



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:50 AM UTC

PDB ID : 4YUT / pdb_00004yut
Title : Crystal structure of photoactivated adenylyl cyclase of a cyanobacteria *Oscillatoria acuminata* in orthorhombic form
Authors : Park, S.-Y.; Ohki, M.; Sugiyama, K.; Kawai, F.; Iseki, M.
Deposited on : 2015-03-19
Resolution : 2.90 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

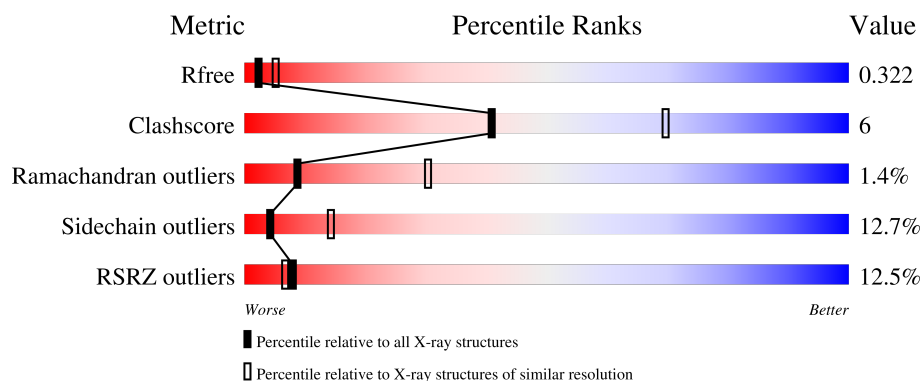
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	382	12% 66% 21% • 8%
1	B	382	12% 66% 22% •• 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5598 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 Family 3 adenylate cyclase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2768	1754	467	536	11			
1	B	351	Total	C	N	O	S	0	0	0
			2768	1754	467	536	11			

There are 32 discrepancies between the modelled and reference sequences:

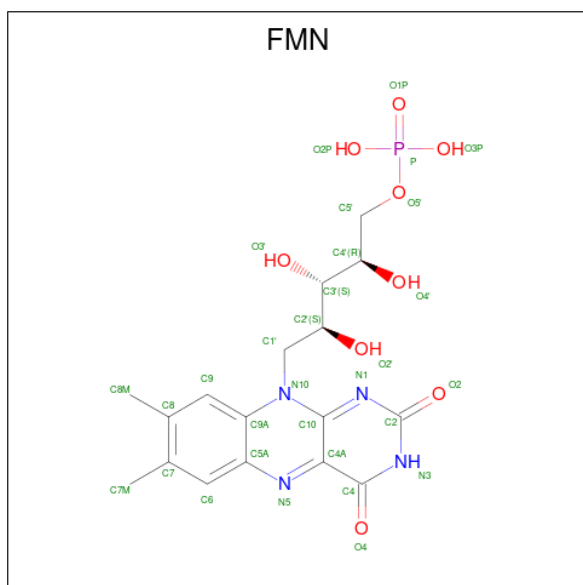
Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	expression tag	UNP K9TLZ5
A	-14	ASN	-	expression tag	UNP K9TLZ5
A	-13	HIS	-	expression tag	UNP K9TLZ5
A	-12	LYS	-	expression tag	UNP K9TLZ5
A	-11	VAL	-	expression tag	UNP K9TLZ5
A	-10	HIS	-	expression tag	UNP K9TLZ5
A	-9	HIS	-	expression tag	UNP K9TLZ5
A	-8	HIS	-	expression tag	UNP K9TLZ5
A	-7	HIS	-	expression tag	UNP K9TLZ5
A	-6	HIS	-	expression tag	UNP K9TLZ5
A	-5	HIS	-	expression tag	UNP K9TLZ5
A	-4	ILE	-	expression tag	UNP K9TLZ5
A	-3	GLU	-	expression tag	UNP K9TLZ5
A	-2	GLY	-	expression tag	UNP K9TLZ5
A	-1	ARG	-	expression tag	UNP K9TLZ5
A	0	HIS	-	expression tag	UNP K9TLZ5
B	-15	MET	-	expression tag	UNP K9TLZ5
B	-14	ASN	-	expression tag	UNP K9TLZ5
B	-13	HIS	-	expression tag	UNP K9TLZ5
B	-12	LYS	-	expression tag	UNP K9TLZ5
B	-11	VAL	-	expression tag	UNP K9TLZ5
B	-10	HIS	-	expression tag	UNP K9TLZ5
B	-9	HIS	-	expression tag	UNP K9TLZ5
B	-8	HIS	-	expression tag	UNP K9TLZ5
B	-7	HIS	-	expression tag	UNP K9TLZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	expression tag	UNP K9TLZ5
B	-5	HIS	-	expression tag	UNP K9TLZ5
B	-4	ILE	-	expression tag	UNP K9TLZ5
B	-3	GLU	-	expression tag	UNP K9TLZ5
B	-2	GLY	-	expression tag	UNP K9TLZ5
B	-1	ARG	-	expression tag	UNP K9TLZ5
B	0	HIS	-	expression tag	UNP K9TLZ5

