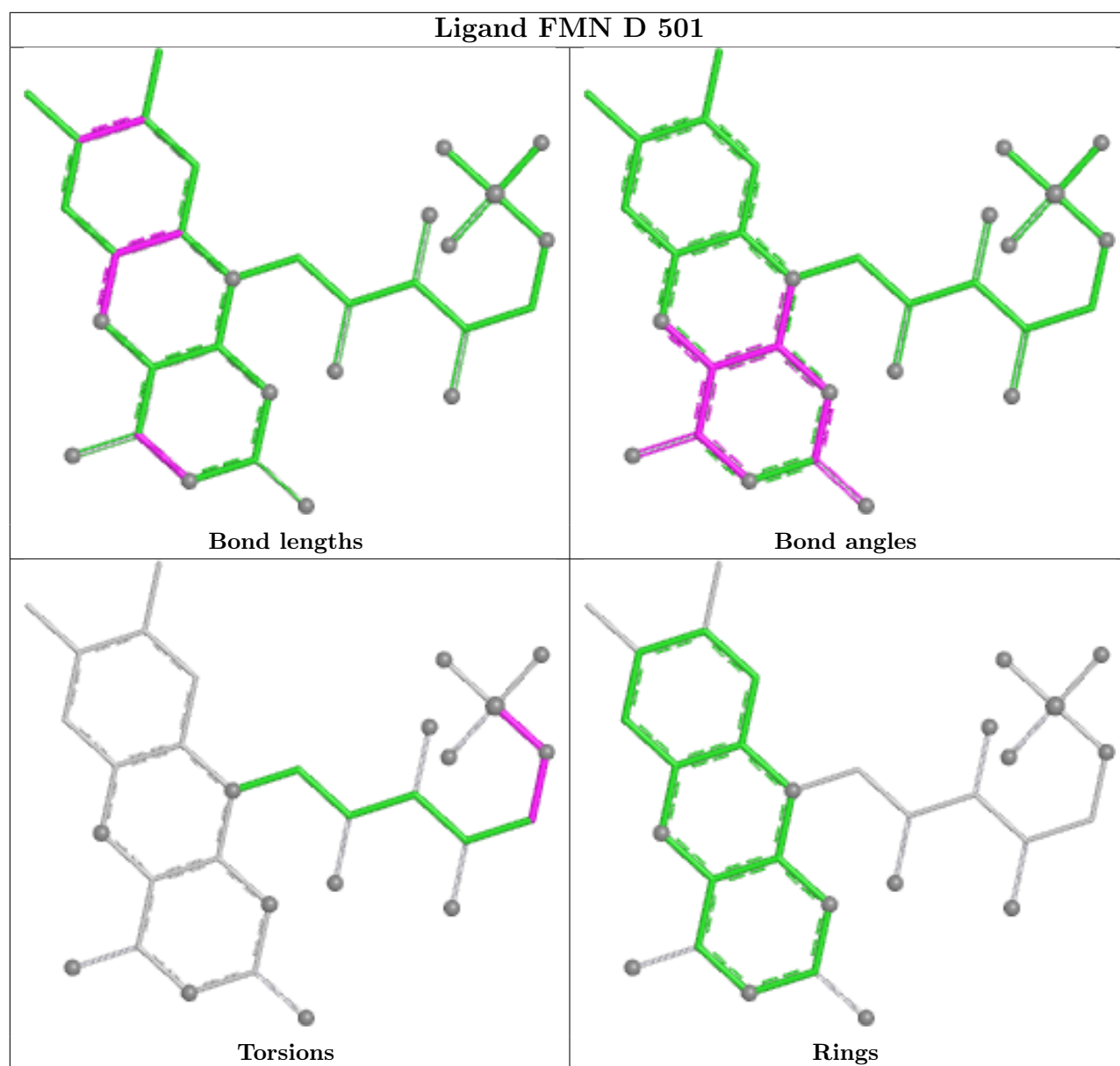
There are no ring outliers.

