Full wwPDB X-ray Structure Validation Report (i)

Jun 22, 2024 – 02:11 PM EDT

PDB ID	:	6EI9
Title	:	Crystal structure of E. coli tRNA-dihydrouridine synthase B (DusB)
Authors	:	Bou-Nader, C.; Hamdane, D.
Deposited on	:	2017-09-18
Resolution	:	2.55 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:

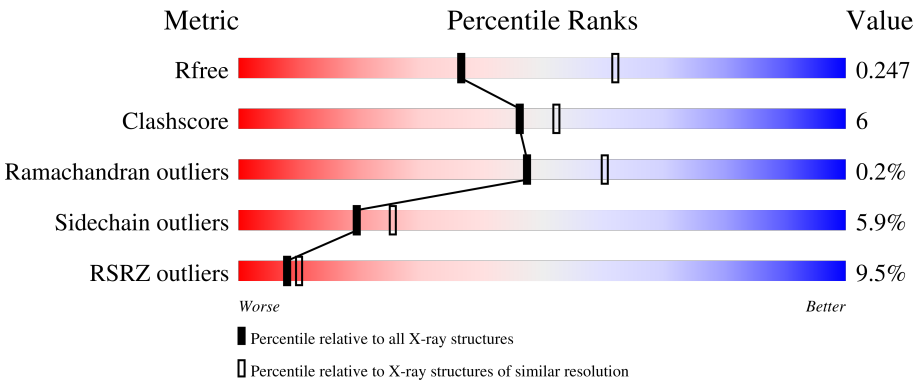
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	340	6% 75% 15% 10%
1	B	340	11% 75% 14% • 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	402	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4941 atoms, of which 71 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 tRNA-dihydrouridine synthase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	306	2326	1466	409	436	15	0	3	0
1	B	306	2275	1425	403	433	14	0	3	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP P0ABT7
A	-17	GLY	-	expression tag	UNP P0ABT7
A	-16	SER	-	expression tag	UNP P0ABT7
A	-15	SER	-	expression tag	UNP P0ABT7
A	-14	HIS	-	expression tag	UNP P0ABT7
A	-13	HIS	-	expression tag	UNP P0ABT7
A	-12	HIS	-	expression tag	UNP P0ABT7
A	-11	HIS	-	expression tag	UNP P0ABT7
A	-10	HIS	-	expression tag	UNP P0ABT7
A	-9	HIS	-	expression tag	UNP P0ABT7
A	-8	SER	-	expression tag	UNP P0ABT7
A	-7	SER	-	expression tag	UNP P0ABT7
A	-6	GLY	-	expression tag	UNP P0ABT7
A	-5	LEU	-	expression tag	UNP P0ABT7
A	-4	VAL	-	expression tag	UNP P0ABT7
A	-3	PRO	-	expression tag	UNP P0ABT7
A	-2	ARG	-	expression tag	UNP P0ABT7
A	-1	GLY	-	expression tag	UNP P0ABT7
A	0	SER	-	expression tag	UNP P0ABT7
B	-18	MET	-	initiating methionine	UNP P0ABT7
B	-17	GLY	-	expression tag	UNP P0ABT7
B	-16	SER	-	expression tag	UNP P0ABT7
B	-15	SER	-	expression tag	UNP P0ABT7
B	-14	HIS	-	expression tag	UNP P0ABT7
B	-13	HIS	-	expression tag	UNP P0ABT7

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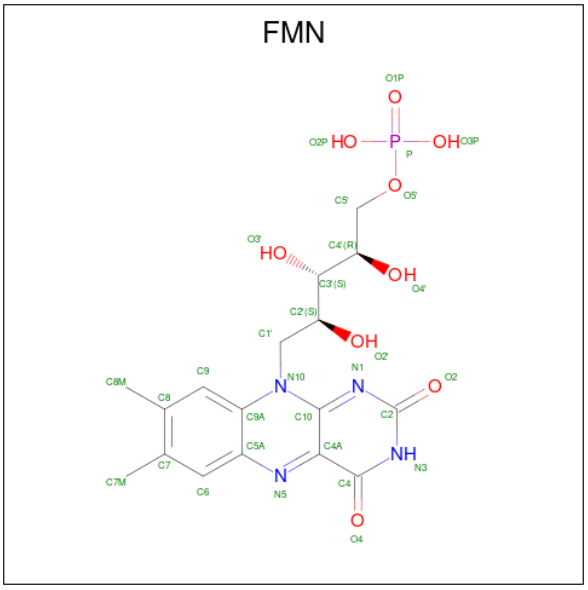
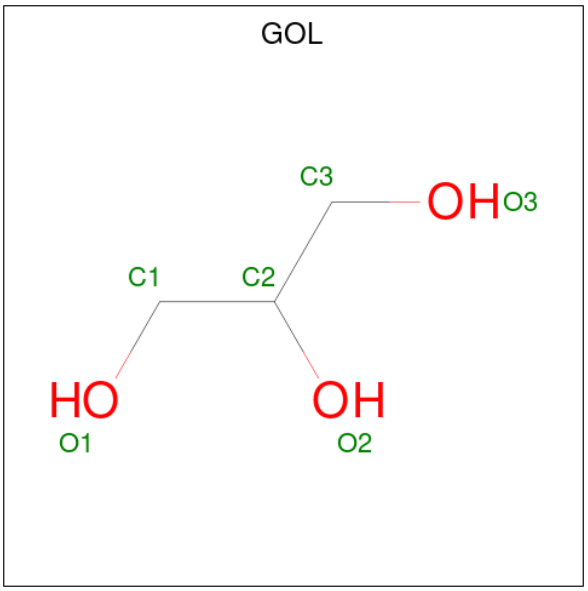
Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP P0ABT7
B	-11	HIS	-	expression tag	UNP P0ABT7
B	-10	HIS	-	expression tag	UNP P0ABT7
B	-9	HIS	-	expression tag	UNP P0ABT7
B	-8	SER	-	expression tag	UNP P0ABT7
B	-7	SER	-	expression tag	UNP P0ABT7
B	-6	GLY	-	expression tag	UNP P0ABT7
B	-5	LEU	-	expression tag	UNP P0ABT7
B	-4	VAL	-	expression tag	UNP P0ABT7
B	-3	PRO	-	expression tag	UNP P0ABT7
B	-2	ARG	-	expression tag	UNP P0ABT7
B	-1	GLY	-	expression tag	UNP P0ABT7
B	0	SER	-	expression tag	UNP P0ABT7

