

# wwPDB X-ray Structure Validation Summary Report (i)

#### Aug 16, 2023 – 01:06 AM EDT

PDB ID	:	1TV5
Title	:	Plasmodium falciparum dihydroorotate dehydrogenase with a bound inhibitor
Authors	:	Hurt, D.E.; Widom, J.; Clardy, J.
Deposited on		
Resolution	:	2.40 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 (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 (1)) were used in the production of this report:

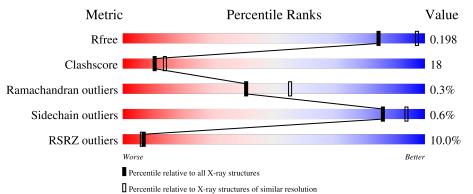
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.40 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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							
			8%						
1	А	443	55%	28%	16%				



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 3282 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 homolog, mitochondrial.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	371	Total 2956	C 1893	N 493	O 554	S 16	0	2	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	127	MET	_	insertion	UNP Q08210
А	128	ARG	-	insertion	UNP Q08210
А	129	GLY	_	insertion	UNP Q08210
А	130	SER	_	insertion	UNP Q08210
А	131	HIS	-	insertion	UNP Q08210
А	132	HIS	-	insertion	UNP Q08210
А	133	HIS	-	insertion	UNP Q08210
А	134	HIS	-	insertion	UNP Q08210
А	135	HIS	-	insertion	UNP Q08210
А	136	HIS	-	insertion	UNP Q08210
А	137	GLY	-	insertion	UNP Q08210
А	138	MET	-	insertion	UNP Q08210
А	139	ALA	_	insertion	UNP Q08210
А	140	SER	-	insertion	UNP Q08210
А	141	MET	-	insertion	UNP Q08210
А	142	THR	-	insertion	UNP Q08210
А	143	GLY	-	insertion	UNP Q08210
А	144	GLY	-	insertion	UNP Q08210
А	145	GLN	-	insertion	UNP Q08210
А	146	GLN	-	insertion	UNP Q08210
А	147	MET	-	insertion	UNP Q08210
А	148	GLY	-	insertion	UNP Q08210
А	149	ARG	-	insertion	UNP Q08210
А	150	ASP	-	insertion	UNP Q08210
А	151	LEU	-	insertion	UNP Q08210
А	152	TYR	-	insertion	UNP Q08210
А	153	ASP	-	insertion	UNP Q08210

There are 31 discrepancies between the modelled and reference sequences:

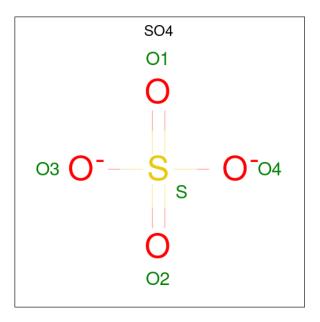
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Chain	Residue	Modelled	Actual	Comment	Reference
A	154	ASP	-	insertion	UNP Q08210
А	155	ASP	-	insertion	UNP Q08210
A	156	ASP	-	insertion	UNP Q08210
A	157	LYS	-	insertion	UNP Q08210

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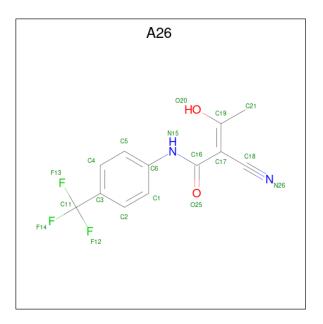
• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 5	0 4	S 1	0	0

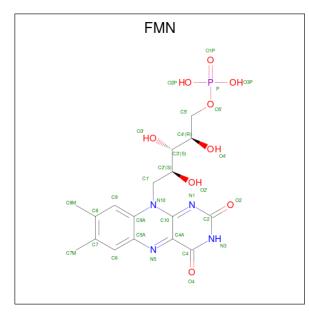
• Molecule 3 is (2Z)-2-cyano-3-hydroxy-N-[4-(trifluoromethyl)phenyl]but-2-enamide (three-letter code: A26) (formula:  $C_{12}H_9F_3N_2O_2$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	А	1	Total	С	F	Ν	Ο	0	0
0	1	Ĩ	19	12	3	2	2		0

