



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:50 PM UTC

PDB ID : 6I55 / pdb_00006i55
Title : Plasmodium falciparum dihydroorotate dehydrogenase (DHODH) co-crystallized with N-(2,2-Diphenylethyl)-4-hydroxy-1,2,5-thiadiazole-3-carboxamide
Authors : Goyal, P.; Sainas, S.; Pippione, A.C.; Boschi, D.; Al-Kadaraghi, S.
Deposited on : 2018-11-12
Resolution : 1.98 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

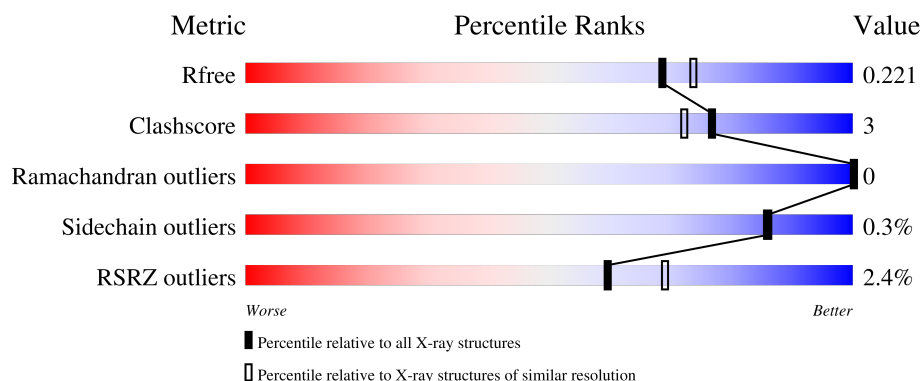
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	405	2% 86% 7% 6%
1	B	405	2% 84% 7% 9%

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	ORO	A	602	-	X	-	-
3	ORO	B	603	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6401 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Dihydroorotate dehydrogenase (quinone), mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			3005	1919	503	568	15			
1	B	368	Total	C	N	O	S	0	1	0
			2922	1871	488	549	14			

There are 106 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	135	MET	-	initiating methionine	UNP Q08210
A	136	HIS	-	expression tag	UNP Q08210
A	137	HIS	-	expression tag	UNP Q08210
A	138	HIS	-	expression tag	UNP Q08210
A	139	HIS	-	expression tag	UNP Q08210
A	140	HIS	-	expression tag	UNP Q08210
A	141	HIS	-	expression tag	UNP Q08210
A	142	SER	-	expression tag	UNP Q08210
A	143	SER	-	expression tag	UNP Q08210
A	144	GLY	-	expression tag	UNP Q08210
A	145	VAL	-	expression tag	UNP Q08210
A	146	ASP	-	expression tag	UNP Q08210
A	147	LEU	-	expression tag	UNP Q08210
A	148	GLY	-	expression tag	UNP Q08210
A	149	THR	-	expression tag	UNP Q08210
A	150	GLU	-	expression tag	UNP Q08210
A	151	ASN	-	expression tag	UNP Q08210
A	152	LEU	-	expression tag	UNP Q08210
A	153	TYR	-	expression tag	UNP Q08210
A	154	PHE	-	expression tag	UNP Q08210
A	155	GLN	-	expression tag	UNP Q08210
A	156	SER	-	expression tag	UNP Q08210
A	157	MET	-	expression tag	UNP Q08210
A	?	-	SER	deletion	UNP Q08210
A	?	-	THR	deletion	UNP Q08210

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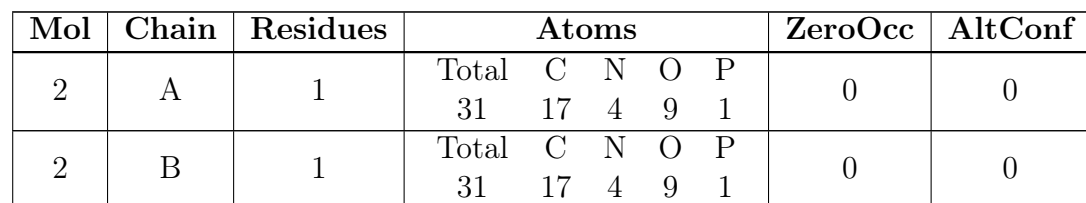
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	TYR	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	GLU	deletion	UNP Q08210
A	?	-	ASP	deletion	UNP Q08210
A	?	-	ASN	deletion	UNP Q08210
A	?	-	LYS	deletion	UNP Q08210
A	?	-	ILE	deletion	UNP Q08210
A	?	-	VAL	deletion	UNP Q08210
A	?	-	GLU	deletion	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
B	135	MET	-	initiating methionine	UNP Q08210
B	136	HIS	-	expression tag	UNP Q08210
B	137	HIS	-	expression tag	UNP Q08210
B	138	HIS	-	expression tag	UNP Q08210
B	139	HIS	-	expression tag	UNP Q08210
B	140	HIS	-	expression tag	UNP Q08210
B	141	HIS	-	expression tag	UNP Q08210
B	142	SER	-	expression tag	UNP Q08210
B	143	SER	-	expression tag	UNP Q08210
B	144	GLY	-	expression tag	UNP Q08210
B	145	VAL	-	expression tag	UNP Q08210
B	146	ASP	-	expression tag	UNP Q08210
B	147	LEU	-	expression tag	UNP Q08210
B	148	GLY	-	expression tag	UNP Q08210