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



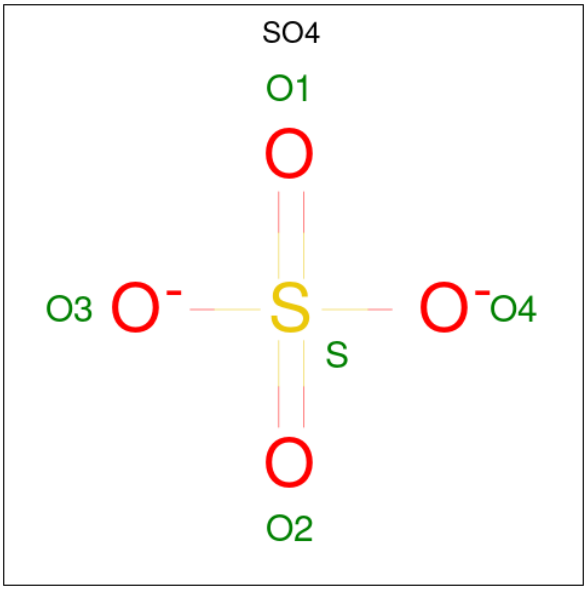
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	P		
2	A	1	50	17	19	4	9	1	0	0
			Total	C	H	N	O	P		
2	B	1	50	17	19	4	9	1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
4	A	1	5	4	1		0	0
			Total	O	S			
4	A	1	5	4	1		0	0

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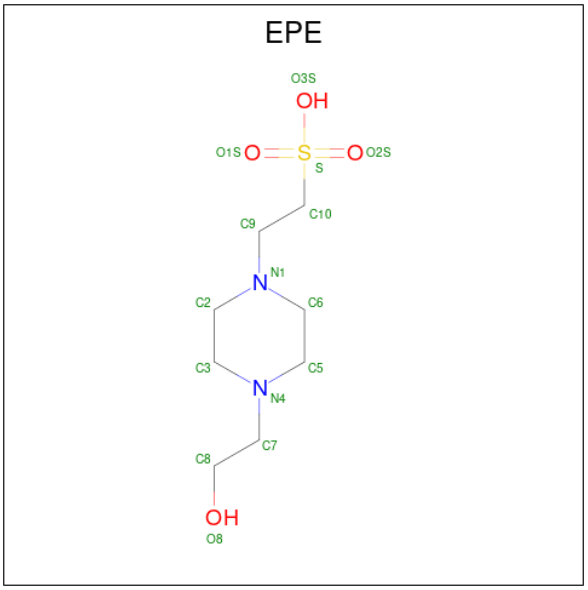
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	A	1	5	4	1	0	0
			Total	O	S		
4	A	1	5	4	1	0	0
			Total	O	S		
4	B	1	5	4	1	0	0
			Total	O	S		
4	B	1	5	4	1	0	0
			Total	O	S		
4	B	1	5	4	1	0	0
			Total	O	S		
4	B	1	5	4	1	0	0

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	S		
5	B	1	32	8	17	2	4	1	0	0

- Molecule 6 is water.

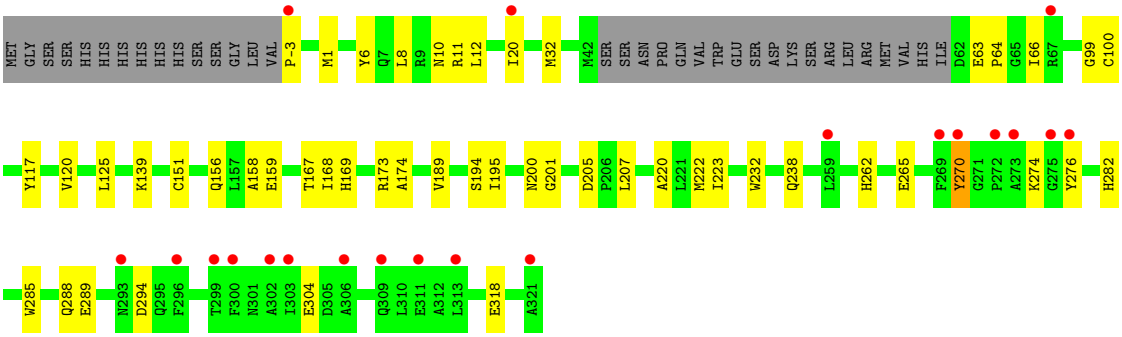
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	62	62	62	0	0
			Total	O		
6	B	78	78	78	0	0

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.