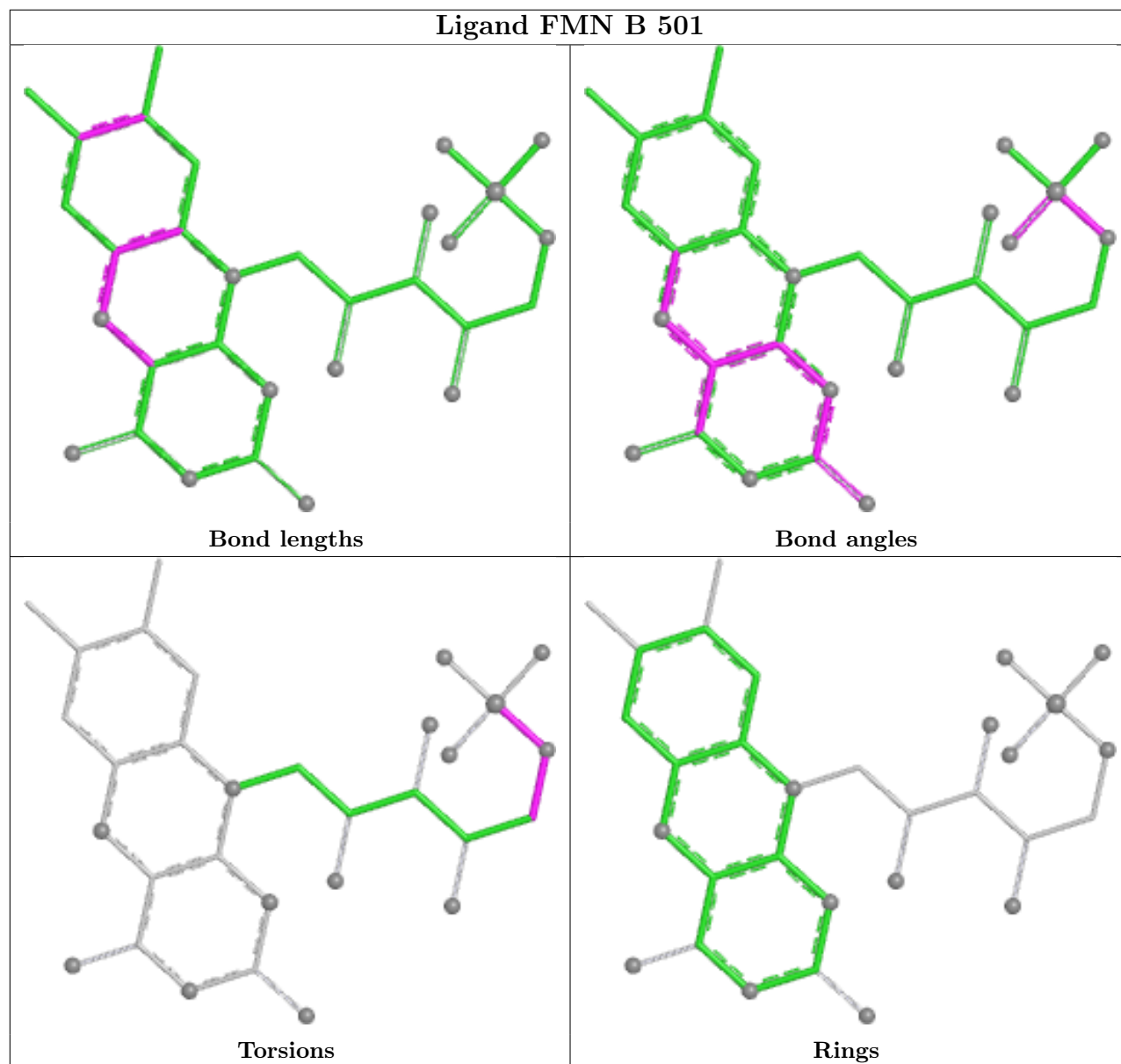
4 monomers are involved in 4 short contacts:

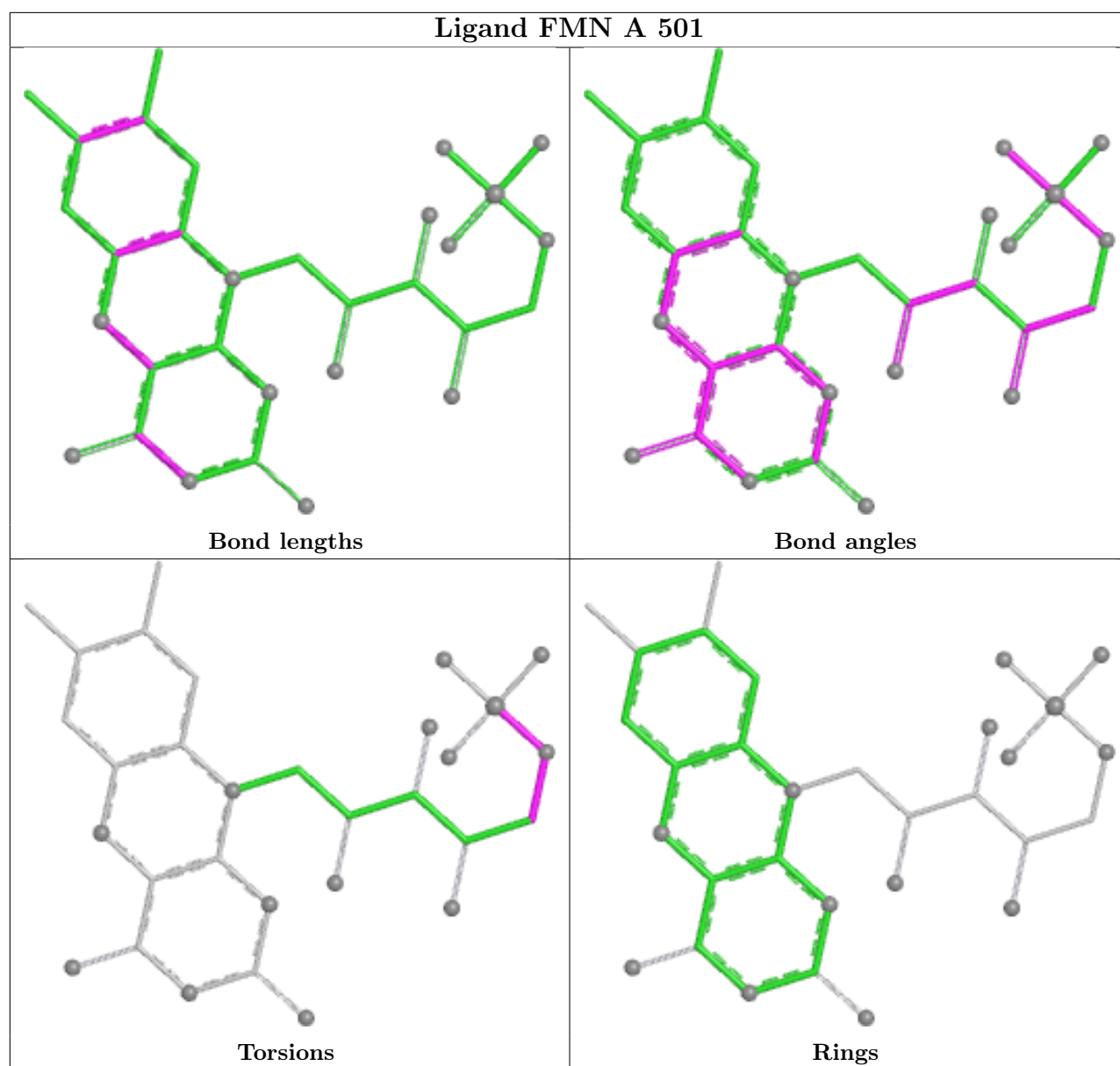
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	FMN	1	0
2	B	501	FMN	1	0
2	A	501	FMN	1	0
3	A	502	ORO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	359/436 (82%)	-1.30	0 100 100	24, 41, 71, 88	0
1	B	362/436 (83%)	-1.28	0 100 100	28, 46, 72, 98	0
1	C	362/436 (83%)	-1.28	0 100 100	28, 44, 72, 102	0
1	D	362/436 (83%)	-1.29	0 100 100	27, 44, 78, 114	0
All	All	1445/1744 (82%)	-1.29	0 100 100	24, 44, 74, 114	0

