Full wwPDB X-ray Structure Validation Report (i)

Sep 23, 2023 – 08:38 PM EDT

PDB ID	:	5TBO
Title	:	Crystal structure of Plasmodium falciparum dihydroorotate dehydrogenase bound with Inhibitor DSM421
Authors	:	Deng, X.; Phillips, M.
Deposited on	:	2016-09-12
Resolution	:	2.15 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:

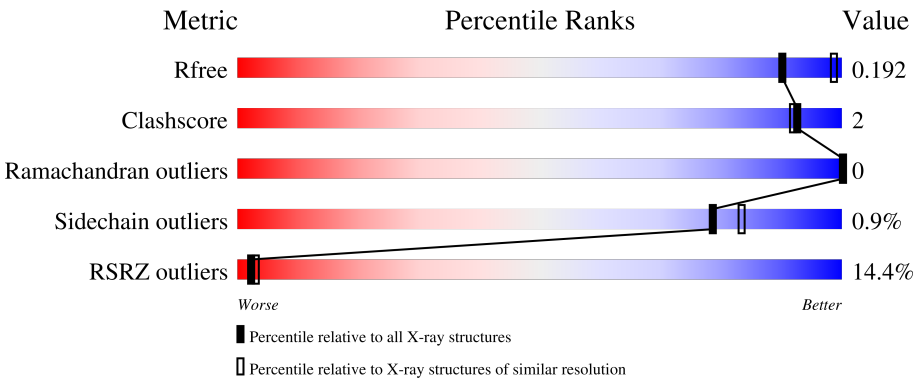
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	13% 86% • 10%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 6099 atoms, of which 3011 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
			Total	C	H	N	O	S			
1	A	362	5811	1845	2933	479	539	15	0	1	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	139	MET	-	initiating methionine	UNP Q08210
A	140	GLY	-	expression tag	UNP Q08210
A	141	HIS	-	expression tag	UNP Q08210
A	142	HIS	-	expression tag	UNP Q08210
A	143	HIS	-	expression tag	UNP Q08210
A	144	HIS	-	expression tag	UNP Q08210
A	145	HIS	-	expression tag	UNP Q08210
A	146	HIS	-	expression tag	UNP Q08210
A	147	ALA	-	expression tag	UNP Q08210
A	148	GLU	-	expression tag	UNP Q08210
A	149	ASN	-	expression tag	UNP Q08210
A	150	LEU	-	expression tag	UNP Q08210
A	151	TYR	-	expression tag	UNP Q08210
A	152	PHE	-	expression tag	UNP Q08210
A	153	GLN	-	expression tag	UNP Q08210
A	154	GLY	-	expression tag	UNP Q08210
A	155	ALA	-	expression tag	UNP Q08210
A	156	ASP	-	expression tag	UNP Q08210
A	157	PRO	-	expression tag	UNP Q08210
A	?	-	SER	deletion	UNP Q08210
A	?	-	THR	deletion	UNP Q08210
A	?	-	TYR	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	GLU	deletion	UNP Q08210
A	?	-	ASP	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	LYS	deletion	UNP Q08210