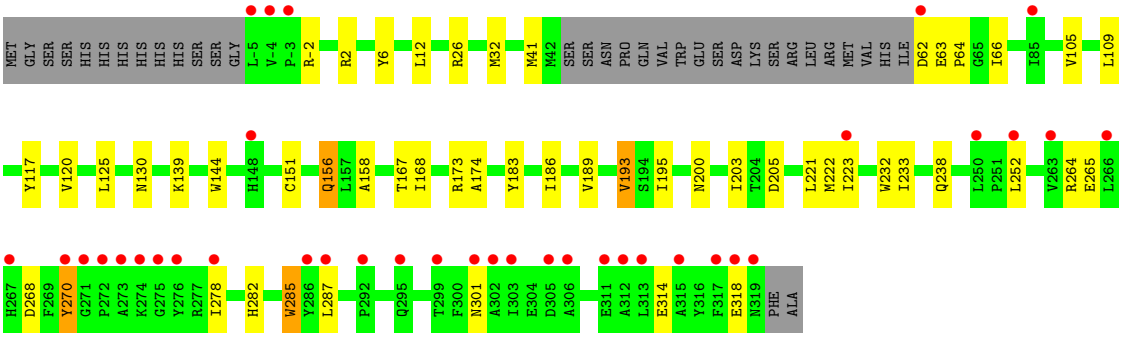
• Molecule 1: tRNA-dihydrouridine synthase B

Chain A:



• Molecule 1: tRNA-dihydrouridine synthase B

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	108.48Å 108.48Å 70.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.51 – 2.55 48.51 – 2.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.51-2.55) 99.9 (48.51-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	1.40 (at 2.54Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.198 , 0.238 0.204 , 0.247	Depositor DCC
R_{free} test set	1344 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	75.1	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 75.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4941	wwPDB-VP
Average B, all atoms (Å^2)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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, GOL, EPE, SO4

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	0.54	0/2381	0.76	2/3231 (0.1%)
1	B	0.55	0/2324	0.79	2/3163 (0.1%)
All	All	0.54	0/4705	0.77	4/6394 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	174[A]	ALA	CA-C-O	6.89	134.57	120.10
1	A	174[B]	ALA	CA-C-O	6.89	134.57	120.10
1	B	174[A]	ALA	CA-C-O	6.83	134.44	120.10
1	B	174[B]	ALA	CA-C-O	6.83	134.44	120.10