There are no RSRZ outliers to report.

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.

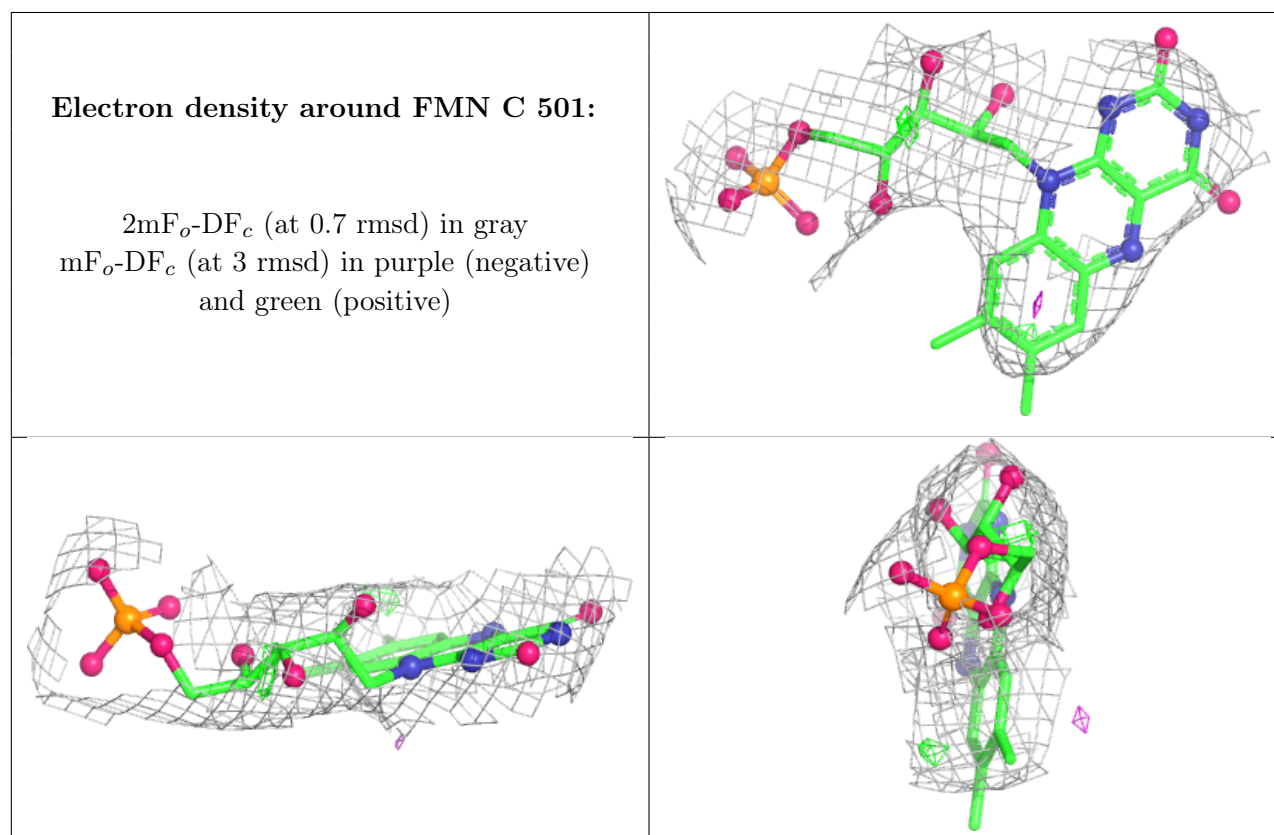
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ORO	B	502	11/11	0.96	0.06	42,43,44,44	0
3	ORO	C	502	11/11	0.97	0.06	47,48,49,49	0
3	ORO	A	502	11/11	0.99	0.04	31,31,32,32	0
2	FMN	C	501	31/31	0.99	0.04	27,29,31,32	0