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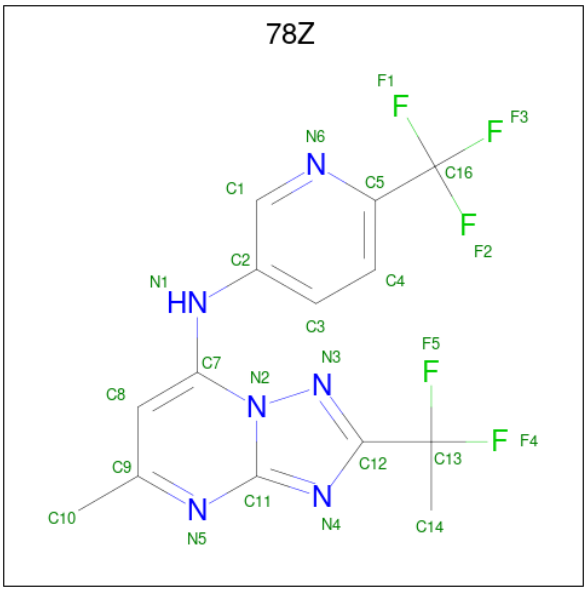
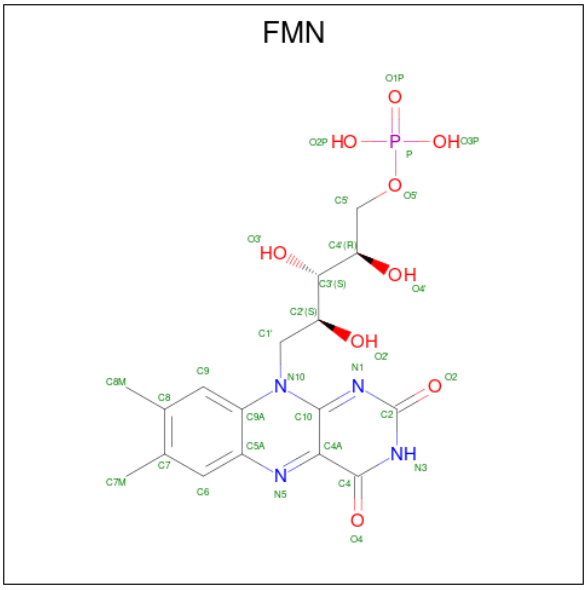
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ILE	deletion	UNP Q08210
A	?	-	VAL	deletion	UNP Q08210
A	?	-	GLU	deletion	UNP Q08210
A	?	-	LYS	deletion	UNP Q08210
A	?	-	LYS	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	PHE	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	LYS	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	SER	deletion	UNP Q08210
A	?	-	HIS	deletion	UNP Q08210
A	?	-	MET	deletion	UNP Q08210
A	?	-	MET	deletion	UNP Q08210
A	?	-	LYS	deletion	UNP Q08210
A	?	-	ASP	deletion	UNP Q08210
A	?	-	ALA	deletion	UNP Q08210
A	?	-	LYS	deletion	UNP Q08210
A	?	-	ASP	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210

- Molecule 2 is 2-(1,1-difluoroethyl)-5-methyl-N-[6-(trifluoromethyl)pyridin-3-yl][1,2,4]triazolo[1,5-a]pyrimidin-7-amine (three-letter code: 78Z) (formula: $C_{14}H_{11}F_5N_6$).



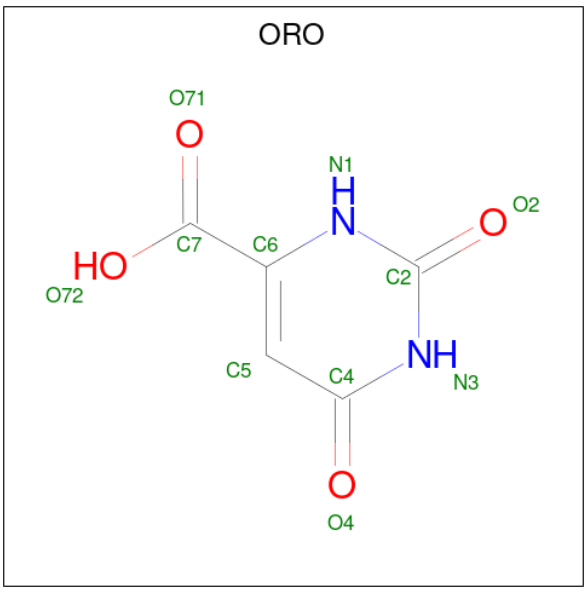
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	H	N		
2	A	1	36	14	5	11	6	0	0

- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



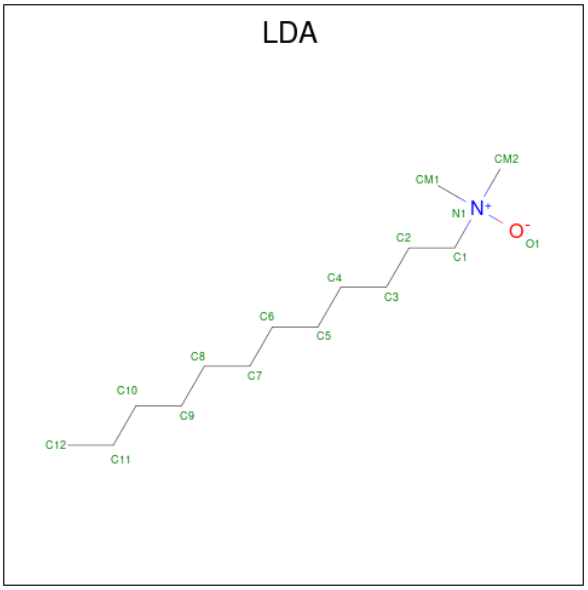
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	P		
3	A	1	49	17	18	4	9	1	0	0