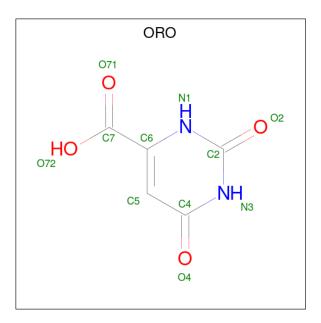
• Molecule 4 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula:  $C_{17}H_{21}N_4O_9P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	Δ	1	Total	С	Ν	0	Р	0	0
4	A	A 1	31	17	4	9	1	0	

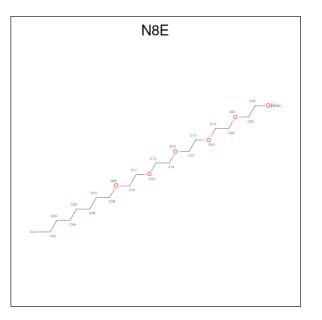
• Molecule 5 is OROTIC ACID (three-letter code: ORO) (formula:  $C_5H_4N_2O_4$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	А	1	Total 11	С 5	N 2	0 4	0	0

• Molecule 6 is 3,6,9,12,15-PENTAOXATRICOSAN-1-OL (three-letter code: N8E) (formula:  $C_{18}H_{38}O_6$ ).



[	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	6	А	1	Total         C         O           24         18         6	0	0
	6	А	1	Total         C         O           24         18         6	0	0



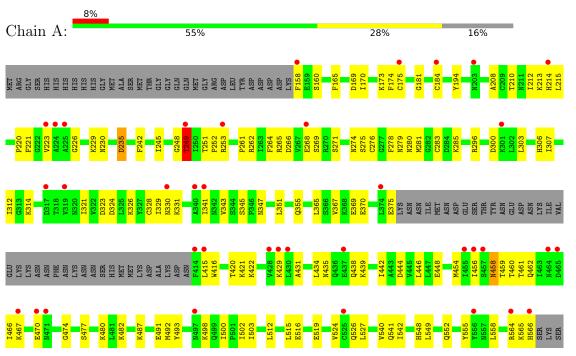
• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	212	Total         O           212         212	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 homolog, mitochondrial



## 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	H 3 2	Depositor	
Cell constants	105.43Å 105.43Å 276.63Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor	
Resolution (Å)	33.48 - 2.40	Depositor	
Resolution (A)	33.48 - 2.40	EDS	
% Data completeness	97.3 (33.48-2.40)	Depositor	
(in resolution range)	97.9 (33.48-2.40)	EDS	
R <sub>merge</sub>	(Not available)	Depositor	
$R_{sym}$	0.07	Depositor	
$< I/\sigma(I) > 1$	$3.80 (at 2.39 \text{\AA})$	Xtriage	
Refinement program	CNS 1.0	Depositor	
D D.	0.201 , $0.243$	Depositor	
$R, R_{free}$	0.197 , $0.198$	DCC	
$R_{free}$ test set	1181 reflections $(5.12\%)$	wwPDB-VP	
Wilson B-factor $(Å^2)$	31.0	Xtriage	
Anisotropy	0.400	Xtriage	
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.40,53.8	EDS	
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
$F_o, F_c$ correlation	0.94	EDS	
Total number of atoms	3282	wwPDB-VP	
Average B, all atoms $(Å^2)$	35.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.19% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: N8E, ORO, FMN, A26, 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	
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.36	0/3007	0.64	2/4048~(0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	249	THR	N-CA-C	-11.33	80.41	111.00
1	А	458	ASN	N-CA-C	-5.68	95.66	111.00

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	А	2956	0	2992	113	0
2	А	5	0	0	1	0
3	А	19	0	9	0	0
4	А	31	0	19	1	0
5	А	11	0	3	2	0
6	А	48	0	76	5	0
7	А	212	0	0	13	0
All	All	3282	0	3099	113	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 18.