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Chain	Residue	Modelled	Actual	Comment	Reference
B	149	THR	-	expression tag	UNP Q08210
B	150	GLU	-	expression tag	UNP Q08210
B	151	ASN	-	expression tag	UNP Q08210
B	152	LEU	-	expression tag	UNP Q08210
B	153	TYR	-	expression tag	UNP Q08210
B	154	PHE	-	expression tag	UNP Q08210
B	155	GLN	-	expression tag	UNP Q08210
B	156	SER	-	expression tag	UNP Q08210
B	157	MET	-	expression tag	UNP Q08210
B	?	-	SER	deletion	UNP Q08210
B	?	-	THR	deletion	UNP Q08210
B	?	-	TYR	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210
B	?	-	GLU	deletion	UNP Q08210
B	?	-	ASP	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210
B	?	-	LYS	deletion	UNP Q08210
B	?	-	ILE	deletion	UNP Q08210
B	?	-	VAL	deletion	UNP Q08210
B	?	-	GLU	deletion	UNP Q08210
B	?	-	LYS	deletion	UNP Q08210
B	?	-	LYS	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210
B	?	-	PHE	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210
B	?	-	LYS	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210
B	?	-	SER	deletion	UNP Q08210
B	?	-	HIS	deletion	UNP Q08210
B	?	-	MET	deletion	UNP Q08210
B	?	-	MET	deletion	UNP Q08210
B	?	-	LYS	deletion	UNP Q08210
B	?	-	ASP	deletion	UNP Q08210
B	?	-	ALA	deletion	UNP Q08210
B	?	-	LYS	deletion	UNP Q08210
B	?	-	ASP	deletion	UNP Q08210
B	?	-	ASN	deletion	UNP Q08210

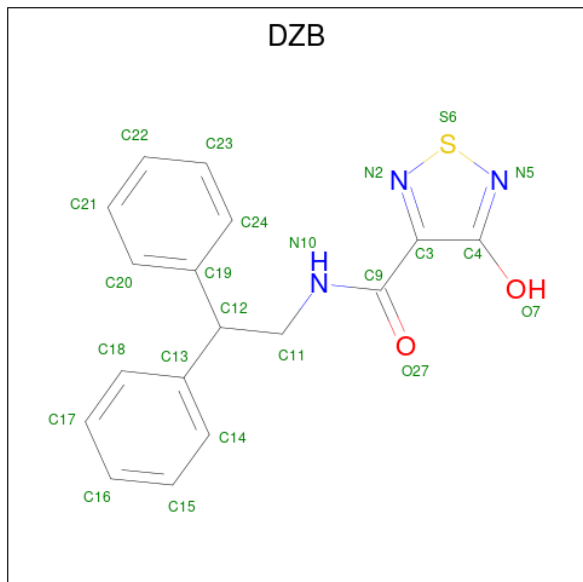
- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).



-
- Chemical structure of Orothione (ORO) is shown. The structure features a pyrimidine ring with a carboxylic acid group at position 6 and a thioamide group at position 2. The atoms are labeled as follows: N1 (blue), N3 (blue), C2 (green), C4 (green), C5 (green), C6 (green), O71 (red), O72 (red), O2 (red), and O4 (red).

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

- Molecule 4 is N-(2,2-Diphenylethyl)-4-hydroxy-1,2,5-thiadiazole-3-carboxamide (CCD ID: DZB) (formula: C₁₇H₁₅N₃O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			23	17	3	2	1		
4	B	1	Total	C	N	O	S	0	0
			23	17	3	2	1		

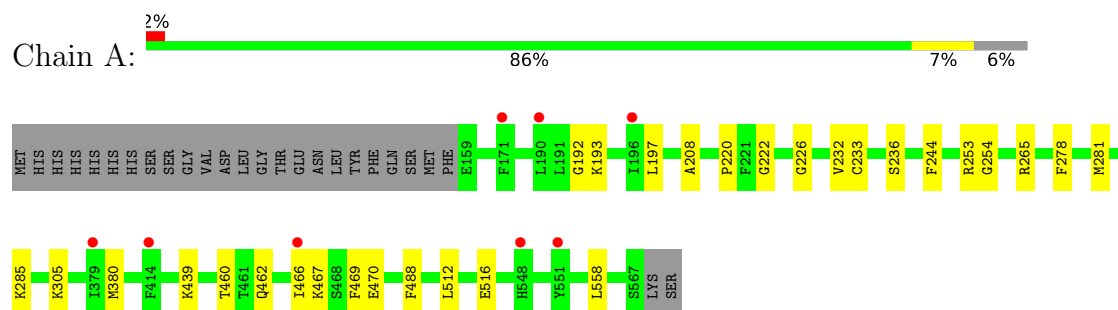
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	157	Total	O	0	0
			157	157		
5	B	187	Total	O	0	0
			187	187		