- Molecule 4 is OROTIC ACID (three-letter code: ORO) (formula: $C_5H_4N_2O_4$).



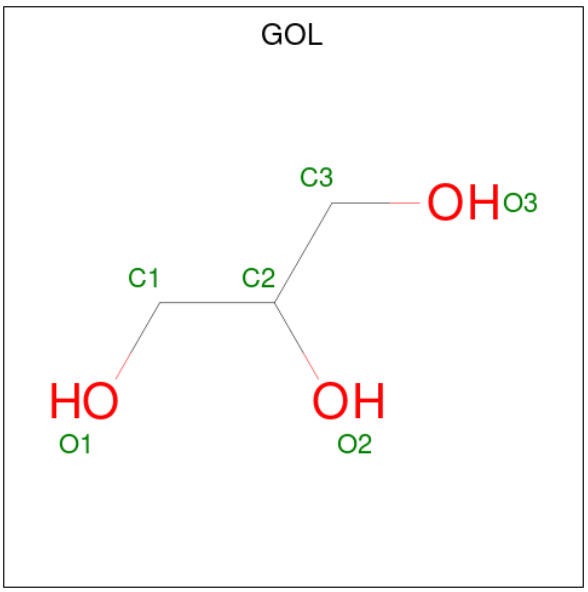
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	14	5	3	2	4	0	0

- Molecule 5 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
5	A	1	47	14	31	1	1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
6	A	1	14	3	8	3	0	0
			Total	C	H	O		
6	A	1	13	3	7	3	0	0

- Molecule 7 is water.

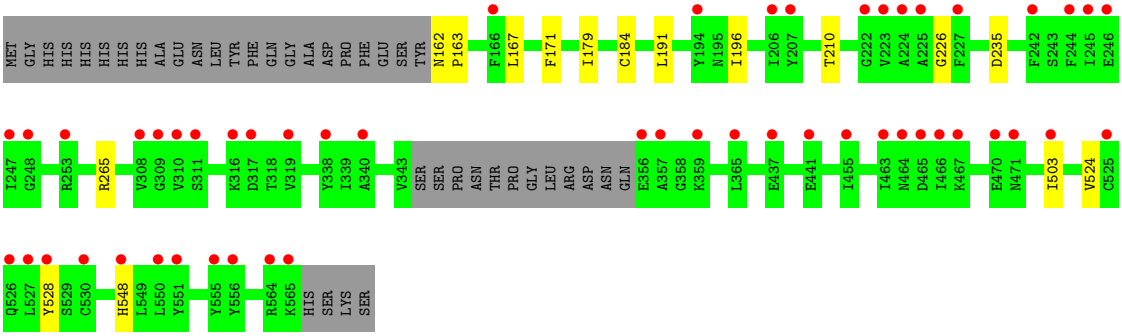
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	115	115	115	0	0

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 (quinone), mitochondrial

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α, β, γ	86.38Å 86.38Å 138.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.55 – 2.15 31.55 – 2.15	Depositor EDS
% Data completeness (in resolution range)	83.5 (31.55-2.15) 83.5 (31.55-2.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.28 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.181 , 0.219 0.187 , 0.192	Depositor DCC
R_{free} test set	1351 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	26.0	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 59.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.052 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6099	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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: LDA, 78Z, GOL, 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	0.25	0/2927	0.41	0/3937

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	2878	2933	2933	9	0
2	A	25	11	0	1	0
3	A	31	18	19	1	0
4	A	11	3	3	0	0
5	A	16	31	31	2	1
6	A	12	15	16	0	1
7	A	115	0	0	0	0
All	All	3088	3011	3002	9	1

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 2.