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

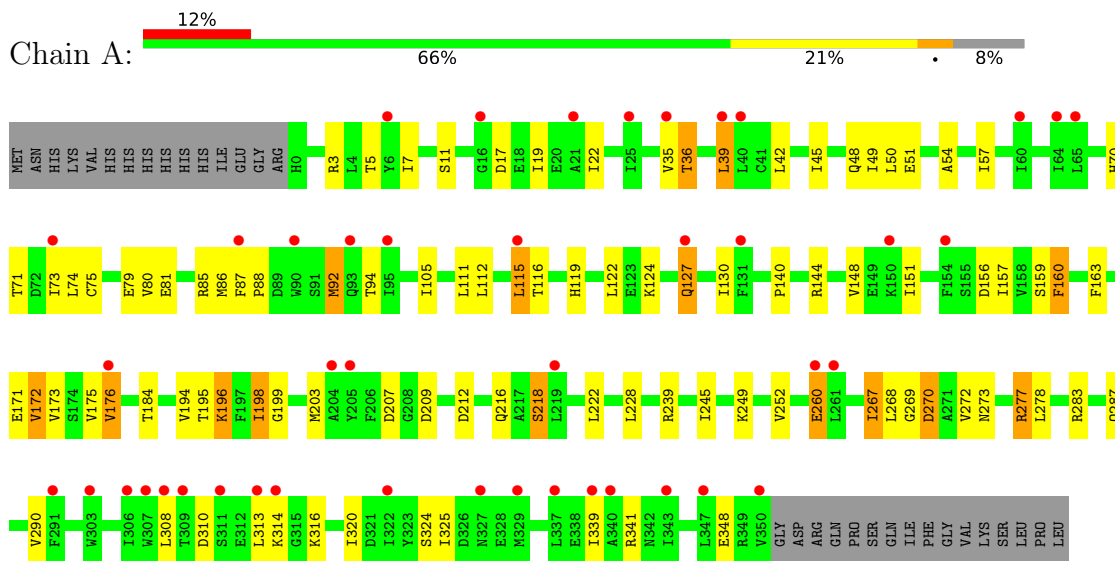


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

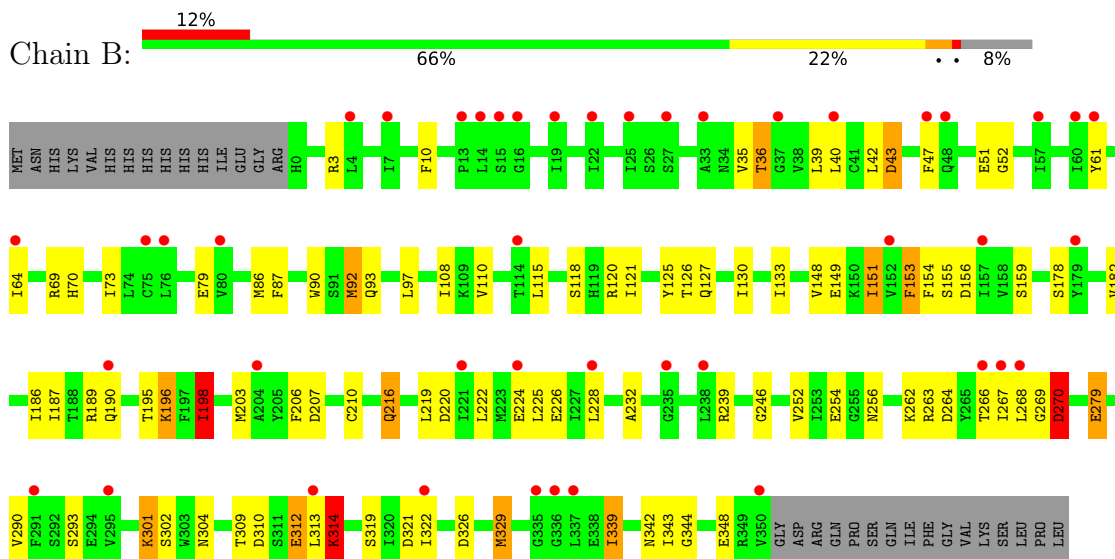
3 Residue-property plots [i](#)

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

- Molecule 1: Family 3 adenylate cyclase



- Molecule 1: Family 3 adenylate cyclase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.35Å 100.70Å 120.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.79 – 2.90 43.79 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.2 (43.79-2.90) 96.2 (43.79-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.90Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.271 , 0.310 0.286 , 0.322	Depositor DCC
R_{free} test set	1205 reflections (5.29%)	wwPDB-VP
Wilson B-factor (Å ²)	70.8	Xtriage
Anisotropy	0.461	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 83.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5598	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% 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

