Full wwPDB X-ray Structure Validation Report (i)

Apr 28, 2024 – 11:55 pm BST

PDB ID	:	4CQA
Title	:	Plasmodium falciparum dihydroorotate dehydrogenase (DHODH) in complex with IDI-6273
Authors	:	Rowland, P.
Deposited on	:	2014-02-12
Resolution	:	2.82 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 (i) 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 (i)) were used in the production of this report:

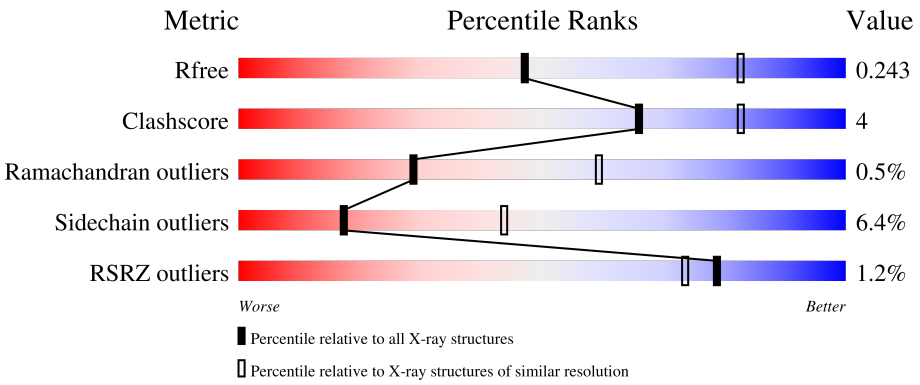
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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 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 <=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	401	2% 78% 14% • 7%
1	B	401	78% 13% • 8%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6119 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	371	2937	1879	494	549	15	0	0	0
1	B	368	2913	1864	490	545	14	0	0	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	139	MET	-	expression tag	UNP Q54A96
A	140	GLY	-	expression tag	UNP Q54A96
A	141	HIS	-	expression tag	UNP Q54A96
A	142	HIS	-	expression tag	UNP Q54A96
A	143	HIS	-	expression tag	UNP Q54A96
A	144	HIS	-	expression tag	UNP Q54A96
A	145	HIS	-	expression tag	UNP Q54A96
A	146	HIS	-	expression tag	UNP Q54A96
A	147	ALA	-	expression tag	UNP Q54A96
A	148	GLU	-	expression tag	UNP Q54A96
A	149	ASN	-	expression tag	UNP Q54A96
A	150	LEU	-	expression tag	UNP Q54A96
A	151	TYR	-	expression tag	UNP Q54A96
A	152	PHE	-	expression tag	UNP Q54A96
A	153	GLN	-	expression tag	UNP Q54A96
A	154	GLY	-	expression tag	UNP Q54A96
A	155	ALA	-	expression tag	UNP Q54A96
A	156	ASP	-	expression tag	UNP Q54A96
A	157	PRO	-	expression tag	UNP Q54A96
B	139	MET	-	expression tag	UNP Q54A96
B	140	GLY	-	expression tag	UNP Q54A96
B	141	HIS	-	expression tag	UNP Q54A96
B	142	HIS	-	expression tag	UNP Q54A96
B	143	HIS	-	expression tag	UNP Q54A96
B	144	HIS	-	expression tag	UNP Q54A96

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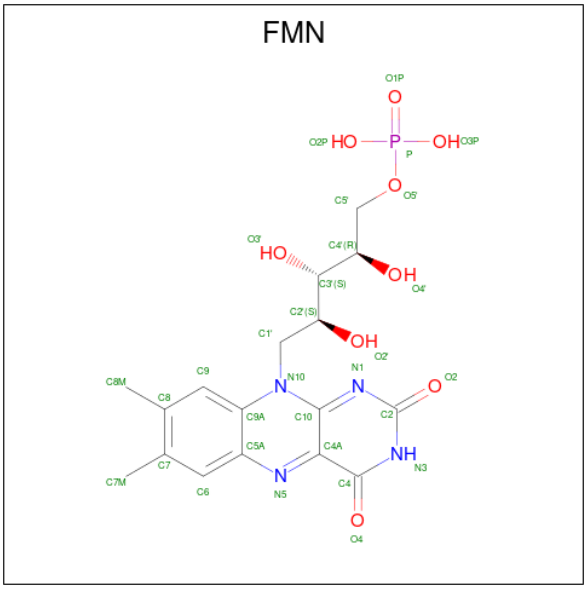
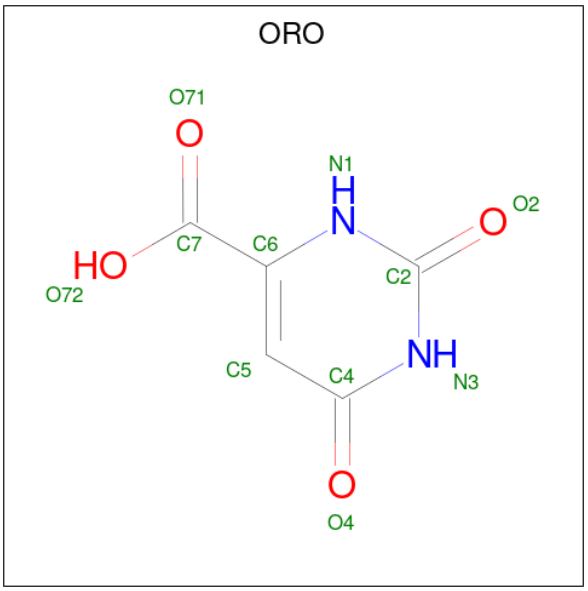
Chain	Residue	Modelled	Actual	Comment	Reference
B	145	HIS	-	expression tag	UNP Q54A96
B	146	HIS	-	expression tag	UNP Q54A96
B	147	ALA	-	expression tag	UNP Q54A96
B	148	GLU	-	expression tag	UNP Q54A96
B	149	ASN	-	expression tag	UNP Q54A96
B	150	LEU	-	expression tag	UNP Q54A96
B	151	TYR	-	expression tag	UNP Q54A96
B	152	PHE	-	expression tag	UNP Q54A96
B	153	GLN	-	expression tag	UNP Q54A96
B	154	GLY	-	expression tag	UNP Q54A96
B	155	ALA	-	expression tag	UNP Q54A96
B	156	ASP	-	expression tag	UNP Q54A96
B	157	PRO	-	expression tag	UNP Q54A96