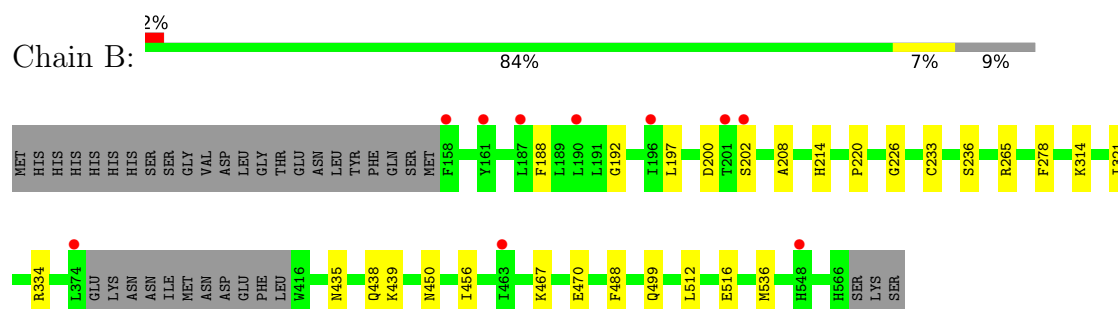
3 Residue-property plots [i](#)

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



- Molecule 1: Dihydroorotate dehydrogenase (quinone), mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.84Å 158.42Å 62.25Å 90.00° 106.56° 90.00°	Depositor
Resolution (Å)	48.73 – 1.98 48.73 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.73-1.98) 99.3 (48.73-1.98)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 1.98Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.173 , 0.218 0.176 , 0.221	Depositor DCC
R_{free} test set	3342 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	38.9	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6401	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.05% 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: DZB, ORO, 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	0.31	0/3056	0.47	0/4115
1	B	0.32	0/2975	0.50	0/4005
All	All	0.32	0/6031	0.48	0/8120

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

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	3005	0	3042	18	0
1	B	2922	0	2964	19	0
2	A	31	0	19	1	0
2	B	31	0	19	1	0
3	A	11	0	3	1	0
3	B	11	0	3	1	0
4	A	23	0	0	0	0
4	B	23	0	0	0	0
5	A	157	0	0	1	0
5	B	187	0	0	4	0
All	All	6401	0	6050	35	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 3.

The worst 5 of 35 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:467:LYS:O	1:B:470:GLU:HG3	1.94	0.67
1:A:197:LEU:HD12	1:A:236:SER:HB3	1.81	0.62
1:A:466:ILE:HG23	1:A:469:PHE:HB2	1.82	0.60
1:A:512:LEU:O	1:A:516:GLU:HG3	2.03	0.59
1:B:197:LEU:HD12	1:B:236:SER:HB3	1.88	0.55

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	377/405 (93%)	371 (98%)	6 (2%)	0	100	100
1	B	365/405 (90%)	354 (97%)	11 (3%)	0	100	100
All	All	742/810 (92%)	725 (98%)	17 (2%)	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	336/360 (93%)	335 (100%)	1 (0%)	86	86
1	B	326/360 (91%)	325 (100%)	1 (0%)	86	86
All	All	662/720 (92%)	660 (100%)	2 (0%)	86	86

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	265	ARG
1	B	265	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	499	GLN
1	B	552	GLN

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 ⓘ

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
2	FMN	A	601	-	33,33,33	2.69	10 (30%)	48,50,50	1.67	8 (16%)
3	ORO	B	603	-	11,11,11	3.03	7 (63%)	14,15,15	2.82	7 (50%)
4	DZB	B	601	-	25,25,25	2.58	8 (32%)	33,33,33	1.44	4 (12%)
4	DZB	A	603	-	25,25,25	2.58	9 (36%)	33,33,33	1.46	4 (12%)
2	FMN	B	602	-	33,33,33	2.62	10 (30%)	48,50,50	1.80	9 (18%)
3	ORO	A	602	-	11,11,11	2.99	7 (63%)	14,15,15	2.62	7 (50%)

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	601	-	-	1/18/18/18	0/3/3/3
3	ORO	B	603	-	-	2/4/4/4	0/1/1/1
4	DZB	B	601	-	-	2/17/17/17	0/3/3/3
4	DZB	A	603	-	-	2/17/17/17	0/3/3/3
2	FMN	B	602	-	-	1/18/18/18	0/3/3/3
3	ORO	A	602	-	-	4/4/4/4	0/1/1/1

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	601	DZB	C9-N10	7.38	1.46	1.33
4	A	603	DZB	C9-N10	6.73	1.45	1.33
2	A	601	FMN	C4A-N5	6.63	1.45	1.30
2	B	602	FMN	C4A-N5	6.38	1.44	1.30
2	A	601	FMN	C10-N1	6.14	1.45	1.33

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	FMN	C7M-C7-C6	-6.51	108.10	119.57
2	A	601	FMN	C7M-C7-C6	-6.16	108.72	119.57
4	A	603	DZB	N5-S6-N2	5.90	107.42	100.70
4	B	601	DZB	N5-S6-N2	5.49	106.96	100.70
2	B	602	FMN	C7M-C7-C8	5.45	131.89	120.76