All (9) 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:265:ARG:HD3	2:A:1001:78Z:N4	2.22	0.54
1:A:503:ILE:HG23	1:A:524:VAL:HG23	1.91	0.53
1:A:191:LEU:HD22	1:A:196:ILE:HD11	1.94	0.49
1:A:171:PHE:HB2	5:A:1004:LDA:H123	1.95	0.48
1:A:226:GLY:HA3	3:A:1002:FMN:N5	2.29	0.47
1:A:179:ILE:HB	1:A:184:CYS:SG	2.56	0.46
1:A:167:LEU:HB3	5:A:1004:LDA:H101	1.98	0.45
1:A:162:ASN:N	1:A:163:PRO:HD2	2.34	0.43
1:A:210:THR:HG21	1:A:524:VAL:HG12	2.02	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1004:LDA:HM11	6:A:1006:GOL:H12[4_545]	1.25	0.35

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	359/401 (90%)	347 (97%)	12 (3%)	0	100 100

There are no Ramachandran outliers to report.

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	321/354 (91%)	318 (99%)	3 (1%)	78 83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	ASP
1	A	528	TYR
1	A	548	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	$\#\|Z\| > 2$
5	LDA	A	1004	-	12,15,15	2.59	1 (8%)	14,17,17	1.32	2 (14%)
3	FMN	A	1002	-	33,33,33	1.06	2 (6%)	48,50,50	1.26	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	78Z	A	1001	-	21,27,27	1.59	4 (19%)	29,42,42	1.64	7 (24%)
4	ORO	A	1003	-	9,11,11	1.25	0	8,15,15	2.58	4 (50%)
6	GOL	A	1006	-	5,5,5	0.57	0	5,5,5	0.53	0
6	GOL	A	1005	-	5,5,5	0.38	0	5,5,5	0.15	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
5	LDA	A	1004	-	-	5/13/13/13	-
3	FMN	A	1002	-	-	1/18/18/18	0/3/3/3
2	78Z	A	1001	-	-	2/14/16/16	0/3/3/3
4	ORO	A	1003	-	-	4/4/4/4	0/1/1/1
6	GOL	A	1006	-	-	4/4/4/4	-
6	GOL	A	1005	-	-	0/4/4/4	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1004	LDA	O1-N1	-8.91	1.21	1.42
3	A	1002	FMN	C4A-N5	3.96	1.38	1.30
2	A	1001	78Z	F4-C13	-3.40	1.34	1.37
2	A	1001	78Z	C11-N4	3.18	1.40	1.35
2	A	1001	78Z	F5-C13	-3.04	1.34	1.37
2	A	1001	78Z	C8-C9	2.60	1.43	1.38
3	A	1002	FMN	C10-N1	2.43	1.38	1.33

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1003	ORO	C6-C5-C4	4.69	119.76	116.73
2	A	1001	78Z	C2-C1-N6	-4.29	120.27	124.13
4	A	1003	ORO	C5-C4-N3	-3.74	119.72	124.08
5	A	1004	LDA	CM1-N1-C1	-3.48	102.92	110.23
2	A	1001	78Z	C16-C5-N6	3.05	118.27	114.61
3	A	1002	FMN	C4-N3-C2	-2.91	120.27	125.64
3	A	1002	FMN	C4A-C10-N10	2.69	120.42	116.48
3	A	1002	FMN	C4A-C4-N3	2.63	119.86	113.19
2	A	1001	78Z	C9-N5-C11	2.57	120.36	117.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1003	ORO	O72-C7-C6	2.54	120.47	114.69
2	A	1001	78Z	F3-C16-C5	-2.45	108.28	112.47
3	A	1002	FMN	O4-C4-C4A	-2.40	120.23	126.60
5	A	1004	LDA	C1-C2-C3	-2.38	101.02	110.67
3	A	1002	FMN	C10-C4A-N5	-2.36	119.85	124.86
4	A	1003	ORO	C7-C6-N1	2.30	119.87	116.48
3	A	1002	FMN	C9A-C5A-N5	-2.26	119.98	122.43
2	A	1001	78Z	F2-C16-C5	-2.24	108.64	112.47
2	A	1001	78Z	C4-C3-C2	-2.22	117.74	120.30
3	A	1002	FMN	C4A-C10-N1	-2.11	119.84	124.73
2	A	1001	78Z	C8-C9-N5	-2.09	120.09	122.57
3	A	1002	FMN	C5A-C9A-N10	2.03	120.05	117.95