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



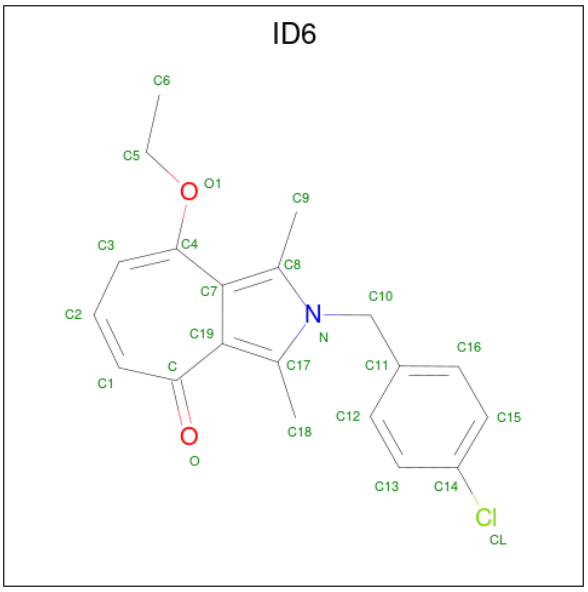
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is OROTIC ACID (three-letter code: ORO) (formula: $C_5H_4N_2O_4$).



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

- Molecule 4 is 2-(4-chlorobenzyl)-8-ethoxy-1,3-dimethylcyclohepta[c]pyrrol-4(2H)-one (three-letter code: ID6) (formula: $C_{20}H_{20}ClNO_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
4	A	1	24	20	1	1	2	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
4	B	1	24	20	1	1	2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	65	65	65	0	0
			Total	O		
5	B	72	72	72	0	0

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: DIHYDROOROTATE DEHYDROGENASE

Chain A: 2% 78% 14% • 7%

MET GLY HIS HIS HIS HIS HIS ALA GLU ASN LEU TYR PHE GLN GLY ALA ASP PRO PHE GLU SER TYR ASN PRO GLU F165 F166 L167 I170 F171 H185 L190 T201 L215 G226 K229 D235 F244 I250 R262 R265 N274 S275 C276 N280

M281 K285 V286 L303 H306 I307 V308 V319 N320 I321 K326 I329 R334 T348 P349 G350 E356 V367 E370 E375 K376 N377 N378 I379 M380 N381 ASP GLU F414 L415 W416 F417 L425 L446 N450 I451 I456 N464 D465 I466 K480

S485 F488 N494 I518 V524 C525 Q526 L531 S538 A539 Y556 N557 L558 I562 S567 LYS SER

• Molecule 1: DIHYDROOROTATE DEHYDROGENASE

Chain B: 78% 13% • 8%

MET GLY HIS HIS HIS HIS HIS ALA GLU ASN LEU TYR PHE GLN GLY ALA ASP PRO PHE GLU SER TYR ASN PRO GLU F165 F166 L167 Y168 D169 I170 K173 H185 F188 L191 T201 A208 L215 G226 K229 D235 F244 I250 G254 R262

N274 S275 C276 N280 V286 L302 L303 H306 I307 V319 K326 I329 R334 T348 P349 G350 E356 V367 K368 E369 E370 L374 N378 ILE MET ASN ASP GLU F414 F417 L425 L446 I451 I456 N464 D465 I466 K467 S468

K480 S485 F488 I518 V524 C525 Q526 L531 S538 L558 I562 S567 LYS SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	52.95Å 166.41Å 63.16Å 90.00° 107.91° 90.00°	Depositor
Resolution (Å)	60.10 – 2.82 60.10 – 2.82	Depositor EDS
% Data completeness (in resolution range)	82.0 (60.10-2.82) 82.0 (60.10-2.82)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.03 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.171 , 0.230 0.189 , 0.243	Depositor DCC
R_{free} test set	847 reflections (4.11%)	wwPDB-VP
Wilson B-factor (Å^2)	52.6	Xtriage
Anisotropy	0.683	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 55.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6119	wwPDB-VP
Average B, all atoms (Å^2)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, ID6, 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	0.48	0/2985	0.71	0/4016
1	B	0.49	0/2961	0.71	0/3984
All	All	0.48	0/5946	0.71	0/8000