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	2326	0	2256	33	0
1	B	2275	0	2191	26	0
2	A	31	19	19	1	0
2	B	31	19	19	2	0
3	A	6	8	8	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	8	8	0	0
4	A	20	0	0	0	0
4	B	20	0	0	0	0
5	B	15	17	18	0	0
6	A	62	0	0	0	0
6	B	78	0	0	1	0
All	All	4870	71	4519	58	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 (58) 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:62:ASP:HB2	1:B:64:PRO:HD2	1.66	0.77
1:B:144:TRP:CE3	1:B:173:ARG:HG3	2.28	0.68
1:A:20:ILE:HG23	1:A:285:TRP:CH2	2.31	0.65
1:A:173:ARG:C	1:A:173:ARG:HD3	2.16	0.65
1:A:1:MET:HG2	1:A:8:LEU:HD12	1.79	0.63
1:A:207:LEU:HD22	1:B:183:TYR:CD2	2.36	0.61
1:B:282:HIS:HA	1:B:285:TRP:CD1	2.35	0.60
1:B:168:ILE:HD11	1:B:189:VAL:HG11	1.83	0.60
1:A:270:TYR:HB3	1:A:274:LYS:HD3	1.85	0.58
1:B:144:TRP:CZ3	1:B:173:ARG:HG3	2.40	0.57
1:B:12:LEU:HD22	1:B:238:GLN:HG2	1.87	0.56
1:A:63:GLU:HG2	1:A:64:PRO:HD2	1.87	0.56
1:B:156:GLN:HG3	6:B:536:HOH:O	2.05	0.56
1:B:117:TYR:HB2	1:B:120:VAL:HG12	1.88	0.56
1:A:10:ASN:HB2	1:A:238:GLN:NE2	2.21	0.55
1:A:117:TYR:HB2	1:A:120:VAL:HG12	1.89	0.55
1:B:144:TRP:O	1:B:173:ARG:HB3	2.08	0.54
1:B:32:MET:HB3	1:B:232:TRP:HA	1.90	0.54
1:A:100[B]:CYS:HA	3:A:402:GOL:H12	1.91	0.53
1:A:12:LEU:HD22	1:A:238:GLN:HG2	1.92	0.52
1:A:100[A]:CYS:HA	3:A:402:GOL:H12	1.91	0.52
1:B:270:TYR:CE1	1:B:278:ILE:HD13	2.45	0.51
1:A:139:LYS:NZ	3:A:402:GOL:H31	2.26	0.51
1:A:262:HIS:HE1	1:A:282:HIS:ND1	2.09	0.50
1:A:99:GLY:HA3	3:A:402:GOL:H32	1.93	0.49
1:A:200:ASN:HB2	1:A:222:MET:HB3	1.95	0.49
1:B:200:ASN:HD21	2:B:401:FMN:H5'1	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:ARG:HH21	1:B:62:ASP:HA	1.77	0.48
1:A:6:TYR:HB3	1:A:66:ILE:HD13	1.96	0.48
1:B:139:LYS:HD3	2:B:401:FMN:O2	2.14	0.47
1:A:-3:PRO:HB3	1:A:11:ARG:HE	1.80	0.47
1:A:32:MET:HB3	1:A:232:TRP:HA	1.97	0.47
1:B:6:TYR:HB3	1:B:66:ILE:HD13	1.97	0.46
1:B:26:ARG:HE	1:B:62:ASP:HB3	1.80	0.46
1:A:168:ILE:HD11	1:A:189:VAL:HG11	1.98	0.46
1:B:200:ASN:HB2	1:B:222:MET:HB3	1.96	0.46
1:A:159:GLU:OE2	1:A:194:SER:HB2	2.16	0.46
1:A:139:LYS:HE2	1:A:222:MET:SD	2.57	0.45
1:A:159:GLU:HG3	1:A:195:ILE:HG23	1.98	0.45
1:B:139:LYS:HG3	1:B:167:THR:HB	2.00	0.44
1:A:169:HIS:HD2	1:A:201:GLY:HA3	1.83	0.43
1:A:139:LYS:HZ2	3:A:402:GOL:C3	2.31	0.43
1:A:139:LYS:HD3	2:A:401:FMN:O2	2.19	0.43
1:A:11:ARG:HB3	1:A:220:ALA:HA	2.00	0.43
1:A:-3:PRO:HB3	1:A:11:ARG:HH21	1.85	0.41
1:A:139:LYS:HG3	1:A:167:THR:HB	2.02	0.41
1:A:169:HIS:CD2	1:A:201:GLY:HA3	2.55	0.41
1:B:193:VAL:HG13	1:B:195:ILE:HG12	2.03	0.41
1:A:276:TYR:CE1	1:A:304:GLU:HA	2.56	0.41
1:B:-2:ARG:HA	1:B:2:ARG:HH12	1.85	0.41
1:B:125:LEU:HD13	1:B:158:ALA:HA	2.03	0.41
1:B:264:ARG:O	1:B:268:ASP:OD2	2.38	0.41
1:A:139:LYS:NZ	3:A:402:GOL:C3	2.84	0.41
1:B:168:ILE:HB	1:B:186:ILE:HG12	2.02	0.41
1:A:99:GLY:HA3	3:A:402:GOL:C3	2.51	0.40
1:B:63:GLU:N	1:B:64:PRO:CD	2.84	0.40
1:B:203:ILE:HD13	1:B:221:LEU:HD22	2.03	0.40
1:A:125:LEU:HD13	1:A:158:ALA:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	305/340 (90%)	294 (96%)	11 (4%)	0	100	100
1	B	305/340 (90%)	290 (95%)	14 (5%)	1 (0%)	41	51
All	All	610/680 (90%)	584 (96%)	25 (4%)	1 (0%)	47	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	41	MET

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	236/280 (84%)	226 (96%)	10 (4%)	30	40
1	B	227/280 (81%)	210 (92%)	17 (8%)	13	17
All	All	463/560 (83%)	436 (94%)	27 (6%)	19	26

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	151	CYS
1	A	156	GLN
1	A	205	ASP
1	A	223	ILE
1	A	265	GLU
1	A	270	TYR
1	A	288	GLN
1	A	289	GLU
1	A	294	ASP
1	A	318	GLU
1	B	105	VAL
1	B	109	LEU

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Mol	Chain	Res	Type
1	B	130	ASN
1	B	151	CYS
1	B	156	GLN
1	B	193	VAL
1	B	205	ASP
1	B	223	ILE
1	B	233	ILE
1	B	252	LEU
1	B	265	GLU
1	B	270	TYR
1	B	285	TRP
1	B	287	LEU
1	B	301	ASN
1	B	314	GLU
1	B	318	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	A	169	HIS
1	A	178	ASN
1	A	238	GLN
1	A	262	HIS
1	A	290	HIS
1	B	116	GLN
1	B	178	ASN
1	B	191	GLN
1	B	200	ASN
1	B	290	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)