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	0.80	0/2810	1.43	15/3794 (0.4%)
1	B	0.81	0/2810	1.39	8/3794 (0.2%)
All	All	0.80	0/5620	1.41	23/7588 (0.3%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	ASP	CA-CB-CG	6.92	119.52	112.60
1	B	339	ILE	N-CA-C	-6.08	106.81	112.83
1	A	172	VAL	CA-C-N	5.87	128.18	120.60
1	A	172	VAL	C-N-CA	5.87	128.18	120.60
1	A	157	ILE	CA-C-N	5.63	129.62	121.18
1	A	157	ILE	C-N-CA	5.63	129.62	121.18
1	A	269	GLY	CA-C-N	5.55	128.51	120.79
1	A	269	GLY	C-N-CA	5.55	128.51	120.79
1	B	310	ASP	CA-CB-CG	5.41	118.01	112.60
1	A	160	PHE	CA-C-N	5.33	127.69	120.38
1	A	160	PHE	C-N-CA	5.33	127.69	120.38
1	A	260	GLU	N-CA-C	-5.33	106.95	113.50
1	A	222	LEU	CA-C-N	5.29	127.63	120.38
1	A	222	LEU	C-N-CA	5.29	127.63	120.38
1	A	348	GLU	CA-C-N	5.29	128.10	120.38
1	A	348	GLU	C-N-CA	5.29	128.10	120.38
1	A	310	ASP	CA-CB-CG	5.19	117.79	112.60
1	B	344	GLY	CA-C-N	5.07	127.07	120.28
1	B	344	GLY	C-N-CA	5.07	127.07	120.28
1	B	10	PHE	CA-CB-CG	5.05	118.85	113.80
1	B	159	SER	CA-C-N	5.04	127.54	120.28
1	B	159	SER	C-N-CA	5.04	127.54	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	270	ASP	CA-CB-CG	5.01	117.61	112.60

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	2768	0	2803	36	0
1	B	2768	0	2803	42	0
2	A	31	0	19	0	0
2	B	31	0	19	0	0
All	All	5598	0	5644	73	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 6.

All (73) 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:36:THR:HG21	1:B:87:PHE:O	1.82	0.79
1:B:127:GLN:O	1:B:130:ILE:HG13	1.85	0.75
1:A:36:THR:OG1	1:A:85:ARG:NH1	2.24	0.71
1:B:312:GLU:HB3	1:B:319:SER:HA	1.73	0.70
1:A:218:SER:HB3	1:A:245:ILE:HG21	1.76	0.66
1:A:36:THR:HG21	1:A:87:PHE:O	1.96	0.64
1:A:198:ILE:HG12	1:B:198:ILE:HG12	1.79	0.63
1:B:293:SER:HB3	1:B:321:ASP:HB2	1.81	0.63
1:A:7:ILE:HD13	1:A:116:THR:HG22	1.80	0.62
1:A:39:LEU:HB3	1:A:94:THR:HG22	1.82	0.61
1:A:196:LYS:HB2	1:A:203:MET:HE2	1.84	0.59
1:B:196:LYS:HE3	1:B:266:THR:HG21	1.83	0.59
1:A:3:ARG:HB2	1:A:79:GLU:HB2	1.84	0.58
1:B:36:THR:CG2	1:B:90:TRP:O	2.52	0.56
1:A:19:ILE:HA	1:A:22:ILE:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:THR:HG22	1:A:194:VAL:HG21	1.86	0.55
1:B:118:SER:HA	1:B:121:ILE:HD12	1.90	0.54
1:B:264:ASP:HB3	1:B:266:THR:HG23	1.89	0.54
1:B:187:ILE:HG12	1:B:206:PHE:HZ	1.74	0.53
1:B:36:THR:HG23	1:B:90:TRP:O	2.08	0.53
1:B:246:GLY:HA2	1:B:290:VAL:O	2.08	0.52
1:A:273:ASN:O	1:A:277:ARG:HG2	2.10	0.52
1:A:159:SER:H	1:A:283:ARG:HH22	1.57	0.51
1:B:40:LEU:HB2	1:B:47:PHE:HB2	1.92	0.51
1:B:270:ASP:HB2	1:B:314:LYS:HE2	1.92	0.51
1:A:48:GLN:HE21	1:A:92:MET:HE2	1.76	0.50
1:A:48:GLN:NE2	1:A:92:MET:HE2	2.27	0.50
1:B:3:ARG:HG2	1:B:51:GLU:HG2	1.93	0.50
1:A:127:GLN:O	1:A:130:ILE:HG13	2.12	0.50
1:B:219:LEU:HA	1:B:222:LEU:HD12	1.94	0.49
1:A:267:ILE:HD12	1:A:272:VAL:HG22	1.94	0.49
1:B:252:VAL:HG12	1:B:269:GLY:HA3	1.95	0.49
1:B:3:ARG:HB2	1:B:79:GLU:HB2	1.95	0.49
1:B:178:SER:O	1:B:182:VAL:HG23	2.13	0.49
1:A:85:ARG:HG3	1:A:88:PRO:HG3	1.94	0.48
1:A:287:GLN:HG3	1:A:308:LEU:HD21	1.94	0.48
1:B:154:PHE:O	1:B:279:GLU:HG3	2.14	0.48
1:A:36:THR:OG1	1:A:85:ARG:CZ	2.61	0.48
1:B:151:ILE:HD12	1:B:207:ASP:O	2.15	0.47
1:B:130:ILE:HA	1:B:133:ILE:HD12	1.95	0.47
1:B:339:ILE:HG23	1:B:342:ASN:HB2	1.97	0.47
1:B:40:LEU:HD23	1:B:97:LEU:HD11	1.97	0.47
1:B:61:TYR:HA	1:B:64:ILE:HD12	1.97	0.46
1:A:140:PRO:HB2	1:B:125:TYR:OH	2.16	0.46
1:A:112:LEU:HD11	1:B:108:ILE:HG23	1.99	0.45
1:B:70:HIS:HB3	1:B:73:ILE:HD11	1.99	0.45
1:B:3:ARG:HD3	1:B:86:MET:HE2	2.00	0.44
1:A:3:ARG:HD3	1:A:86:MET:HE2	1.98	0.44
1:A:122:LEU:HD22	1:B:126:THR:HG21	1.99	0.43
1:B:254:GLU:HB2	1:B:267:ILE:HG22	1.99	0.43
1:B:35:VAL:HG12	1:B:52:GLY:HA3	2.00	0.43
1:B:304:ASN:ND2	1:B:326:ASP:HB3	2.33	0.43
1:A:160:PHE:HA	1:A:163:PHE:HD2	1.84	0.43
1:B:290:VAL:HG13	1:B:322:ILE:HG23	2.00	0.43
1:B:301:LYS:HD2	1:B:302:SER:N	2.34	0.43
1:A:172:VAL:O	1:A:176:VAL:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:ASN:HB3	1:B:263:ARG:HD3	2.01	0.42
1:A:73:ILE:HD12	1:A:73:ILE:H	1.83	0.42
1:B:190:GLN:NE2	1:B:216:GLN:HB3	2.35	0.42
1:A:70:HIS:HB3	1:A:73:ILE:HD11	2.02	0.42
1:A:49:ILE:HG21	1:A:86:MET:HE3	2.01	0.42
1:A:39:LEU:HD23	1:A:48:GLN:HB2	2.01	0.42
1:A:115:LEU:O	1:A:119:HIS:HB2	2.20	0.41
1:A:308:LEU:HD11	1:A:324:SER:HB2	2.02	0.41
1:A:171:GLU:O	1:A:175:VAL:HG23	2.20	0.41
1:B:232:ALA:HB3	1:B:239:ARG:HG2	2.01	0.41
1:A:50:LEU:HB3	1:A:57:ILE:HD12	2.03	0.41
1:B:153:PHE:CE2	1:B:155:SER:HB3	2.55	0.41
1:A:278:LEU:HB3	1:A:290:VAL:HG12	2.03	0.41
1:A:151:ILE:HG13	1:A:249:LYS:HB2	2.03	0.41
1:B:226:GLU:HB2	1:B:329:MET:HE1	2.02	0.41
1:A:124:LYS:O	1:B:262:LYS:HA	2.21	0.40
1:B:186:ILE:HG21	1:B:220:ASP:HB2	2.03	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	349/382 (91%)	325 (93%)	20 (6%)	4 (1%)	11	36
1	B	349/382 (91%)	321 (92%)	22 (6%)	6 (2%)	7	26
All	All	698/764 (91%)	646 (93%)	42 (6%)	10 (1%)	9	30