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2937	0	2992	24	0
1	B	2913	0	2966	24	0
2	A	31	0	19	0	0
2	B	31	0	19	0	0
3	A	11	0	3	0	0
3	B	11	0	3	0	0
4	A	24	0	20	1	0
4	B	24	0	20	4	0
5	A	65	0	0	2	0
5	B	72	0	0	1	0
All	All	6119	0	6042	48	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 (48) 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:368:LYS:HE2	5:B:2045:HOH:O	1.89	0.71
1:B:456:ILE:HG23	1:B:488:PHE:CD2	2.32	0.65
1:A:456:ILE:HG23	1:A:488:PHE:CD2	2.32	0.64
1:A:334:ARG:HH21	1:A:417:PHE:HB2	1.63	0.63
1:B:185:HIS:HD2	4:B:1000:ID6:H51C	1.64	0.62
1:A:494:ASN:HB3	5:A:2036:HOH:O	2.00	0.61
1:A:326:LYS:HG2	1:A:370:GLU:HG3	1.82	0.61
4:B:1000:ID6:O1	4:B:1000:ID6:H91C	2.01	0.59
1:B:185:HIS:CD2	4:B:1000:ID6:H51C	2.37	0.59
1:A:308:VAL:HG12	5:A:2031:HOH:O	2.04	0.57
1:A:185:HIS:HD2	4:A:1000:ID6:H51C	1.71	0.56
1:A:450:ASN:HB2	1:B:254:GLY:O	2.06	0.56
1:A:329:ILE:HD11	1:A:367:VAL:HG13	1.90	0.54
1:A:303:LEU:HA	1:A:306:HIS:HD2	1.75	0.52
1:B:329:ILE:HD11	1:B:367:VAL:HG13	1.91	0.51
1:B:334:ARG:HH21	1:B:417:PHE:HB2	1.75	0.51
1:B:446:LEU:HD22	1:B:451:ILE:HG21	1.91	0.51
1:B:244:PHE:HE2	1:B:526:GLN:HE21	1.58	0.51
1:A:446:LEU:HD22	1:A:451:ILE:HG21	1.92	0.50
1:B:303:LEU:HA	1:B:306:HIS:HD2	1.76	0.50
1:B:188:PHE:HA	1:B:191:LEU:HD12	1.93	0.50
1:A:466:ILE:HD11	1:A:480:LYS:HG3	1.92	0.50
1:A:244:PHE:HE2	1:A:526:GLN:HE21	1.59	0.49
1:A:377:ASN:O	1:A:378:ASN:HB2	2.13	0.48
1:B:466:ILE:HD11	1:B:480:LYS:HG3	1.94	0.48
1:A:166:PHE:CE2	1:A:170:ILE:HD11	2.49	0.47
1:B:326:LYS:HG2	1:B:370:GLU:HG3	1.96	0.47
1:A:281:MET:HB2	1:A:281:MET:HE2	1.73	0.46
1:A:375:GLU:HG3	1:A:416:TRP:HZ2	1.79	0.46
1:A:262:ARG:HD2	1:A:276:CYS:HA	1.98	0.46
1:B:185:HIS:HD2	4:B:1000:ID6:C5	2.28	0.46
1:A:215:LEU:HD22	1:A:425:LEU:HD12	1.98	0.45
1:A:518:ILE:HG23	1:A:562:ILE:HG12	1.98	0.45
1:B:262:ARG:HD2	1:B:276:CYS:HA	1.98	0.45
1:B:518:ILE:HG23	1:B:562:ILE:HG12	1.99	0.44
1:B:250:ILE:HG21	1:B:286:VAL:HG11	2.00	0.44
1:B:215:LEU:HD22	1:B:425:LEU:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:LEU:HA	1:B:170:ILE:HD12	2.00	0.43
1:A:250:ILE:HG21	1:A:286:VAL:HG11	2.00	0.43
1:B:467:LYS:HE3	1:B:467:LYS:H	1.84	0.43
1:B:226:GLY:HA2	1:B:229:LYS:HE2	2.01	0.43
1:A:281:MET:HE3	1:A:285:LYS:HG3	2.00	0.42
1:B:349:PRO:HA	1:B:350:GLY:HA2	1.82	0.42
1:A:349:PRO:HA	1:A:350:GLY:HA2	1.83	0.42
1:B:244:PHE:HB3	1:B:307:ILE:HB	2.03	0.41
1:B:303:LEU:HA	1:B:306:HIS:CD2	2.55	0.41
1:A:244:PHE:HB3	1:A:307:ILE:HB	2.02	0.41
1:A:226:GLY:HA2	1:A:229:LYS:HE2	2.02	0.41

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	367/401 (92%)	342 (93%)	22 (6%)	3 (1%)	19 47
1	B	364/401 (91%)	343 (94%)	20 (6%)	1 (0%)	41 70
All	All	731/802 (91%)	685 (94%)	42 (6%)	4 (0%)	29 59

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	ASN
1	A	538	SER
1	B	538	SER
1	A	376	LYS

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	328/354 (93%)	308 (94%)	20 (6%)	18	46
1	B	325/354 (92%)	303 (93%)	22 (7%)	16	40
All	All	653/708 (92%)	611 (94%)	42 (6%)	17	44

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	167	LEU
1	A	170	ILE
1	A	171	PHE
1	A	190	LEU
1	A	229	LYS
1	A	235	ASP
1	A	265	ARG
1	A	274	ASN
1	A	280	ASN
1	A	319	VAL
1	A	321	ILE
1	A	348	THR
1	A	356	GLU
1	A	417	PHE
1	A	464	ASN
1	A	465	ASP
1	A	485	SER
1	A	524	VAL
1	A	531	LEU
1	A	558	LEU
1	B	165	PHE
1	B	166	PHE
1	B	167	LEU
1	B	169	ASP
1	B	173	LYS
1	B	229	LYS
1	B	235	ASP