13 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	SO4	B	404	-	4,4,4	0.27	0	6,6,6	0.20	0
4	SO4	A	406	-	4,4,4	0.26	0	6,6,6	0.08	0
5	EPE	B	407	-	15,15,15	2.05	1 (6%)	19,20,20	1.13	1 (5%)
4	SO4	A	405	-	4,4,4	0.31	0	6,6,6	0.09	0
3	GOL	A	402	-	5,5,5	0.65	0	5,5,5	0.49	0
3	GOL	B	402	-	5,5,5	0.46	0	5,5,5	0.51	0
4	SO4	A	404	-	4,4,4	0.30	0	6,6,6	0.11	0
4	SO4	B	406	-	4,4,4	0.30	0	6,6,6	0.13	0
2	FMN	A	401	-	33,33,33	1.51	3 (9%)	48,50,50	1.66	11 (22%)
4	SO4	B	403	-	4,4,4	0.33	0	6,6,6	0.63	0
2	FMN	B	401	-	33,33,33	1.62	5 (15%)	48,50,50	1.42	11 (22%)
4	SO4	A	403	-	4,4,4	0.30	0	6,6,6	0.20	0
4	SO4	B	405	-	4,4,4	0.27	0	6,6,6	0.08	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	EPE	B	407	-	-	2/9/19/19	0/1/1/1
3	GOL	A	402	-	-	2/4/4/4	-
3	GOL	B	402	-	-	4/4/4/4	-
2	FMN	A	401	-	-	10/18/18/18	0/3/3/3
2	FMN	B	401	-	-	4/18/18/18	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	407	EPE	C10-S	-7.53	1.67	1.77
2	B	401	FMN	C9A-C5A	5.63	1.50	1.41
2	A	401	FMN	C9A-C5A	4.89	1.49	1.41
2	A	401	FMN	C8-C7	3.95	1.50	1.40
2	B	401	FMN	C8-C7	3.56	1.49	1.40
2	B	401	FMN	C4-N3	-2.69	1.33	1.38
2	A	401	FMN	C4A-N5	2.43	1.36	1.30
2	B	401	FMN	C4A-N5	2.32	1.35	1.30
2	B	401	FMN	C10-N10	2.24	1.42	1.37

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	FMN	C4-C4A-N5	4.83	124.88	118.21
2	B	401	FMN	C4-C4A-N5	3.97	123.69	118.21
2	A	401	FMN	O2'-C2'-C3'	3.49	117.42	109.25
2	A	401	FMN	O2-C2-N1	-2.99	116.84	121.80
2	A	401	FMN	C5A-N5-C4A	2.82	122.66	118.09
2	B	401	FMN	C5'-C4'-C3'	-2.73	107.07	112.22
2	B	401	FMN	C4A-C10-N1	-2.53	118.38	124.59
2	A	401	FMN	C10-C4A-N5	-2.52	119.66	124.81
2	A	401	FMN	C10-N1-C2	2.50	122.27	116.85
2	B	401	FMN	C10-N1-C2	2.45	122.15	116.85
2	B	401	FMN	O4'-C4'-C5'	2.43	115.34	109.99
2	B	401	FMN	C4A-C10-N10	2.40	119.92	116.48
2	A	401	FMN	O4'-C4'-C3'	-2.34	103.77	109.25
2	A	401	FMN	O3P-P-O5'	-2.27	100.74	106.67
2	A	401	FMN	O4-C4-C4A	-2.18	120.77	126.53
2	B	401	FMN	O3P-P-O5'	-2.17	101.00	106.67
2	B	401	FMN	C10-C4A-N5	-2.15	120.42	124.81
2	B	401	FMN	C4A-C4-N3	2.11	118.62	113.25
2	B	401	FMN	O5'-C5'-C4'	2.06	114.86	109.36
2	A	401	FMN	C9A-C5A-N5	-2.05	120.27	122.45
2	B	401	FMN	O2-C2-N1	-2.01	118.46	121.80
2	A	401	FMN	C4'-C3'-C2'	-2.01	110.22	113.57
5	B	407	EPE	O1S-S-C10	2.00	109.75	106.73

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	FMN	N10-C1'-C2'-O2'
2	A	401	FMN	N10-C1'-C2'-C3'
2	A	401	FMN	C1'-C2'-C3'-O3'
2	A	401	FMN	C1'-C2'-C3'-C4'
2	A	401	FMN	O2'-C2'-C3'-O3'
2	A	401	FMN	O2'-C2'-C3'-C4'
2	A	401	FMN	C5'-O5'-P-O1P
2	A	401	FMN	C5'-O5'-P-O2P
2	A	401	FMN	C5'-O5'-P-O3P
2	B	401	FMN	C3'-C4'-C5'-O5'
2	B	401	FMN	O4'-C4'-C5'-O5'
3	B	402	GOL	O2-C2-C3-O3
2	A	401	FMN	C4'-C5'-O5'-P
3	B	402	GOL	O1-C1-C2-C3
3	B	402	GOL	C1-C2-C3-O3
2	B	401	FMN	C4'-C5'-O5'-P
3	A	402	GOL	O2-C2-C3-O3
2	B	401	FMN	C2'-C3'-C4'-O4'
5	B	407	EPE	N4-C7-C8-O8
3	B	402	GOL	O1-C1-C2-O2
3	A	402	GOL	C1-C2-C3-O3
5	B	407	EPE	C9-C10-S-O2S

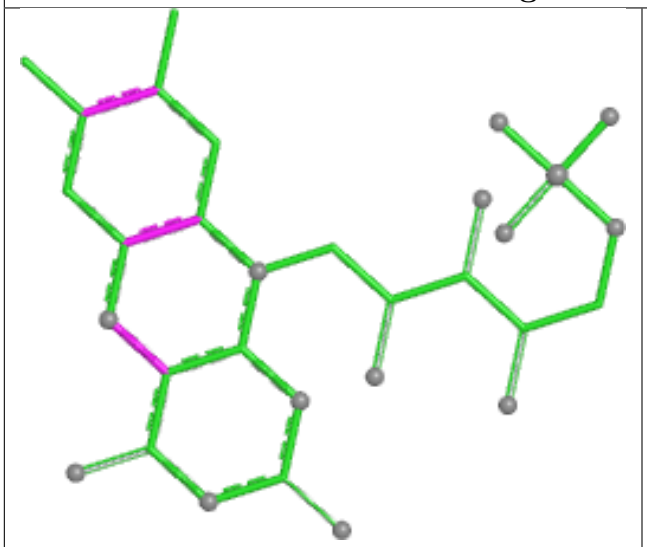
There are no ring outliers.