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

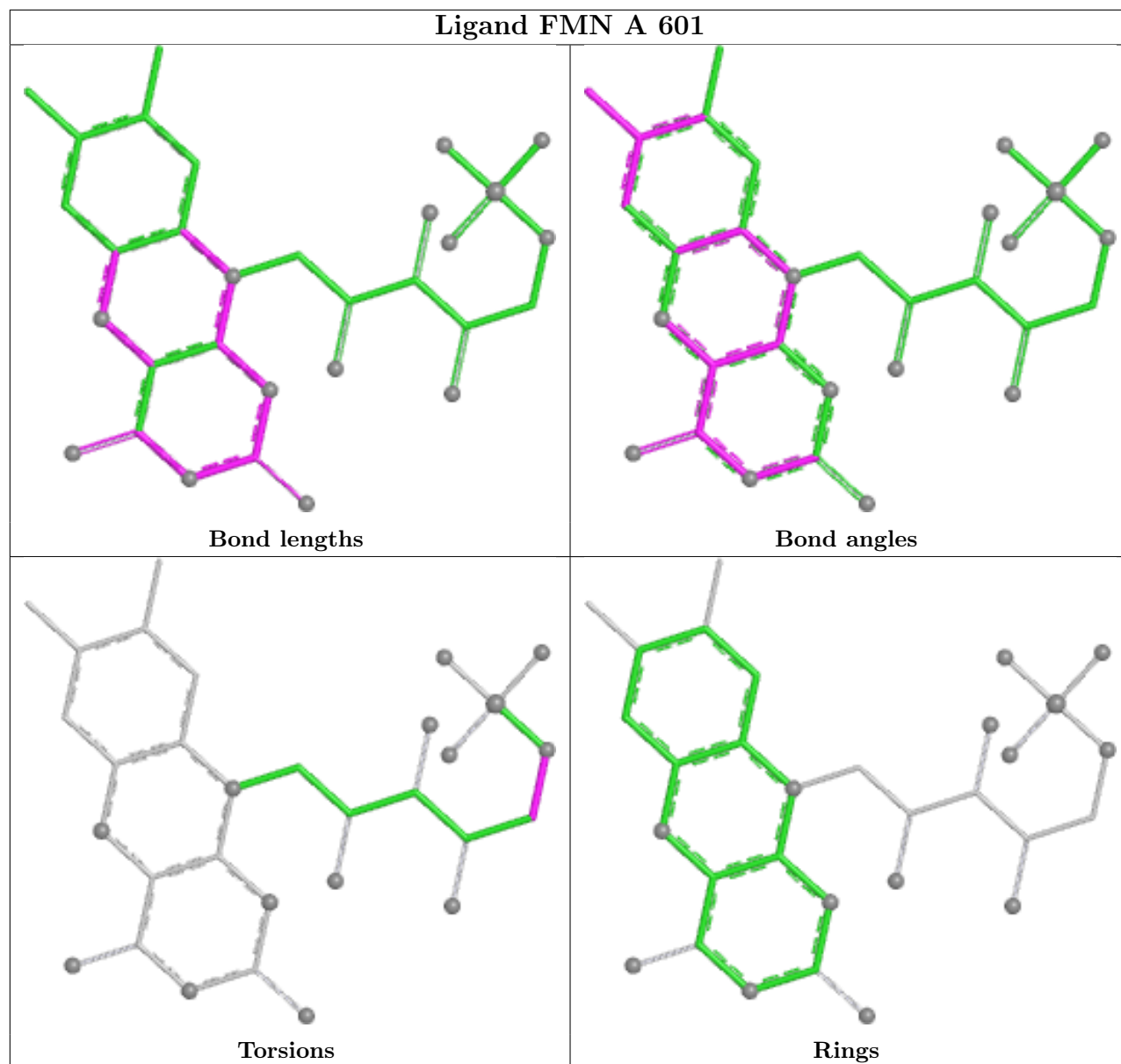
Mol	Chain	Res	Type	Atoms
3	A	602	ORO	N1-C6-C7-O71
3	A	602	ORO	N1-C6-C7-O72
3	A	602	ORO	C5-C6-C7-O71
3	A	602	ORO	C5-C6-C7-O72
3	B	603	ORO	N1-C6-C7-O71

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	FMN	1	0
3	B	603	ORO	1	0
2	B	602	FMN	1	0
3	A	602	ORO	1	0

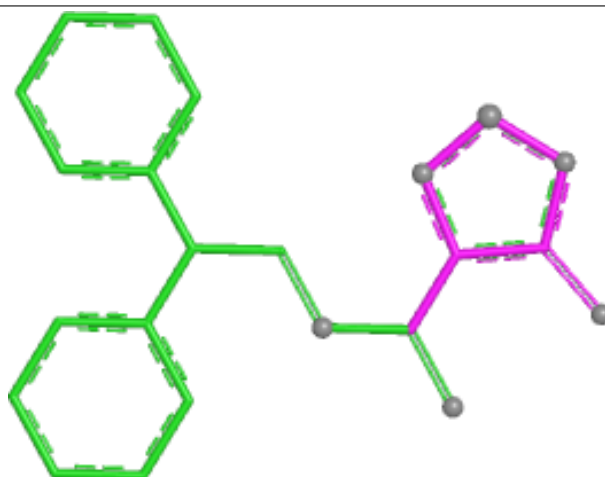
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