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Mol	Chain	Res	Type
1	B	274	ASN
1	B	280	ASN
1	B	302	LEU
1	B	319	VAL
1	B	348	THR
1	B	356	GLU
1	B	374	LEU
1	B	464	ASN
1	B	465	ASP
1	B	467	LYS
1	B	468	SER
1	B	485	SER
1	B	524	VAL
1	B	531	LEU
1	B	558	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	HIS
1	A	306	HIS
1	A	330	ASN
1	A	381	ASN
1	A	566	HIS
1	B	185	HIS
1	B	306	HIS
1	B	330	ASN
1	B	494	ASN
1	B	566	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	$\#\|Z\| > 2$
4	ID6	B	1000	-	25,26,26	0.71	1 (4%)	24,37,37	0.42	0
4	ID6	A	1000	-	25,26,26	0.75	1 (4%)	24,37,37	0.47	0
2	FMN	B	800	-	33,33,33	0.36	0	48,50,50	0.47	0
3	ORO	B	900	-	9,11,11	1.69	2 (22%)	8,15,15	3.54	2 (25%)
3	ORO	A	900	-	9,11,11	1.75	3 (33%)	8,15,15	3.52	2 (25%)
2	FMN	A	800	-	33,33,33	0.38	0	48,50,50	0.47	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ID6	B	1000	-	-	3/7/7/7	0/3/3/3
4	ID6	A	1000	-	-	3/7/7/7	0/3/3/3
2	FMN	B	800	-	-	3/18/18/18	0/3/3/3
3	ORO	B	900	-	-	4/4/4/4	0/1/1/1
3	ORO	A	900	-	-	4/4/4/4	0/1/1/1
2	FMN	A	800	-	-	3/18/18/18	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	900	ORO	C6-N1	3.31	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	900	ORO	C6-N1	3.22	1.39	1.34
3	A	900	ORO	C4-N3	3.19	1.38	1.33
3	B	900	ORO	C4-N3	3.03	1.38	1.33
4	A	1000	ID6	C7-C19	3.01	1.47	1.40
4	B	1000	ID6	C7-C19	2.86	1.47	1.40
3	A	900	ORO	C6-C7	-2.12	1.47	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	900	ORO	C5-C4-N3	-7.78	115.00	124.08
3	A	900	ORO	C5-C4-N3	-7.71	115.08	124.08
3	A	900	ORO	C6-C5-C4	5.78	120.46	116.73
3	B	900	ORO	C6-C5-C4	5.76	120.45	116.73

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	900	ORO	N1-C6-C7-O71
3	A	900	ORO	N1-C6-C7-O72
3	A	900	ORO	C5-C6-C7-O71
3	A	900	ORO	C5-C6-C7-O72
3	B	900	ORO	N1-C6-C7-O71
3	B	900	ORO	N1-C6-C7-O72
3	B	900	ORO	C5-C6-C7-O71
3	B	900	ORO	C5-C6-C7-O72
4	A	1000	ID6	C3-C4-O1-C5
4	B	1000	ID6	C3-C4-O1-C5
2	A	800	FMN	C5'-O5'-P-O1P
2	B	800	FMN	C5'-O5'-P-O1P
4	A	1000	ID6	N-C10-C11-C12
4	A	1000	ID6	N-C10-C11-C16
4	B	1000	ID6	N-C10-C11-C12
4	B	1000	ID6	N-C10-C11-C16
2	B	800	FMN	C4'-C5'-O5'-P
2	A	800	FMN	C4'-C5'-O5'-P
2	A	800	FMN	C5'-O5'-P-O2P
2	B	800	FMN	C5'-O5'-P-O2P

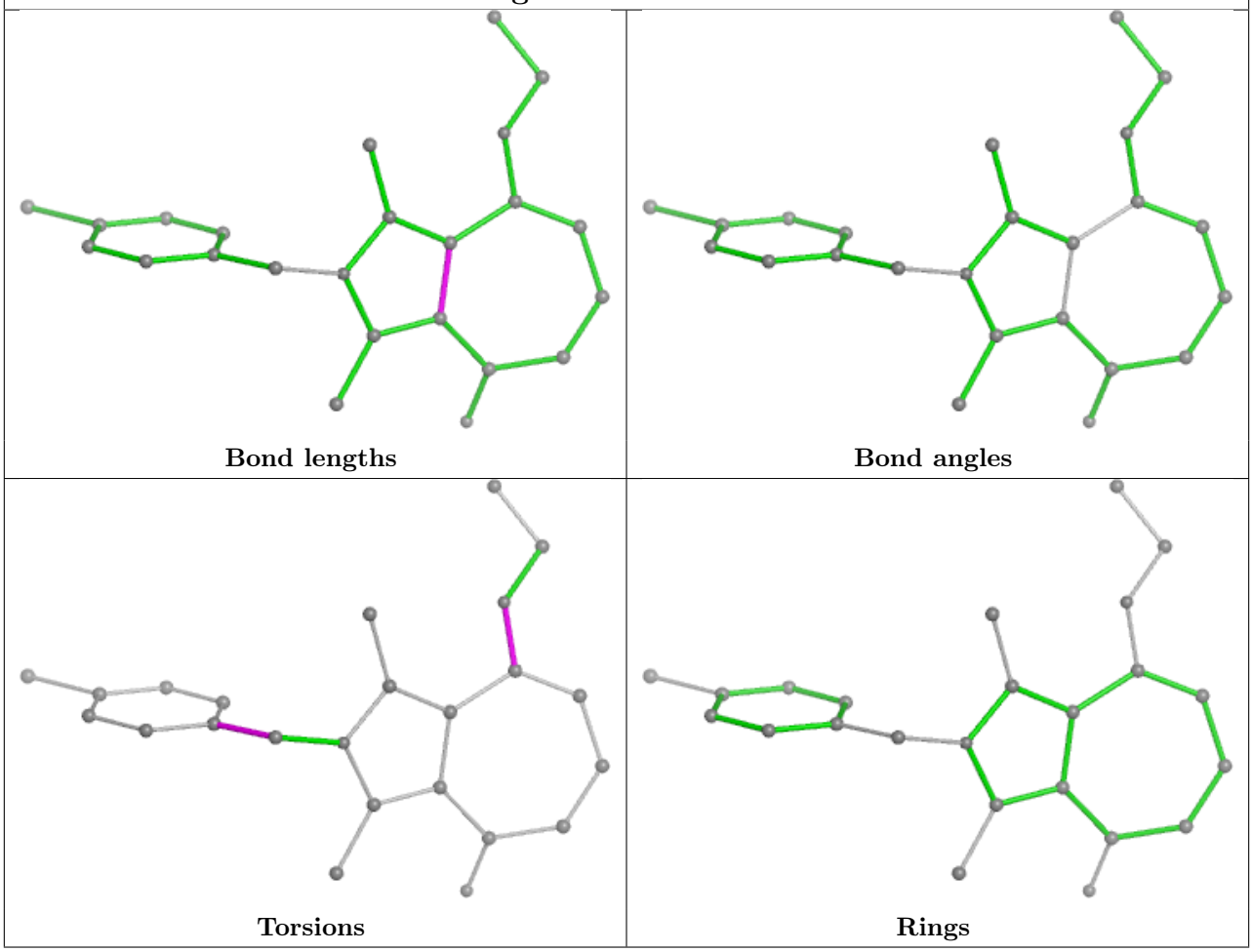
There are no ring outliers.