3 monomers are involved in 10 short contacts:

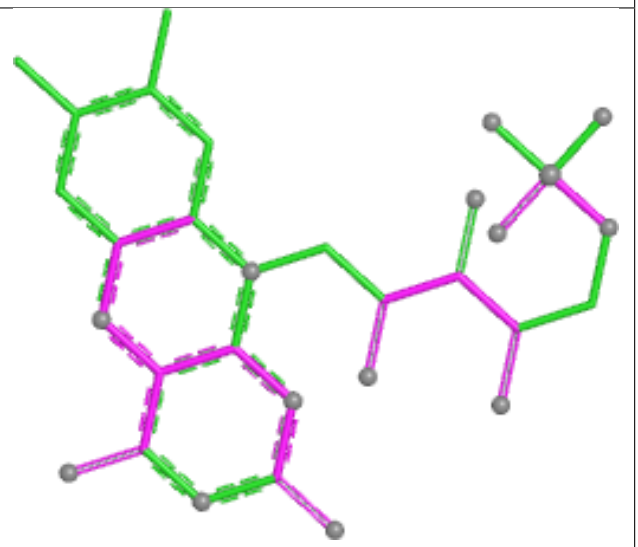
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	GOL	7	0
2	A	401	FMN	1	0
2	B	401	FMN	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