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	43	ASP

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Mol	Chain	Res	Type
1	B	210	CYS
1	B	314	LYS
1	A	54	ALA
1	A	314	LYS
1	B	92	MET
1	B	309	THR
1	A	80	VAL
1	B	198	ILE
1	A	199	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	310/338 (92%)	265 (86%)	45 (14%)	3	10
1	B	310/338 (92%)	276 (89%)	34 (11%)	6	20
All	All	620/676 (92%)	541 (87%)	79 (13%)	4	14

All (79) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	11	SER
1	A	17	ASP
1	A	35	VAL
1	A	36	THR
1	A	39	LEU
1	A	42	LEU
1	A	45	ILE
1	A	51	GLU
1	A	71	THR
1	A	74	LEU
1	A	75	CYS
1	A	81	GLU
1	A	92	MET

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Mol	Chain	Res	Type
1	A	105	ILE
1	A	111	LEU
1	A	115	LEU
1	A	127	GLN
1	A	144	ARG
1	A	148	VAL
1	A	156	ASP
1	A	173	VAL
1	A	176	VAL
1	A	195	THR
1	A	196	LYS
1	A	198	ILE
1	A	207	ASP
1	A	209	ASP
1	A	212	ASP
1	A	216	GLN
1	A	218	SER
1	A	228	LEU
1	A	239	ARG
1	A	252	VAL
1	A	260	GLU
1	A	267	ILE
1	A	268	LEU
1	A	270	ASP
1	A	277	ARG
1	A	313	LEU
1	A	316	LYS
1	A	320	ILE
1	A	325	ILE
1	A	339	ILE
1	A	341	ARG
1	B	36	THR
1	B	39	LEU
1	B	42	LEU
1	B	43	ASP
1	B	69	ARG
1	B	92	MET
1	B	93	GLN
1	B	110	VAL
1	B	115	LEU
1	B	120	ARG
1	B	148	VAL