2 monomers are involved in 5 short contacts:

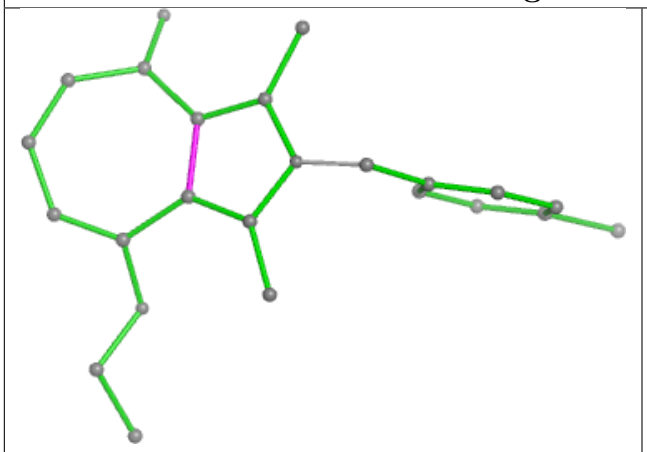
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1000	ID6	4	0
4	A	1000	ID6	1	0

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 then 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.

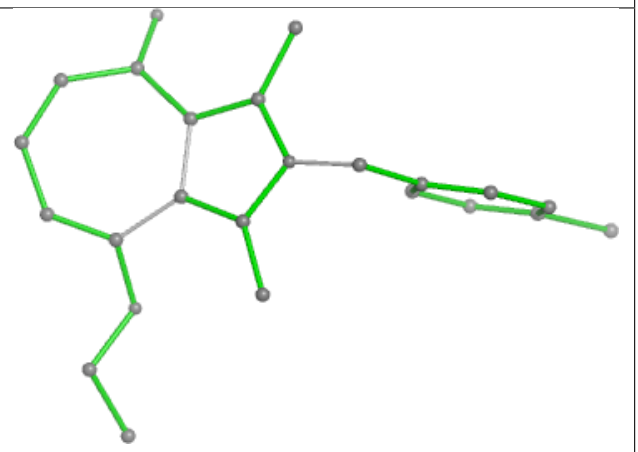
Ligand ID6 B 1000



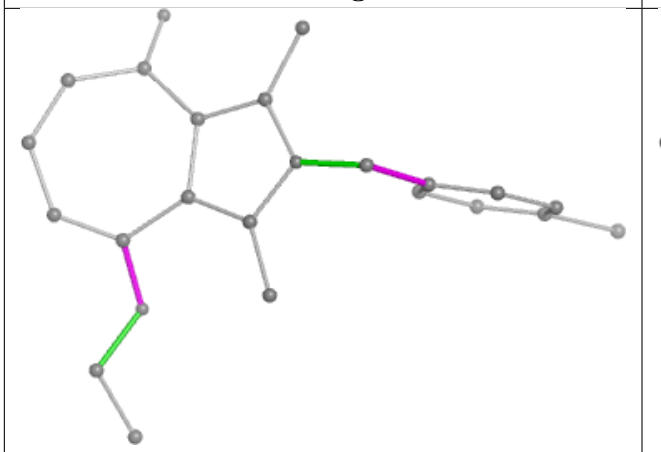
Ligand ID6 A 1000



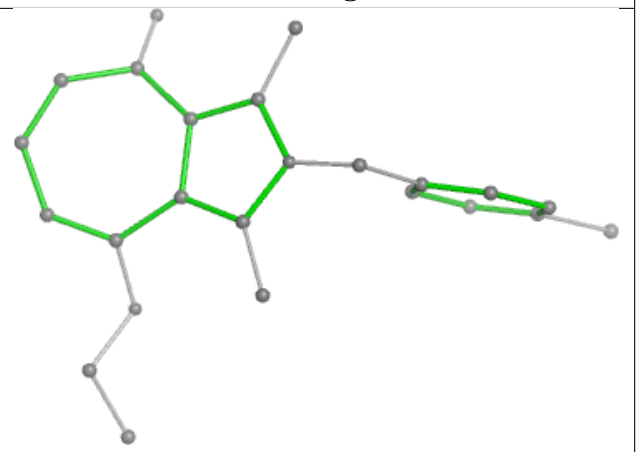
Bond lengths



Bond angles

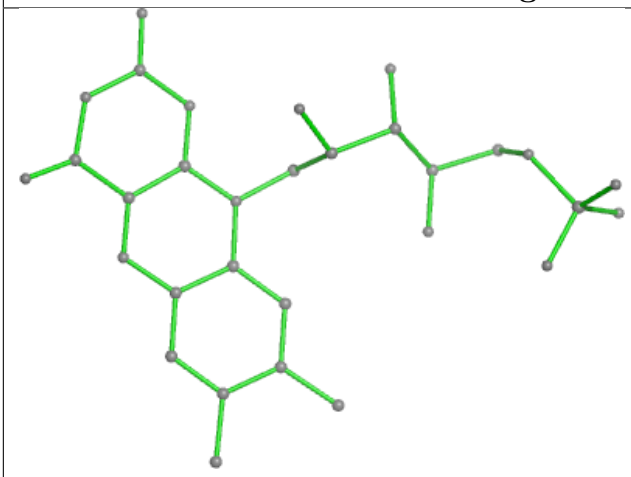


Torsions

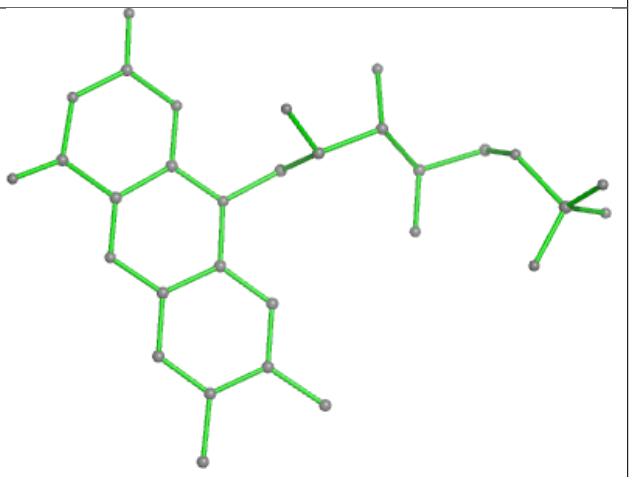


Rings

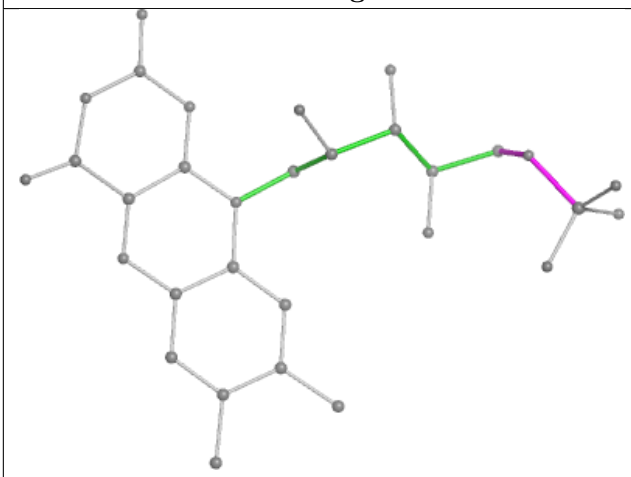
Ligand FMN B 800