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1003	ORO	N1-C6-C7-O71
4	A	1003	ORO	N1-C6-C7-O72
4	A	1003	ORO	C5-C6-C7-O71
4	A	1003	ORO	C5-C6-C7-O72
6	A	1006	GOL	O1-C1-C2-C3
5	A	1004	LDA	C5-C6-C7-C8
6	A	1006	GOL	C1-C2-C3-O3
6	A	1006	GOL	O1-C1-C2-O2
5	A	1004	LDA	C6-C7-C8-C9
2	A	1001	78Z	N3-C12-C13-F5
5	A	1004	LDA	C2-C3-C4-C5
6	A	1006	GOL	O2-C2-C3-O3
5	A	1004	LDA	C3-C4-C5-C6
2	A	1001	78Z	N3-C12-C13-F4
3	A	1002	FMN	C4'-C5'-O5'-P
5	A	1004	LDA	C9-C10-C11-C12

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1004	LDA	2	1
3	A	1002	FMN	1	0
2	A	1001	78Z	1	0

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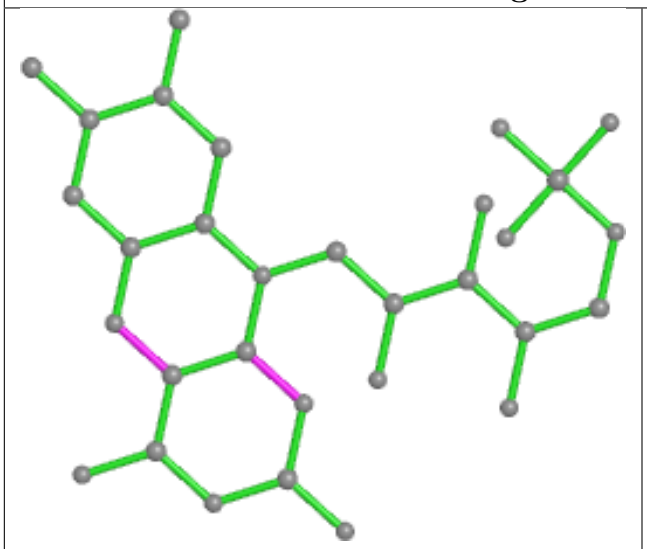
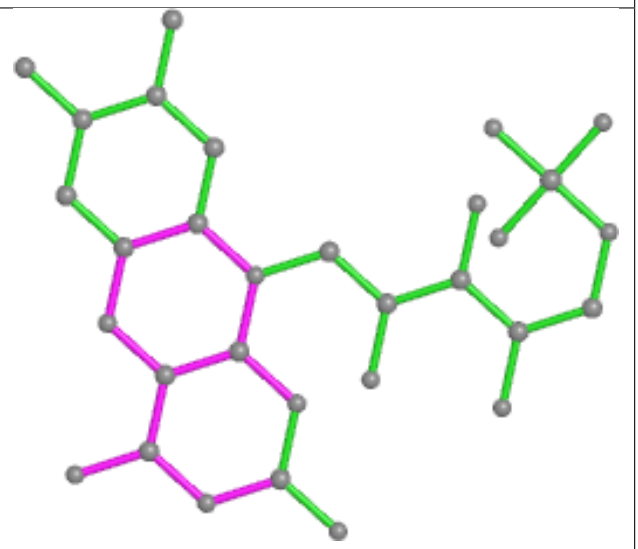
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1006	GOL	0	1

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.