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Mol	Chain	Res	Type
1	B	149	GLU
1	B	151	ILE
1	B	153	PHE
1	B	156	ASP
1	B	189	ARG
1	B	195	THR
1	B	196	LYS
1	B	198	ILE
1	B	203	MET
1	B	216	GLN
1	B	224	GLU
1	B	225	LEU
1	B	228	LEU
1	B	268	LEU
1	B	270	ASP
1	B	279	GLU
1	B	301	LYS
1	B	312	GLU
1	B	313	LEU
1	B	314	LYS
1	B	329	MET
1	B	343	ILE
1	B	348	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	GLN
1	A	127	GLN
1	A	190	GLN
1	A	213	GLN
1	A	230	ASN
1	A	256	ASN
1	A	273	ASN
1	B	93	GLN
1	B	190	GLN
1	B	213	GLN
1	B	216	GLN
1	B	256	ASN
1	B	304	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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	A	401	-	33,33,33	0.27	0	48,50,50	0.47	0
2	FMN	B	401	-	33,33,33	0.33	0	48,50,50	0.80	1 (2%)

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	A	401	-	-	3/18/18/18	0/3/3/3
2	FMN	B	401	-	-	8/18/18/18	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	FMN	C4'-C3'-C2'	3.85	119.98	113.57

There are no chirality outliers.

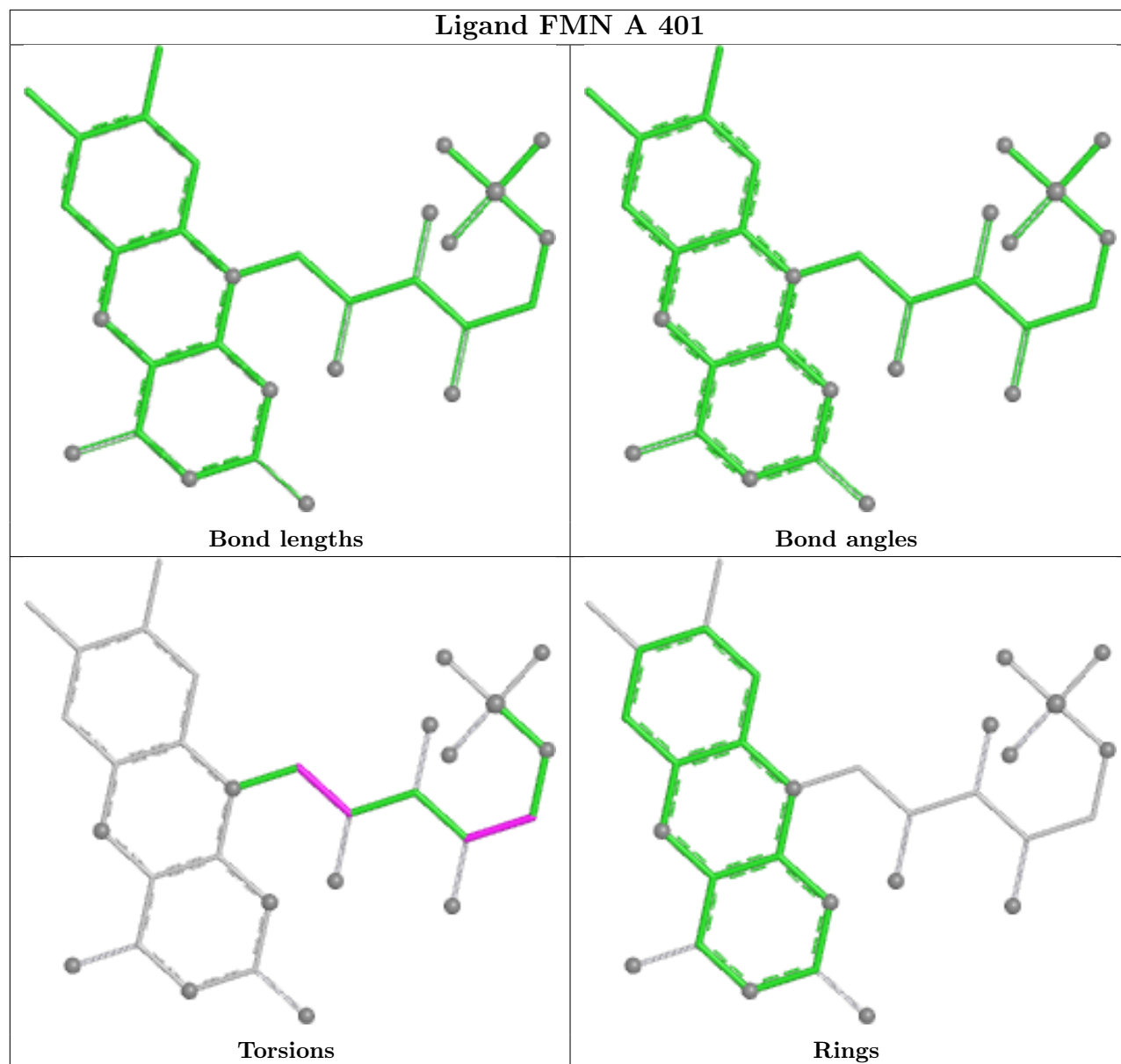
All (11) torsion outliers are listed below:

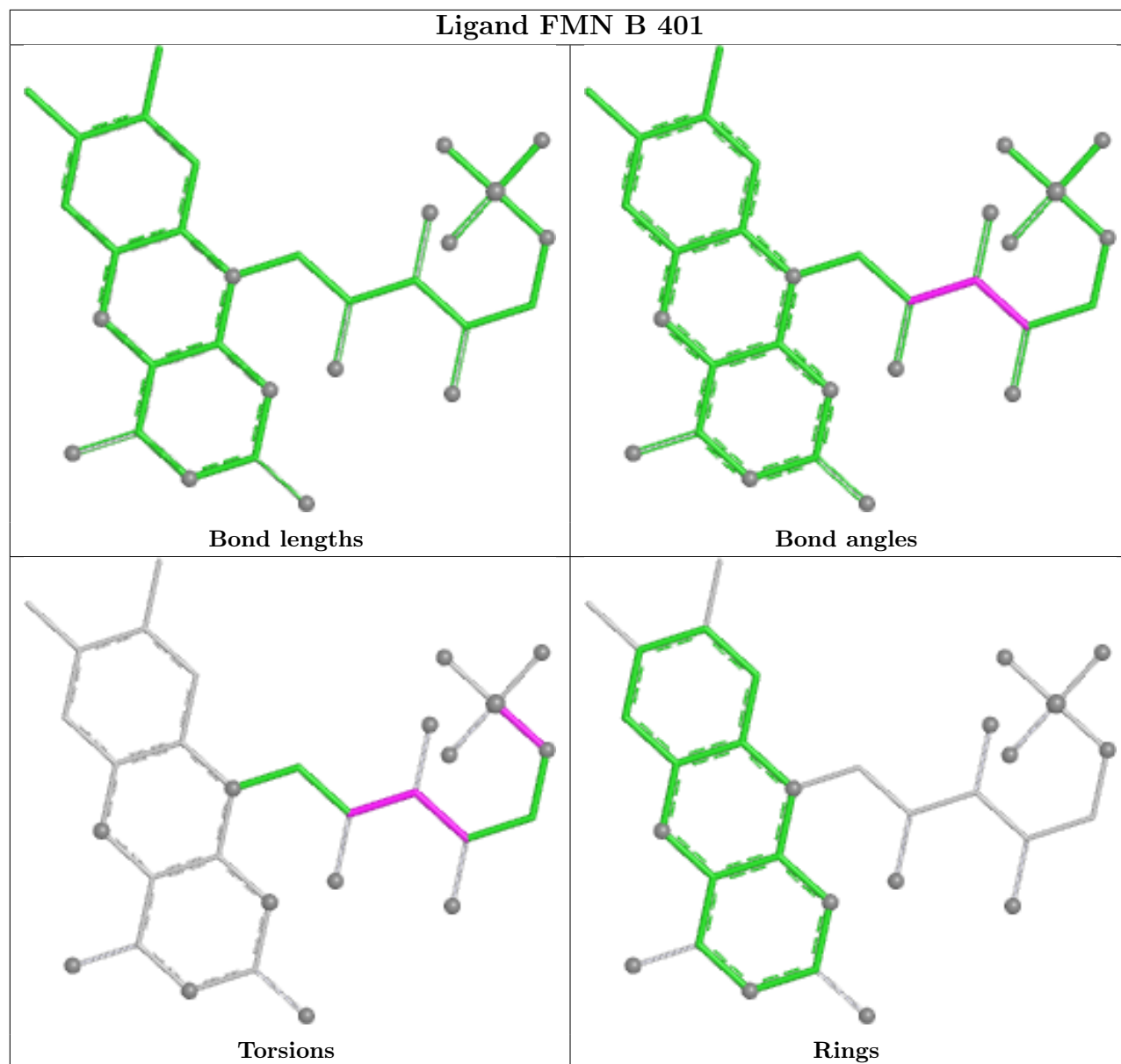
Mol	Chain	Res	Type	Atoms
2	A	401	FMN	C3'-C4'-C5'-O5'
2	A	401	FMN	O4'-C4'-C5'-O5'
2	B	401	FMN	C1'-C2'-C3'-O3'
2	B	401	FMN	C1'-C2'-C3'-C4'
2	B	401	FMN	O2'-C2'-C3'-C4'
2	B	401	FMN	O2'-C2'-C3'-O3'
2	B	401	FMN	O3'-C3'-C4'-C5'
2	B	401	FMN	C2'-C3'-C4'-C5'
2	B	401	FMN	C5'-O5'-P-O1P
2	B	401	FMN	O3'-C3'-C4'-O4'
2	A	401	FMN	N10-C1'-C2'-O2'

There are no ring outliers.

No monomer is involved in short contacts.