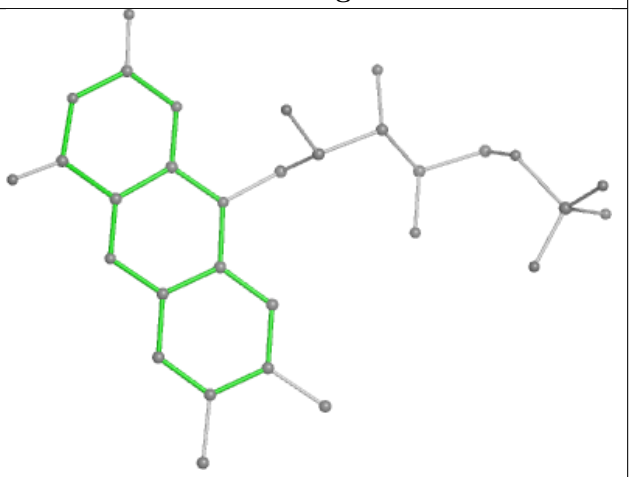
Bond lengths



Bond angles

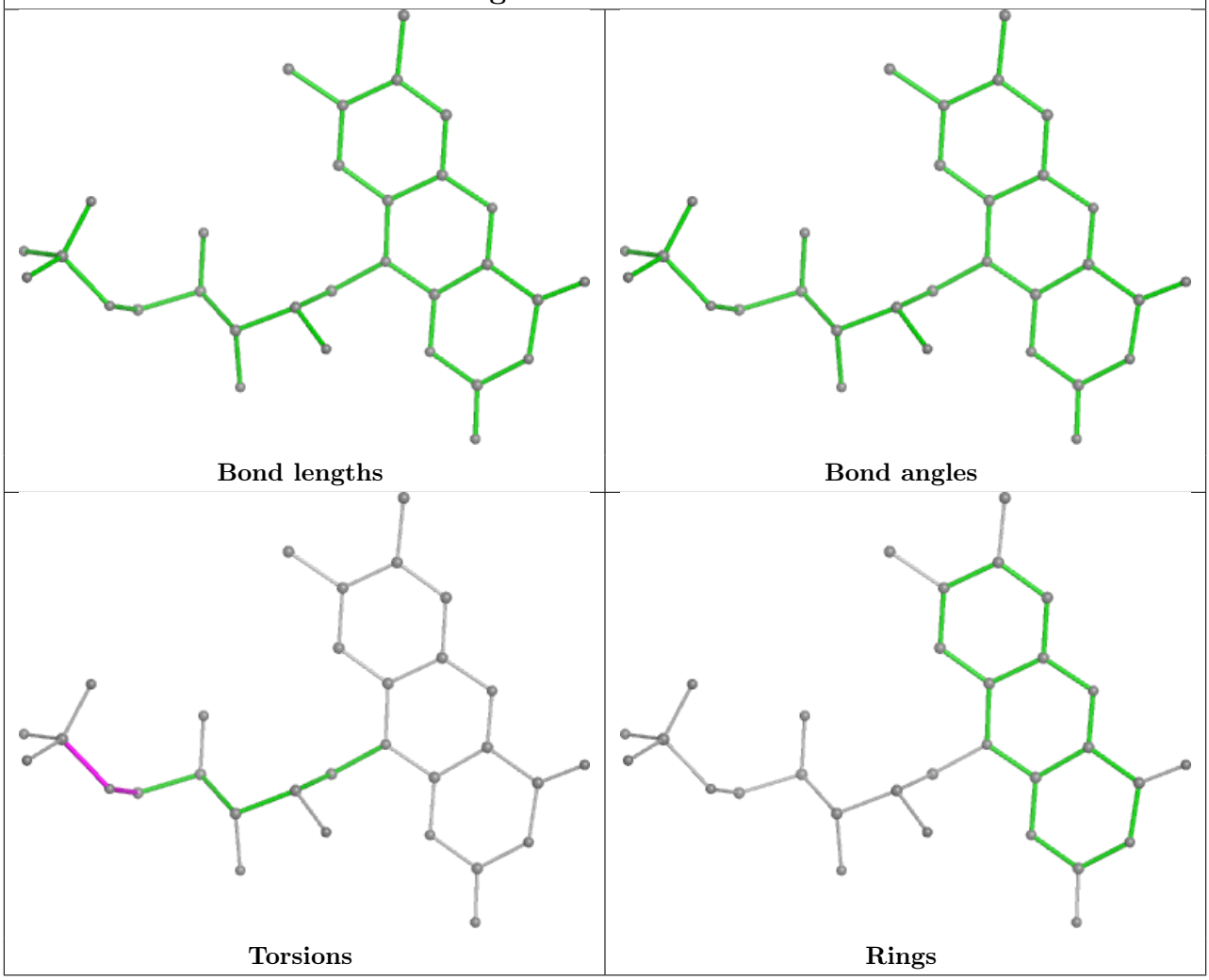


Torsions



Rings

Ligand FMN A 800



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	371/401 (92%)	-0.18	7 (1%)	66	59	35, 61, 101, 128	0
1	B	368/401 (91%)	-0.21	2 (0%)	91	88	35, 62, 103, 125	0
All	All	739/802 (92%)	-0.19	9 (1%)	79	73	35, 62, 102, 128	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	381	ASN	3.5
1	A	201	THR	3.0
1	A	414	PHE	2.6
1	A	380	MET	2.4
1	B	201	THR	2.3
1	A	539	ALA	2.2
1	A	556	TYR	2.2
1	B	208	ALA	2.1
1	A	171	PHE	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 monosaccharides 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,