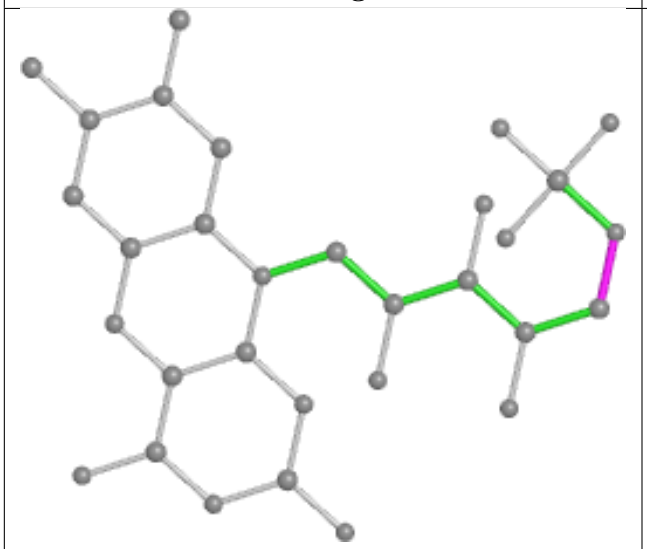
Ligand FMN A 1002



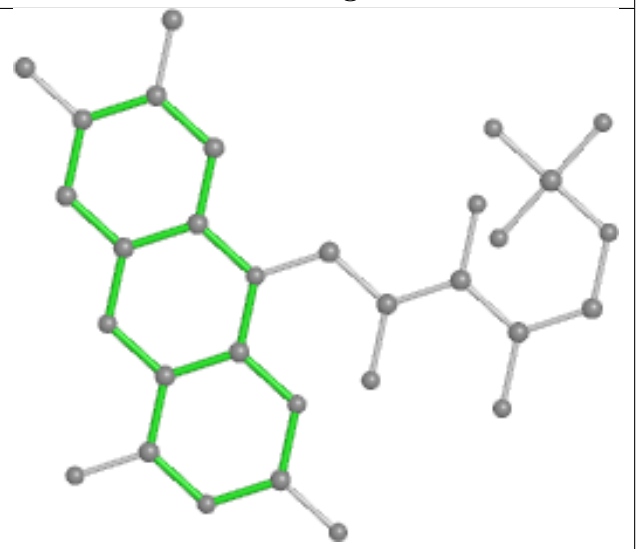
Bond lengths



Bond angles

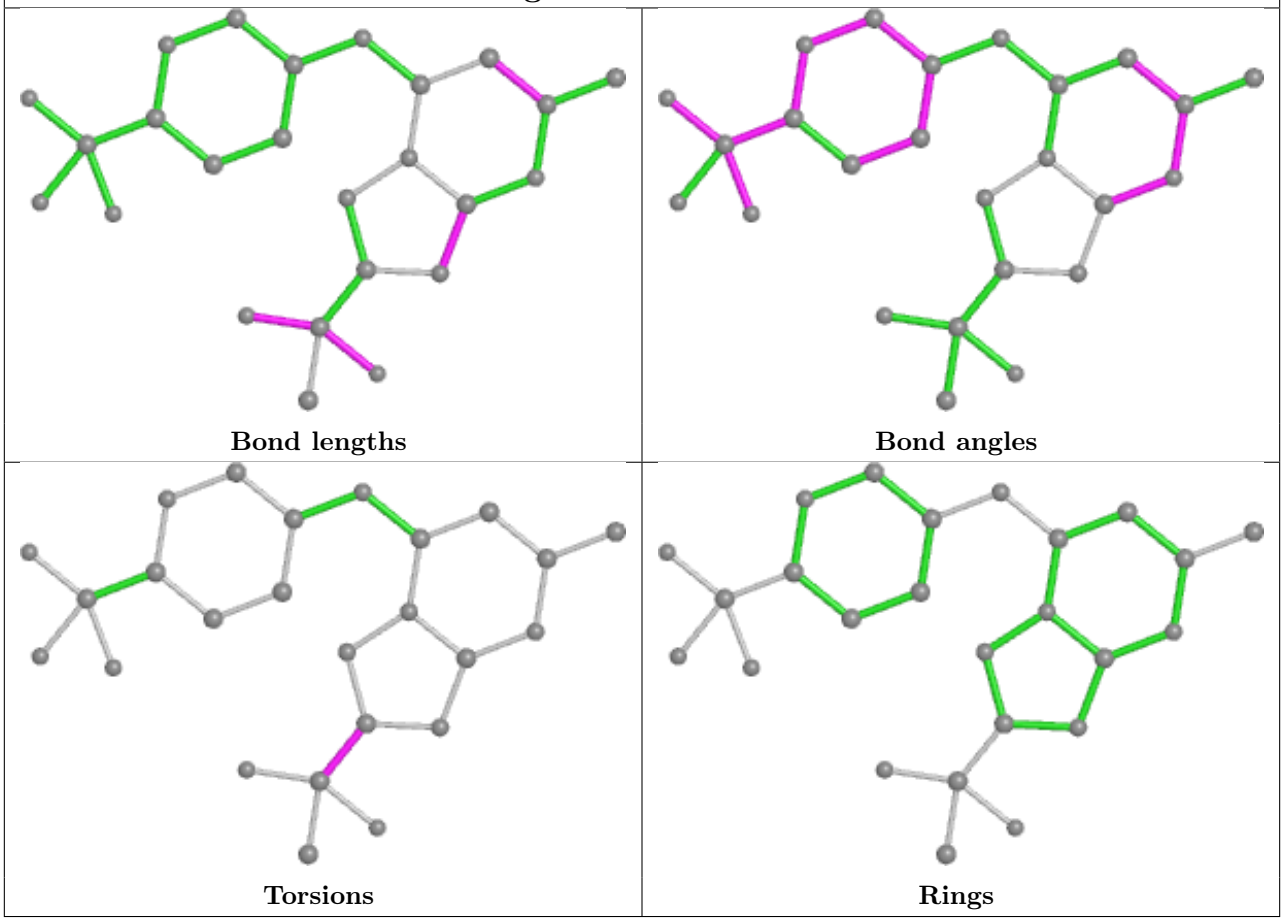


Torsions



Rings

Ligand 78Z A 1001



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	362/401 (90%)	0.68	52 (14%) 2 3	15, 37, 72, 99	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	564	ARG	4.7
1	A	556	TYR	4.6
1	A	551	TYR	4.6
1	A	464	ASN	4.4
1	A	467	LYS	4.3
1	A	463	ILE	4.0
1	A	225	ALA	4.0
1	A	319	VAL	4.0
1	A	223	VAL	3.9
1	A	224	ALA	3.8
1	A	310	VAL	3.7
1	A	338	TYR	3.6
1	A	465	ASP	3.6
1	A	555	TYR	3.6
1	A	317	ASP	3.5
1	A	311	SER	3.2
1	A	455	ILE	3.2
1	A	565	LYS	3.2
1	A	244	PHE	3.2
1	A	309	GLY	3.2
1	A	222	GLY	3.1
1	A	357	ALA	3.1
1	A	245	ILE	3.1
1	A	441	GLU	3.0
1	A	206	ILE	3.0
1	A	207	TYR	3.0
1	A	340	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	527	LEU	2.9
1	A	466	ILE	2.8
1	A	470	GLU	2.8
1	A	253	ARG	2.7
1	A	550	LEU	2.7
1	A	526	GLN	2.6
1	A	242	PHE	2.5
1	A	503	ILE	2.5
1	A	194	TYR	2.5
1	A	437	GLU	2.4
1	A	356	GLU	2.4
1	A	528	TYR	2.3
1	A	166	PHE	2.3
1	A	359	LYS	2.3
1	A	525	CYS	2.3
1	A	227	PHE	2.2
1	A	247	ILE	2.2
1	A	248	GLY	2.2
1	A	308	VAL	2.2
1	A	316	LYS	2.1
1	A	548	HIS	2.1
1	A	365	LEU	2.1
1	A	530	CYS	2.1
1	A	246	GLU	2.0
1	A	471	ASN	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)