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	351/382 (91%)	1.03	44 (12%) 8 7	27, 89, 134, 160	0
1	B	351/382 (91%)	1.00	44 (12%) 8 7	46, 97, 155, 171	0
All	All	702/764 (91%)	1.02	88 (12%) 8 7	27, 94, 147, 171	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	22	ILE	5.8
1	B	337	LEU	5.1
1	B	15	SER	4.9
1	A	90	TRP	4.6
1	A	307	TRP	4.4
1	A	329	MET	4.1
1	A	350	VAL	3.9
1	B	336	GLY	3.7
1	A	25	ILE	3.4
1	B	60	ILE	3.4
1	A	343	ILE	3.4
1	A	337	LEU	3.3
1	B	13	PRO	3.3
1	A	339	ILE	3.3
1	A	65	LEU	3.3
1	A	327	ASN	3.2
1	A	205	TYR	3.2
1	B	19	ILE	3.2
1	A	308	LEU	3.2
1	B	33	ALA	3.1
1	B	14	LEU	3.0
1	B	238	LEU	3.0
1	A	219	LEU	2.9
1	A	260	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	303	TRP	2.8
1	B	40	LEU	2.8
1	B	16	GLY	2.8
1	A	347	LEU	2.8
1	B	37	GLY	2.8
1	B	224	GLU	2.7
1	A	322	ILE	2.7
1	B	204	ALA	2.7
1	A	314	LYS	2.7
1	B	335	GLY	2.7
1	A	204	ALA	2.7
1	B	48	GLN	2.7
1	B	76	LEU	2.7
1	B	313	LEU	2.7
1	B	268	LEU	2.6
1	B	267	ILE	2.6
1	A	64	ILE	2.6
1	B	64	ILE	2.6
1	A	291	PHE	2.6
1	A	115	LEU	2.5
1	B	7	ILE	2.5
1	B	27	SER	2.5
1	B	57	ILE	2.5
1	A	73	ILE	2.5
1	B	295	VAL	2.5
1	A	309	THR	2.5
1	B	114	THR	2.5
1	B	75	CYS	2.4
1	B	221	ILE	2.4
1	B	190	GLN	2.4
1	B	4	LEU	2.4
1	A	131	PHE	2.4
1	A	127	GLN	2.4
1	A	21	ALA	2.4
1	A	261	LEU	2.4
1	A	16	GLY	2.3
1	A	39	LEU	2.3
1	A	40	LEU	2.3
1	B	228	LEU	2.3
1	B	80	VAL	2.3
1	A	95	ILE	2.2
1	A	6	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	47	PHE	2.2
1	A	93	GLN	2.2
1	B	291	PHE	2.2
1	A	313	LEU	2.2
1	B	322	ILE	2.2
1	A	176	VAL	2.2
1	B	350	VAL	2.2
1	A	60	ILE	2.1
1	B	266	THR	2.1
1	A	306	ILE	2.1
1	B	25	ILE	2.1
1	A	35	VAL	2.1
1	A	87	PHE	2.1
1	A	340	ALA	2.1
1	B	152	VAL	2.1
1	B	157	ILE	2.1
1	A	311	SER	2.0
1	B	235	GLY	2.0
1	A	150	LYS	2.0
1	A	154	PHE	2.0
1	B	61	TYR	2.0
1	B	179	TYR	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.

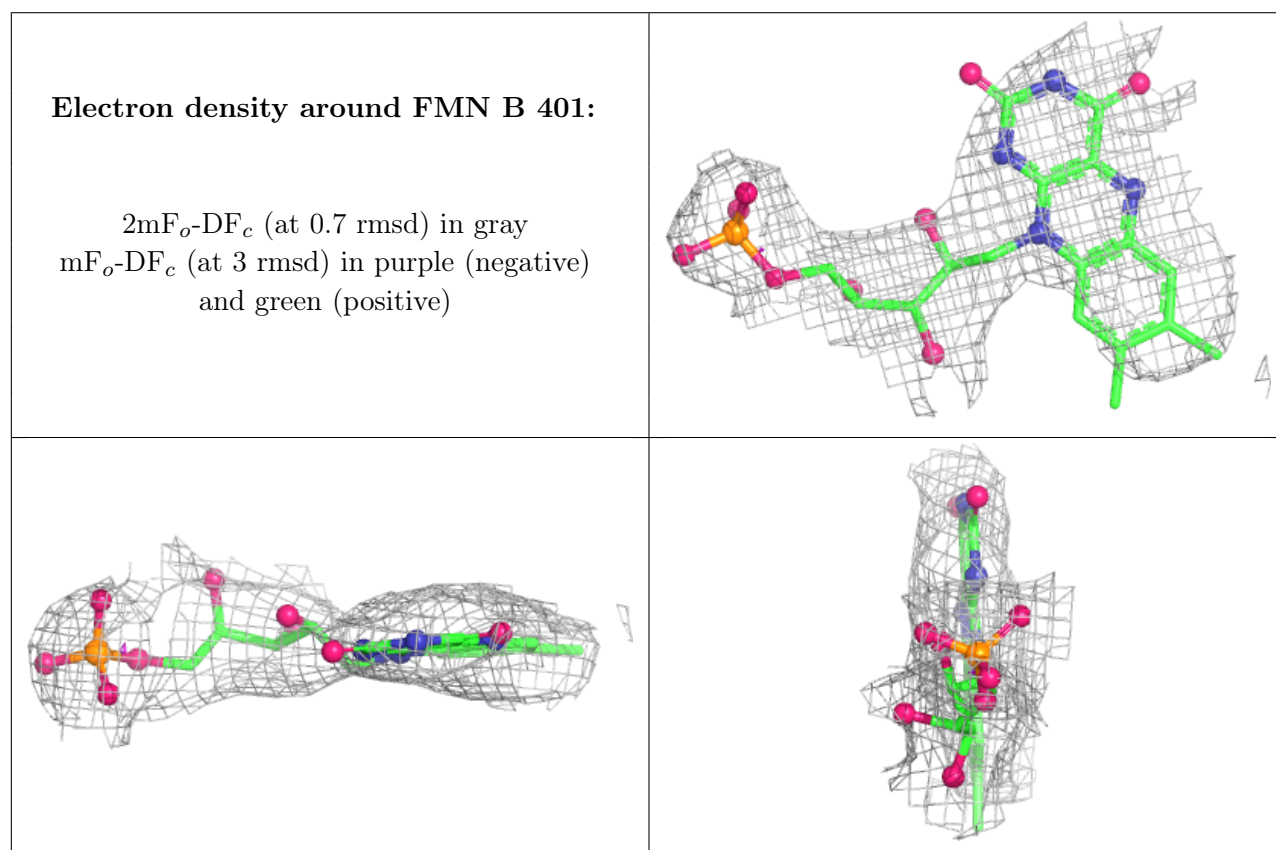
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FMN	B	401	31/31	0.77	0.13	121,127,145,145	0