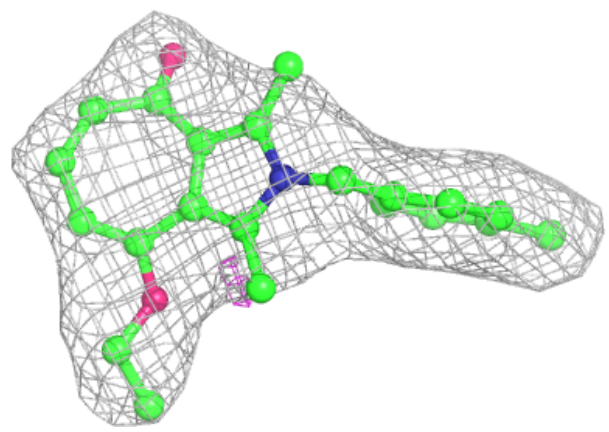
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

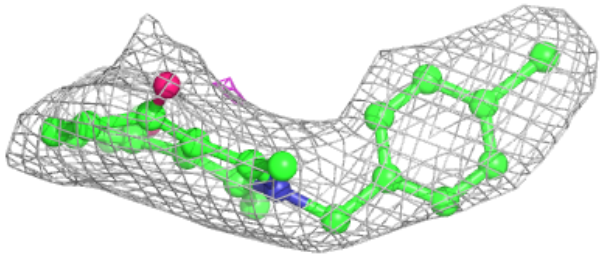
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	ID6	A	1000	24/24	0.96	0.19	58,68,84,90	0
3	ORO	B	900	11/11	0.97	0.14	46,53,58,60	0
3	ORO	A	900	11/11	0.97	0.17	48,54,63,68	0
4	ID6	B	1000	24/24	0.97	0.22	70,75,90,99	0
2	FMN	B	800	31/31	0.98	0.15	49,55,65,70	0
2	FMN	A	800	31/31	0.99	0.17	41,47,53,57	0

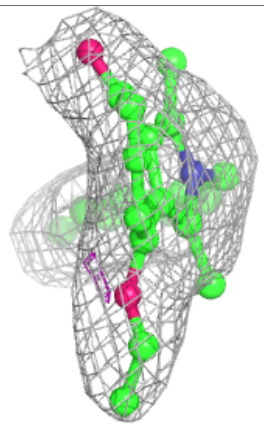
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ID6 A 1000:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