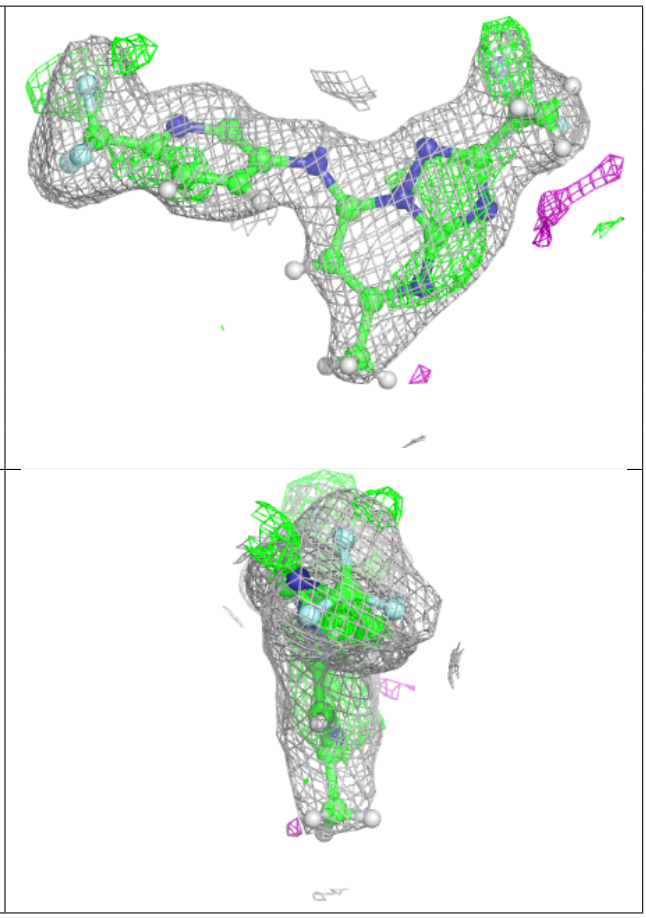
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	LDA	A	1004	16/16	0.71	0.31	49,59,59,59	0
6	GOL	A	1005	6/6	0.81	0.28	45,58,70,70	0
6	GOL	A	1006	6/6	0.82	0.18	45,58,70,70	0
2	78Z	A	1001	25/25	0.94	0.23	17,36,60,94	0
4	ORO	A	1003	11/11	0.96	0.11	16,20,27,36	0
3	FMN	A	1002	31/31	0.96	0.22	8,20,32,39	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.

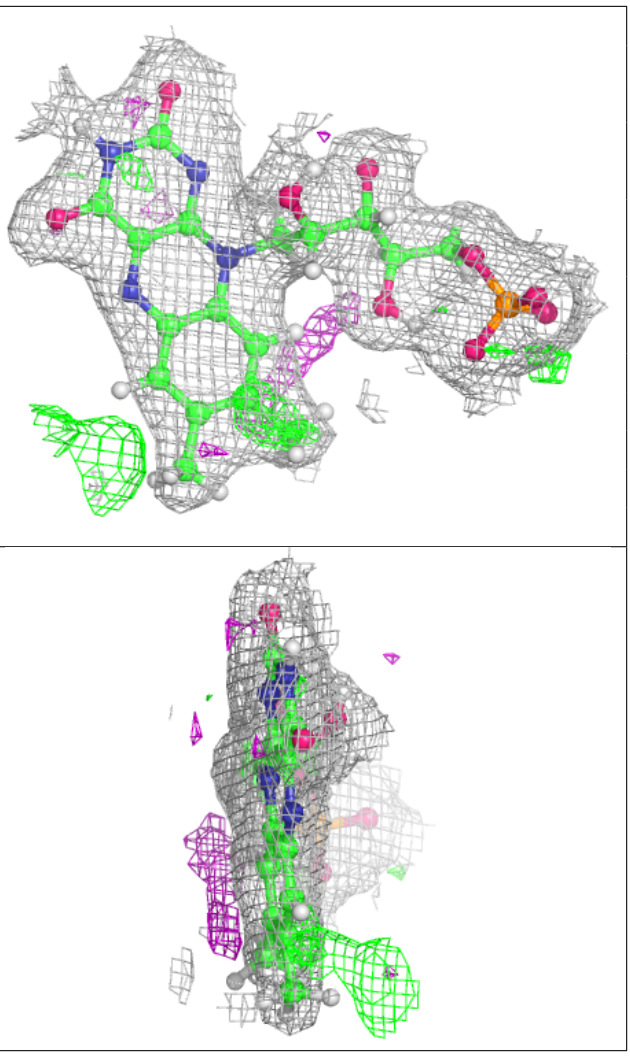
Electron density around 78Z A 1001:

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 1002:

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.