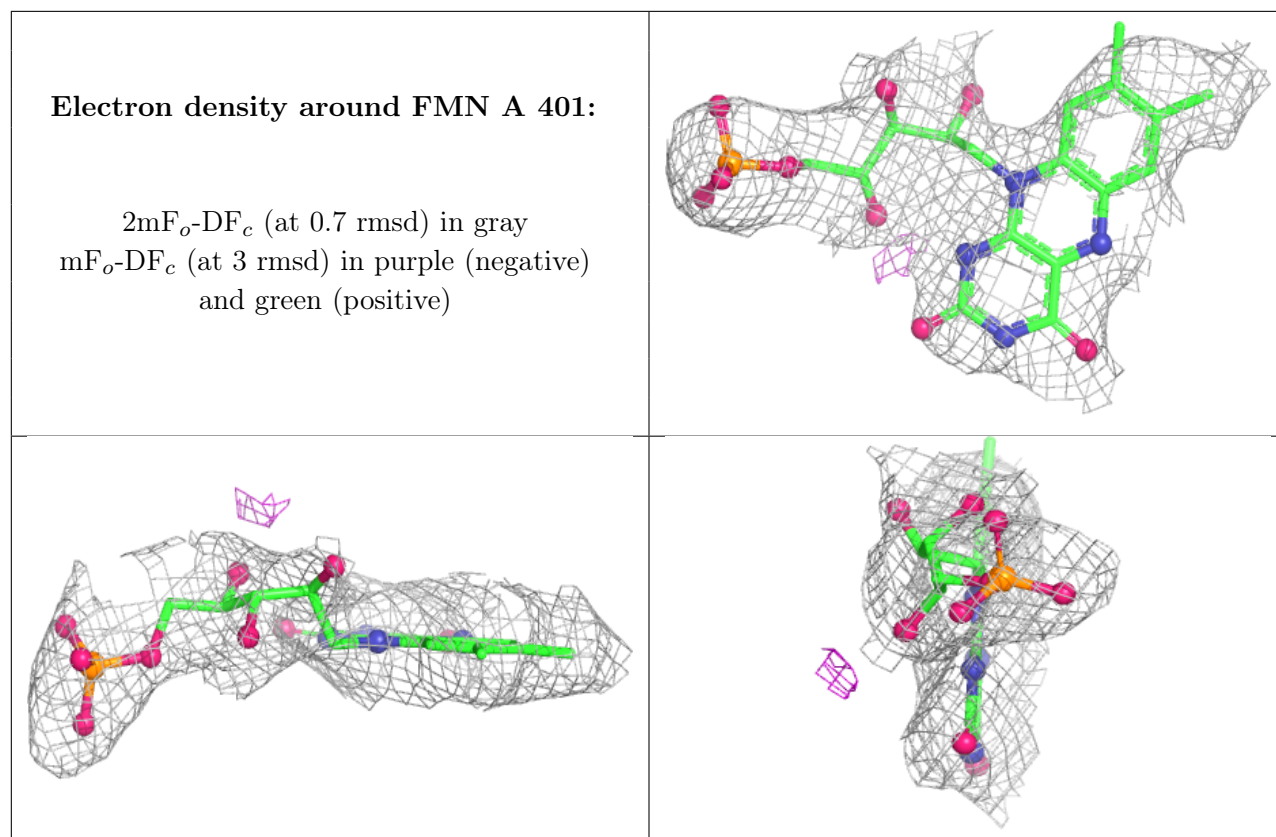
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FMN	A	401	31/31	0.82	0.12	102,107,117,118	0

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.





6.5 Other polymers [i](#)

There are no such residues in this entry.