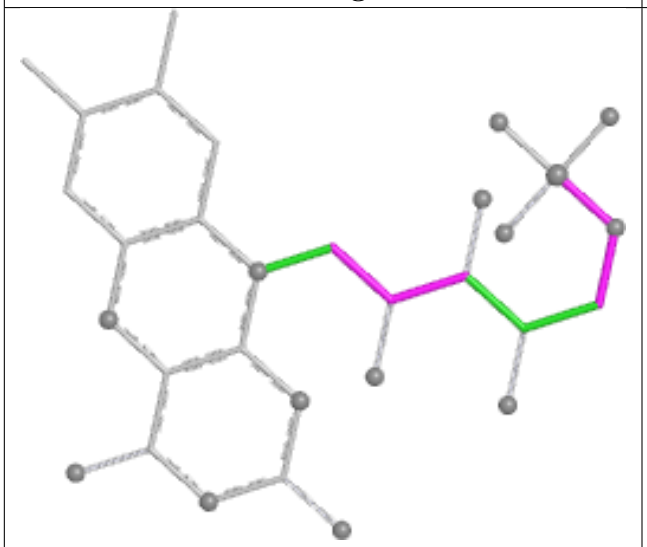
Ligand FMN A 401



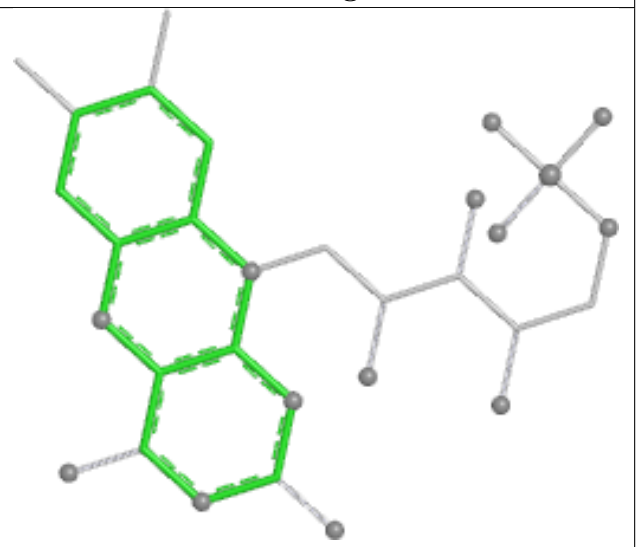
Bond lengths



Bond angles

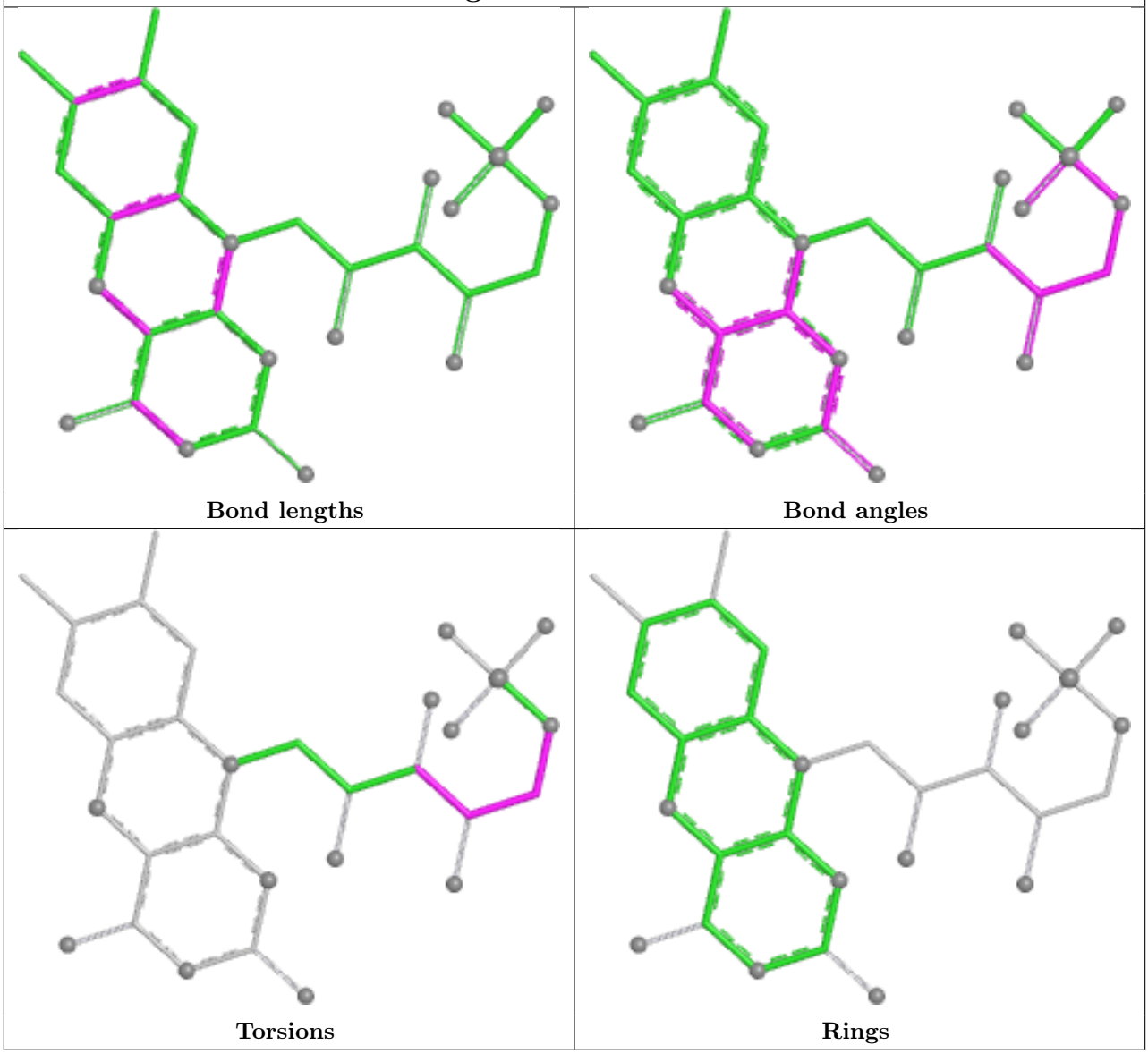


Torsions



Rings

Ligand FMN B 401



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	306/340 (90%)	0.45	21 (6%) 16 20	56, 88, 133, 155	0
1	B	306/340 (90%)	0.66	37 (12%) 4 5	52, 80, 182, 214	0
All	All	612/680 (90%)	0.56	58 (9%) 8 10	52, 84, 153, 214	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	273	ALA	8.3
1	B	302	ALA	7.6
1	B	313	LEU	7.4
1	B	272	PRO	7.0
1	A	270	TYR	6.0
1	B	275	GLY	5.4
1	B	303	ILE	4.9
1	B	299	THR	4.7
1	A	321	ALA	4.7
1	B	287	LEU	4.6
1	B	286	TYR	4.3
1	B	266	LEU	4.2
1	A	302	ALA	4.0
1	A	273	ALA	3.9
1	A	303	ILE	3.9
1	B	-3	PRO	3.9
1	B	-4	VAL	3.8
1	A	272	PRO	3.8
1	A	-3	PRO	3.7
1	B	301	ASN	3.6
1	B	276	TYR	3.6
1	A	276	TYR	3.5
1	B	270	TYR	3.4
1	A	311	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	274	LYS	3.2
1	A	306	ALA	3.2
1	A	296	PHE	3.1
1	B	312	ALA	3.1
1	B	263	VAL	2.9
1	B	306	ALA	2.9
1	B	292	PRO	2.9
1	A	20	ILE	2.8
1	B	315	ALA	2.7
1	B	267	HIS	2.6
1	A	293	ASN	2.6
1	B	85	ILE	2.5
1	B	-5	LEU	2.5
1	A	275	GLY	2.5
1	B	278	ILE	2.5
1	B	305	ASP	2.5
1	A	67	ARG	2.4
1	B	271	GLY	2.4
1	B	318	GLU	2.4
1	A	259	LEU	2.4
1	B	250	LEU	2.3
1	A	313	LEU	2.3
1	A	300	PHE	2.3
1	B	295	GLN	2.3
1	A	299	THR	2.2
1	B	319	ASN	2.2
1	B	311	GLU	2.1
1	B	223	ILE	2.1
1	A	309	GLN	2.1
1	B	317	PHE	2.1
1	B	148	HIS	2.1
1	B	252	LEU	2.1
1	A	269	PHE	2.0
1	B	62	ASP	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)