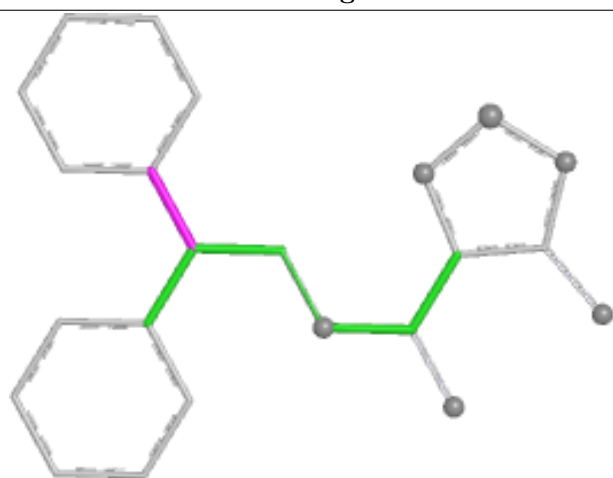
Ligand DZB B 601



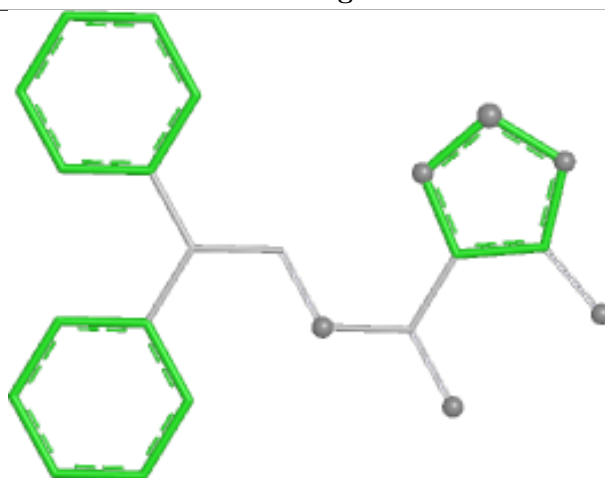
Bond lengths



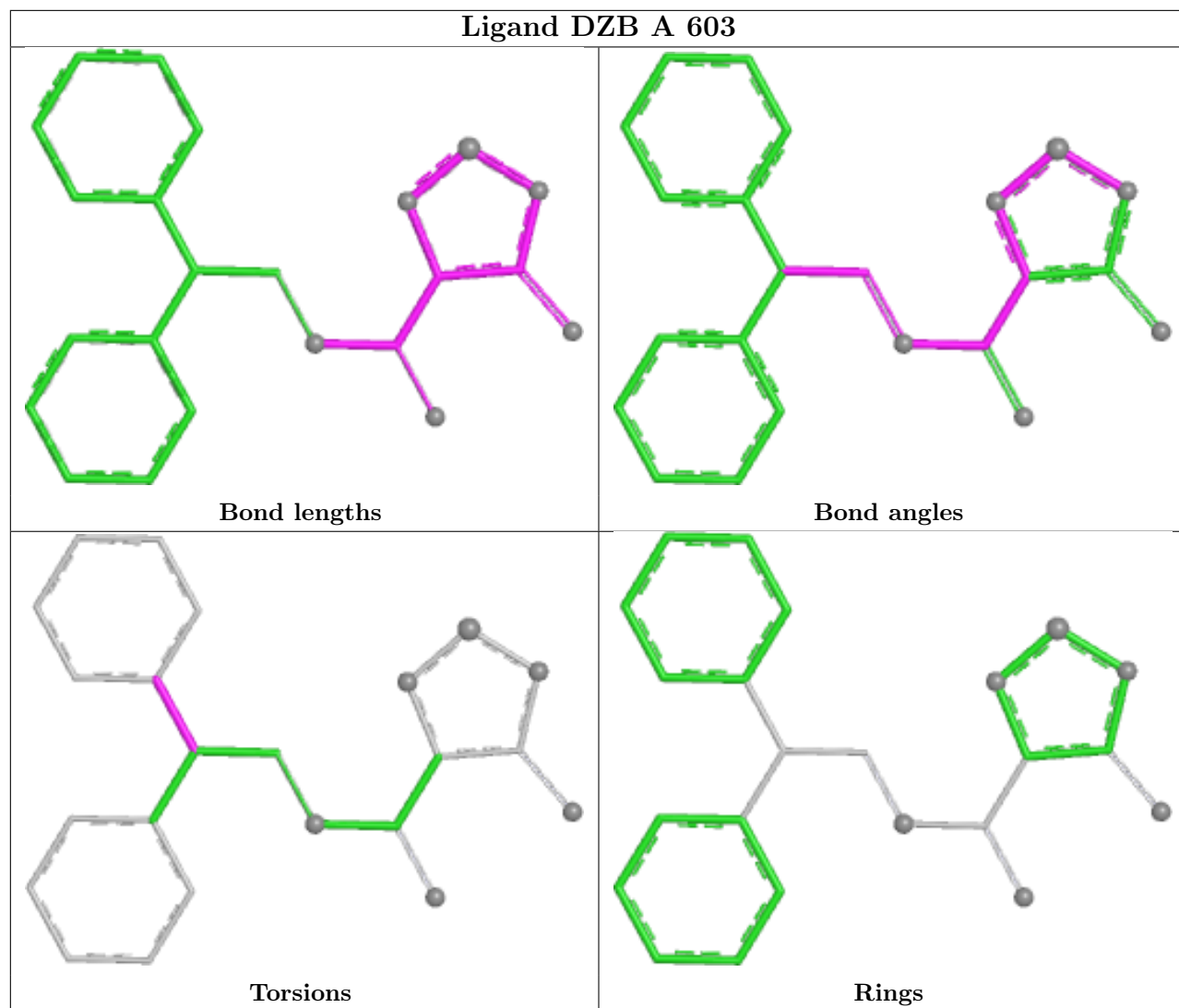
Bond angles

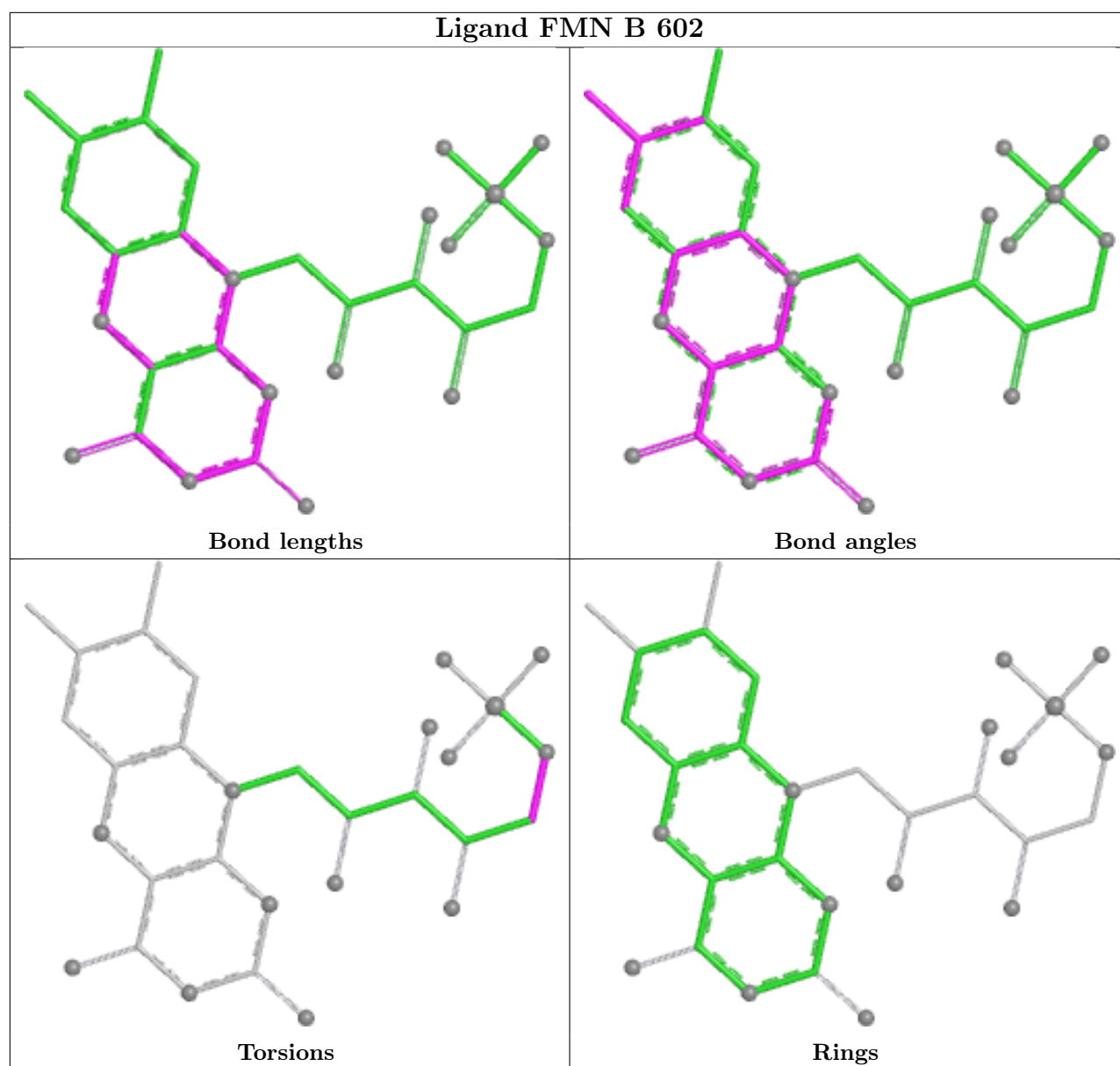


Torsions



Rings





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	379/405 (93%)	0.21	8 (2%) 63 72	33, 47, 78, 101	0
1	B	368/405 (90%)	0.14	10 (2%) 56 66	30, 44, 73, 104	1 (0%)
All	All	747/810 (92%)	0.18	18 (2%) 59 69	30, 46, 76, 104	1 (0%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	201	THR	4.7
1	B	158	PHE	4.0
1	A	466	ILE	3.6
1	A	190	LEU	3.4
1	A	551	TYR	3.3

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](#)