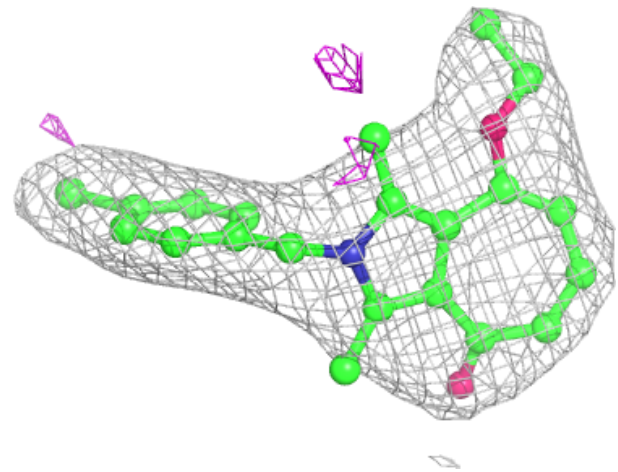


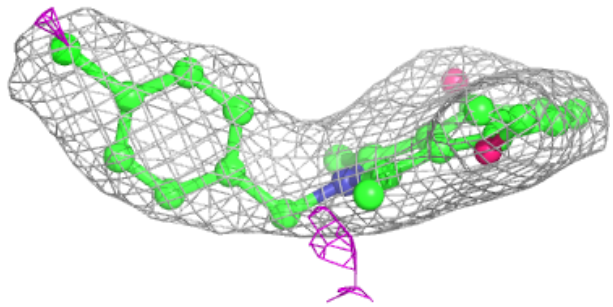


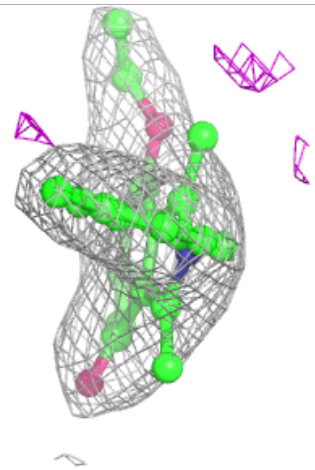


Electron density around ID6 B 1000:

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

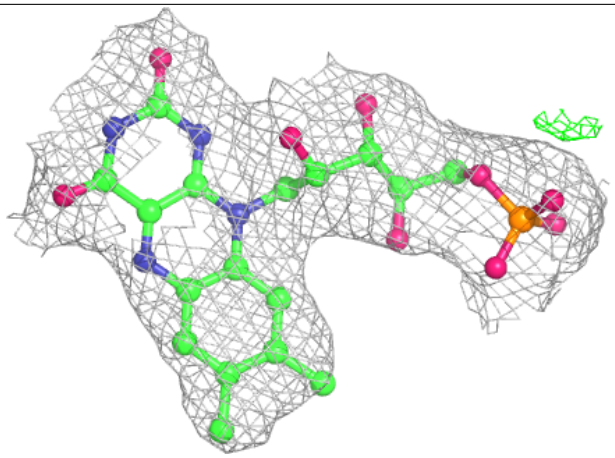


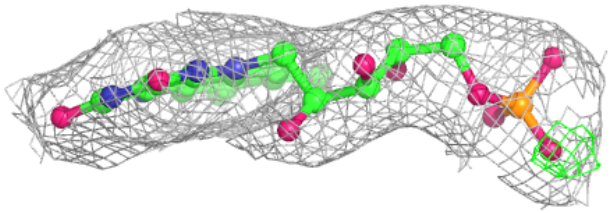


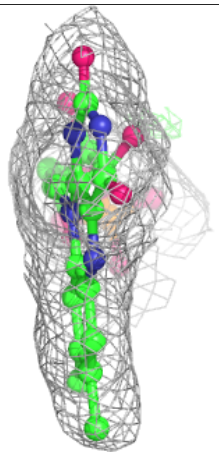


Electron density around FMN B 800:

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

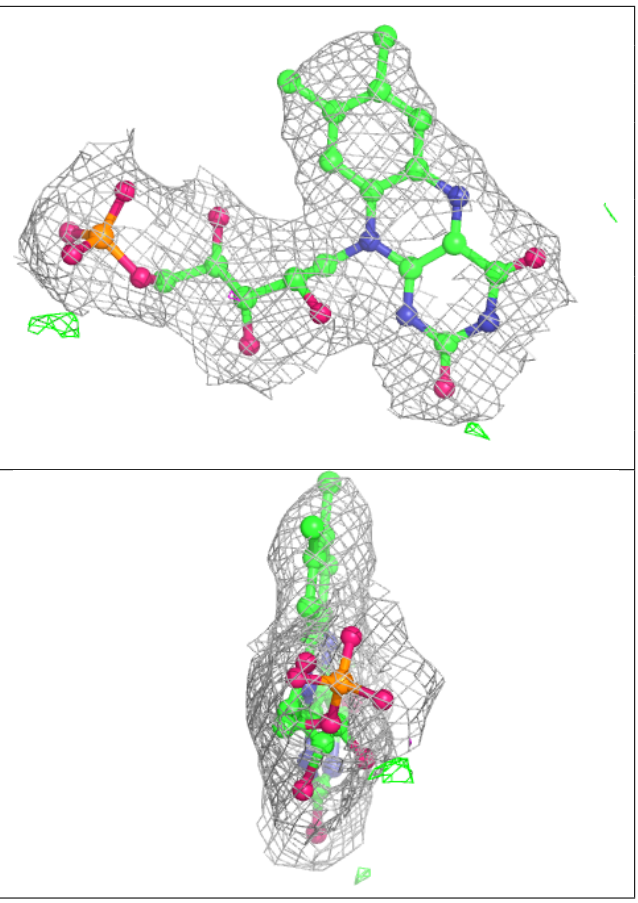






Electron density around FMN A 800:

$2mF_o$-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.