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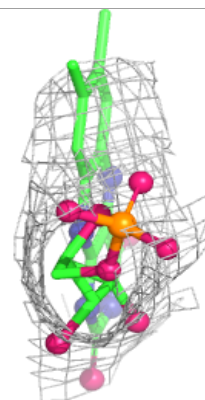
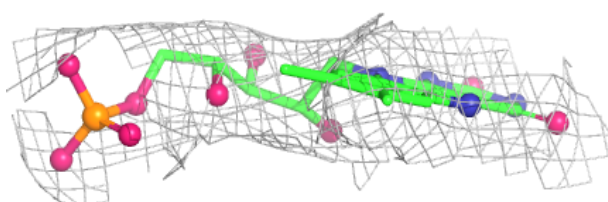
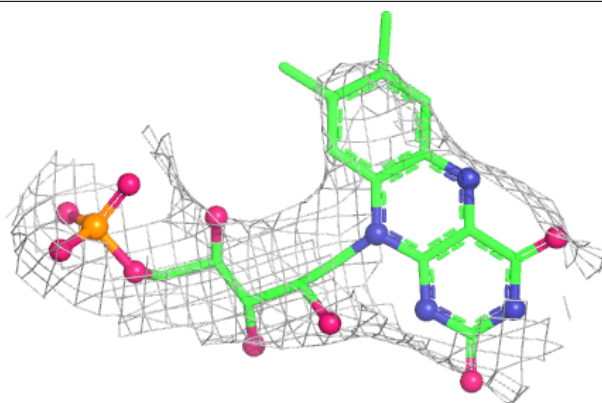
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FMN	D	501	31/31	0.99	0.04	34,35,40,41	0
3	ORO	D	502	11/11	0.99	0.04	40,40,40,40	0
2	FMN	A	501	31/31	1.00	0.03	28,29,31,32	0
2	FMN	B	501	31/31	1.00	0.03	29,30,31,32	0

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.

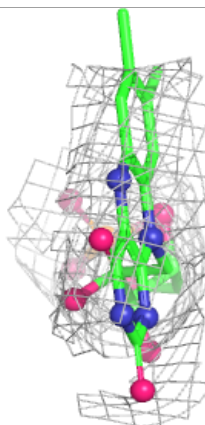
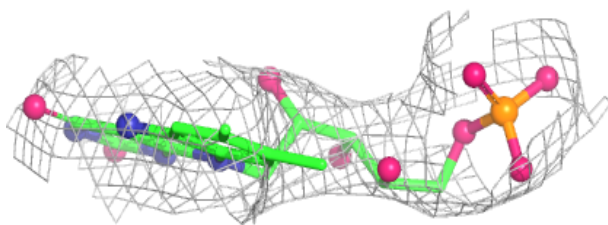
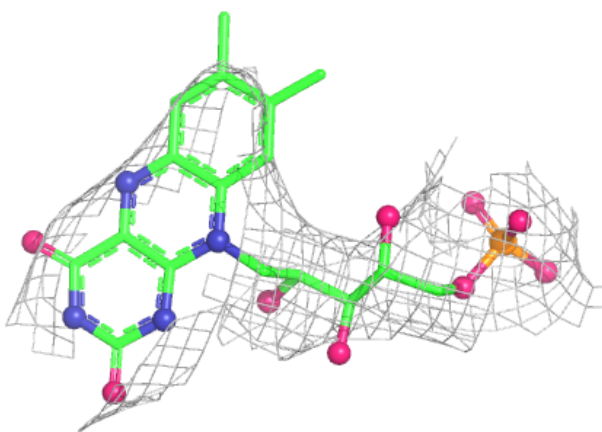