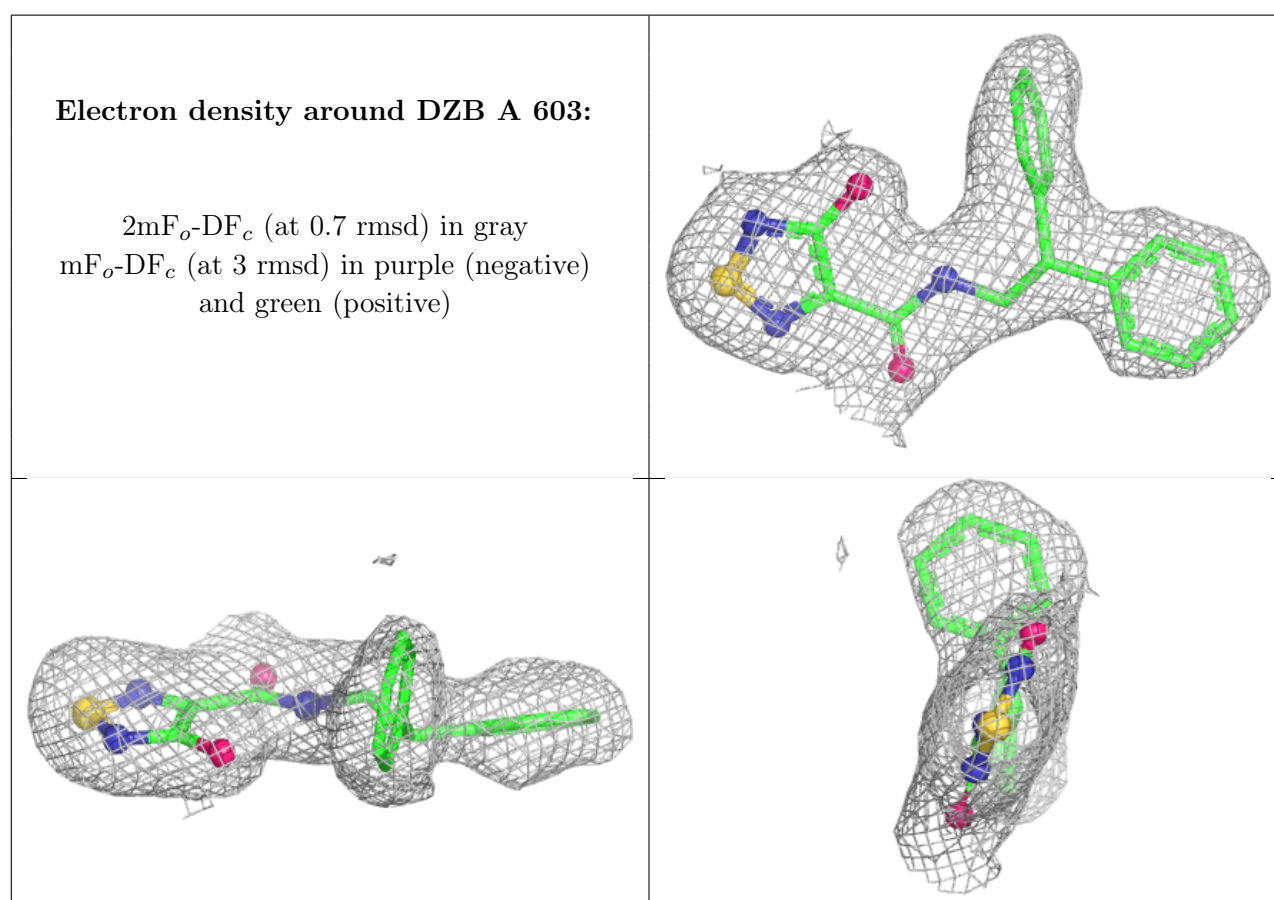
There are no oligosaccharides in this entry.

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.

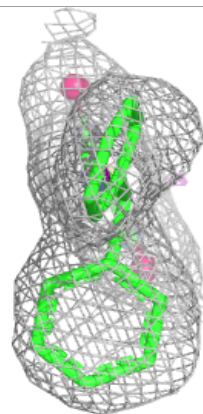
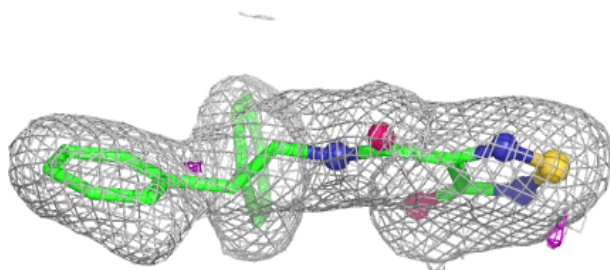
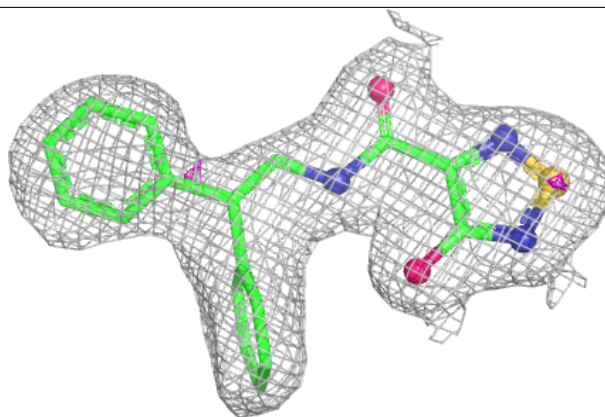
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	DZB	A	603	23/23	0.96	0.10	46,60,82,84	0
4	DZB	B	601	23/23	0.96	0.09	42,56,63,64	0
3	ORO	A	602	11/11	0.97	0.06	35,41,48,48	0
3	ORO	B	603	11/11	0.97	0.05	34,38,45,46	0
2	FMN	A	601	31/31	0.97	0.07	34,39,43,45	0
2	FMN	B	602	31/31	0.97	0.07	30,35,38,40	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.