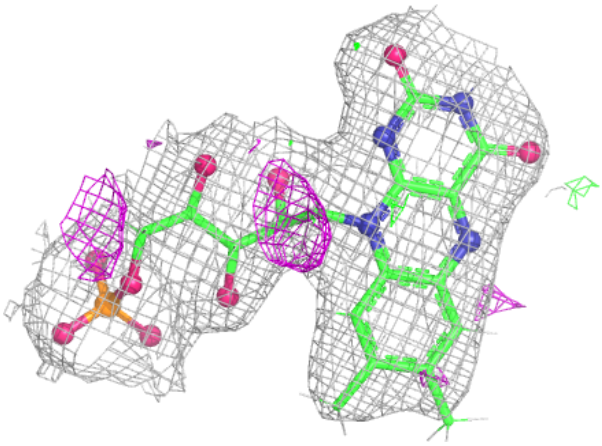
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

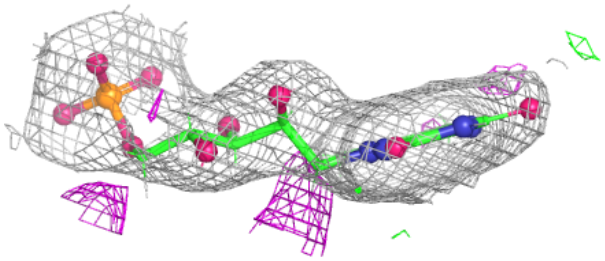
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	B	402	6/6	0.59	0.34	109,114,121,122	0
5	EPE	B	407	15/15	0.59	0.34	181,186,190,191	0
4	SO4	B	405	5/5	0.74	0.30	173,173,175,175	0
4	SO4	B	406	5/5	0.81	0.47	171,173,174,178	0
4	SO4	A	403	5/5	0.81	0.27	161,161,162,165	0
4	SO4	A	406	5/5	0.82	0.37	200,201,205,205	0
4	SO4	A	405	5/5	0.82	0.22	180,182,182,185	0
4	SO4	A	404	5/5	0.86	0.35	169,171,172,175	0
4	SO4	B	404	5/5	0.87	0.21	123,127,127,131	0
3	GOL	A	402	6/6	0.93	0.27	75,76,79,79	0
2	FMN	A	401	31/31	0.95	0.17	63,72,80,82	0
4	SO4	B	403	5/5	0.95	0.28	118,118,120,120	0
2	FMN	B	401	31/31	0.96	0.17	59,63,72,74	0

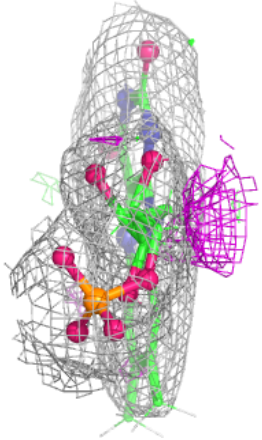
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FMN A 401:

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

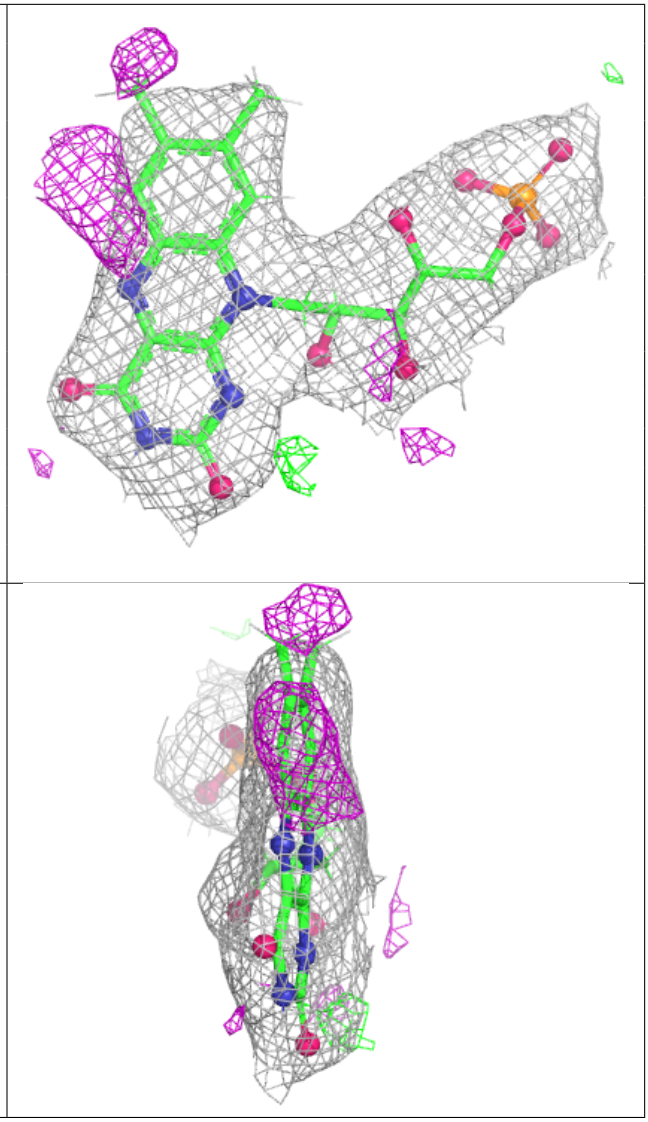






Electron density around FMN B 401:

$2mF_o$-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.