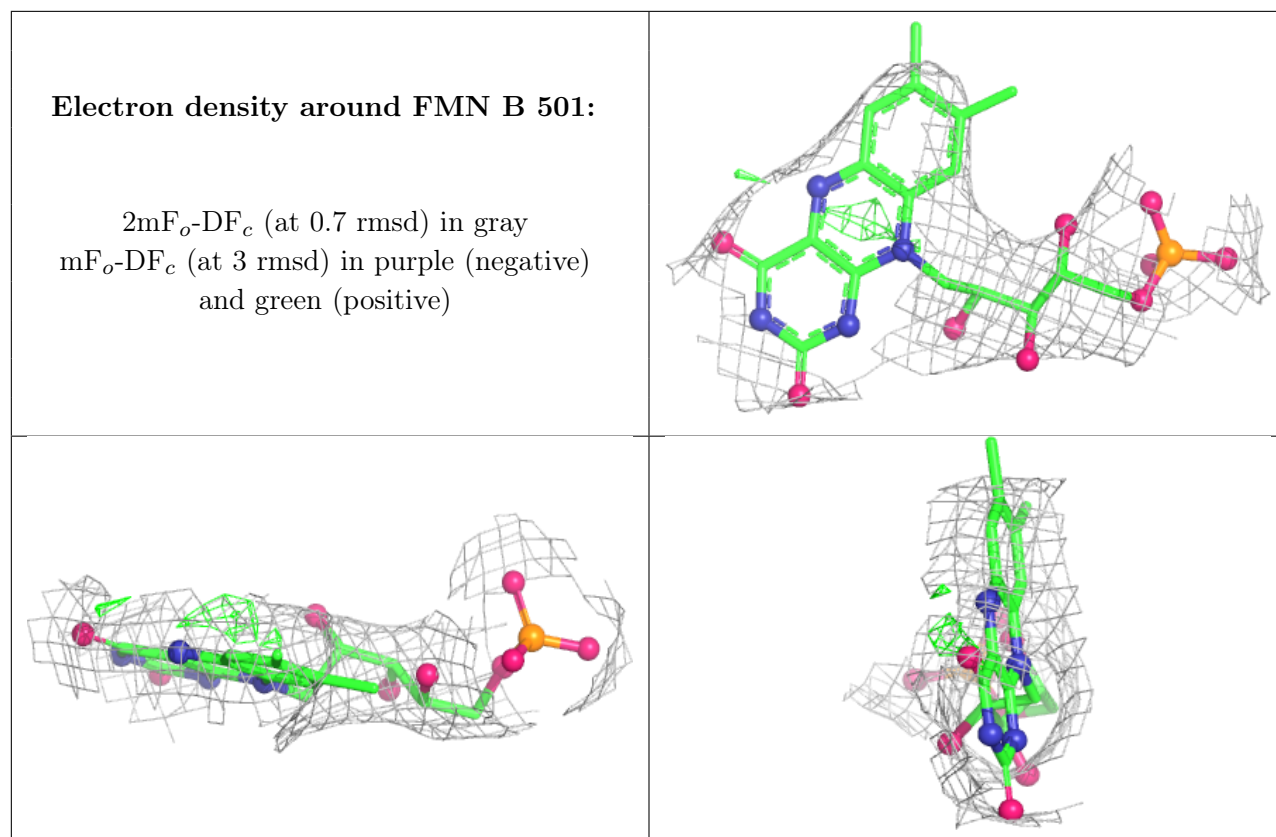
Electron density around FMN D 501:

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

**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)





6.5 Other polymers [i](#)

There are no such residues in this entry.