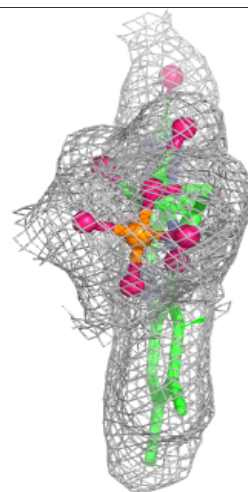
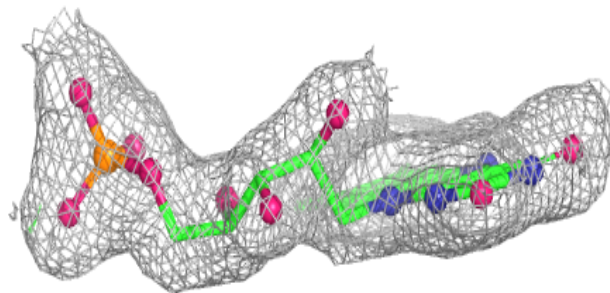
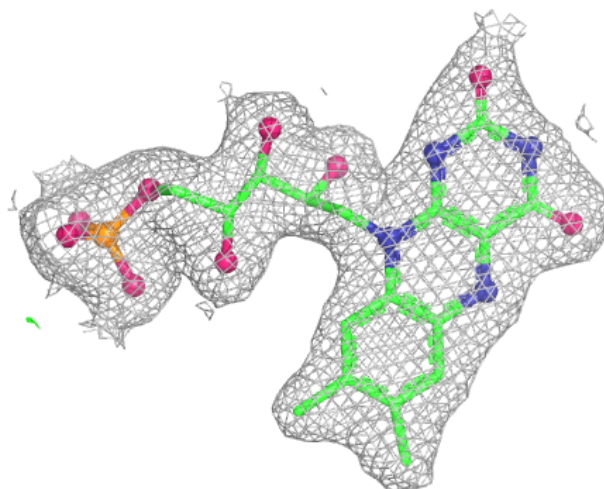
Electron density around DZB B 601:

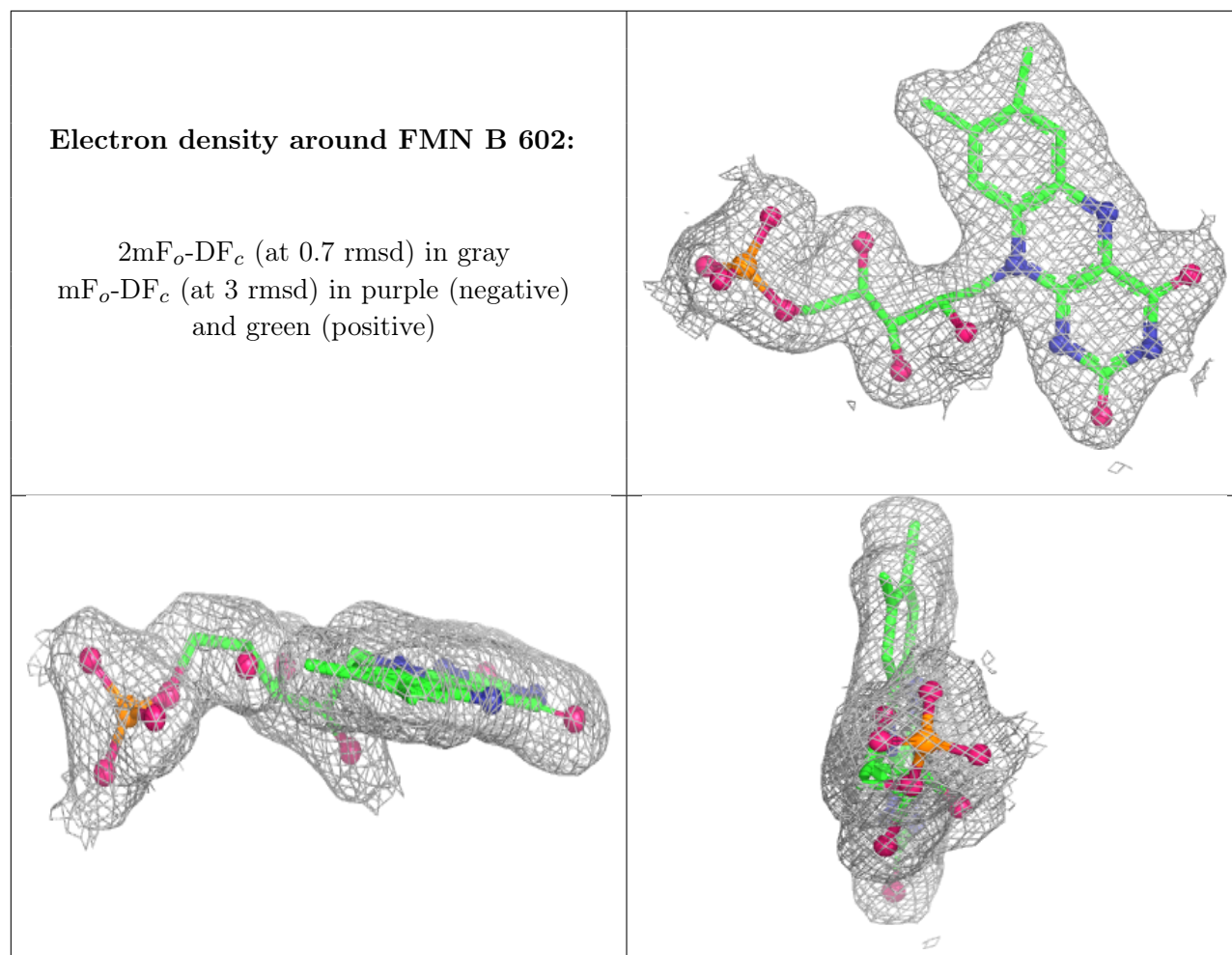
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FMN A 601:

$2mF_o-DF_c$ (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.