The worst 5 of 113 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:229:LYS:O	1:A:248:GLY:HA2	1.77	0.83
1:A:249:THR:HG22	1:A:249:THR:O	1.81	0.79
1:A:323:ASP:HA	1:A:326:LYS:HE2	1.65	0.79
1:A:213:LYS:HE3	7:A:1125:HOH:O	1.82	0.79
1:A:223:VAL:HG22	1:A:245:ILE:HG13	1.65	0.76

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 Allowe		Outliers	Percentiles	
1	А	369/443~(83%)	348~(94%)	20~(5%)	1 (0%)	41 55	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	А	249	THR	

#### 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	А	330/393~(84%)	328~(99%)	2(1%)	86 94	

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

Mol	Chain	Res	Type
1	А	235	ASP
1	А	249	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	548	HIS
1	А	355	GLN
1	А	330	ASN
1	А	320	ASN
1	А	347	ASN

#### 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).



Mal	Mol Type Chain		Res Link		Bond lengths			Bond angles		
10101	Type Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
3	A26	А	1001	-	$19,\!19,\!19$	2.47	5 (26%)	27,27,27	2.14	7 (25%)
6	N8E	А	1004	-	23,23,23	0.38	0	22,22,22	0.64	0
4	FMN	А	1002	-	33,33,33	1.37	6 (18%)	48,50,50	0.96	2(4%)
6	N8E	А	1005	-	23,23,23	0.44	0	22,22,22	0.87	0
2	SO4	А	1006	-	$4,\!4,\!4$	1.93	2 (50%)	$6,\!6,\!6$	0.97	0
5	ORO	А	1003	-	9,11,11	2.26	2 (22%)	8,15,15	3.25	4 (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
3	A26	А	1001	-	-	0/20/20/20	0/1/1/1
6	N8E	А	1004	-	-	2/21/21/21	-
6	N8E	А	1005	-	-	5/21/21/21	-
4	FMN	А	1002	-	-	1/18/18/18	0/3/3/3
5	ORO	А	1003	-	-	4/4/4/4	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
3	А	1001	A26	F14-C11	-6.40	1.09	1.32
5	А	1003	ORO	C6-N1	4.35	1.40	1.34
5	А	1003	ORO	C4-N3	4.04	1.40	1.33
3	А	1001	A26	C5-C6	3.86	1.45	1.39
3	А	1001	A26	F12-C11	-3.75	1.19	1.32

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
5	А	1003	ORO	C5-C4-N3	-7.48	115.34	124.08
3	А	1001	A26	C18-C17-C19	5.57	125.16	118.75
3	А	1001	A26	F14-C11-F12	4.57	122.49	105.72
3	А	1001	A26	O25-C16-C17	-4.43	115.81	120.83
5	А	1003	ORO	O72-C7-C6	-3.19	107.43	114.69

There are no chirality outliers.

5 of 12 torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
5	А	1003	ORO	N1-C6-C7-O71
5	А	1003	ORO	N1-C6-C7-O72
5	А	1003	ORO	C5-C6-C7-O71
5	А	1003	ORO	C5-C6-C7-O72
6	А	1005	N8E	O12-C13-C14-O15

There are no ring outliers.

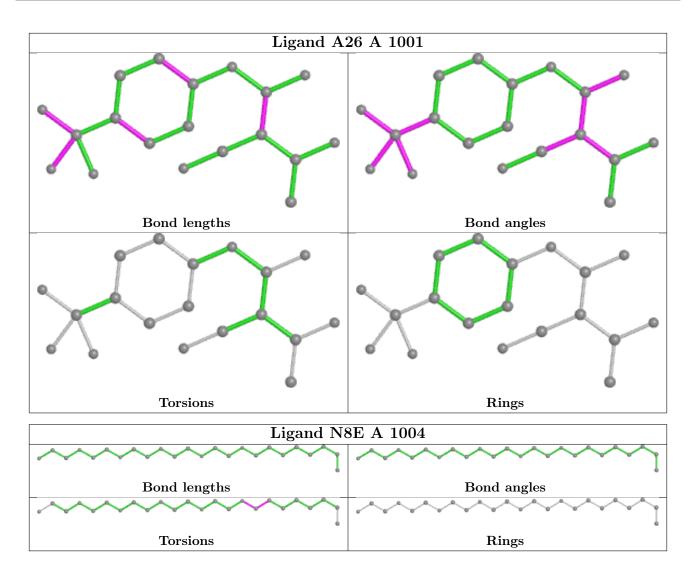
5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	А	1004	N8E	2	0
4	А	1002	FMN	1	0
6	А	1005	N8E	3	0
2	А	1006	SO4	1	0
5	А	1003	ORO	2	0

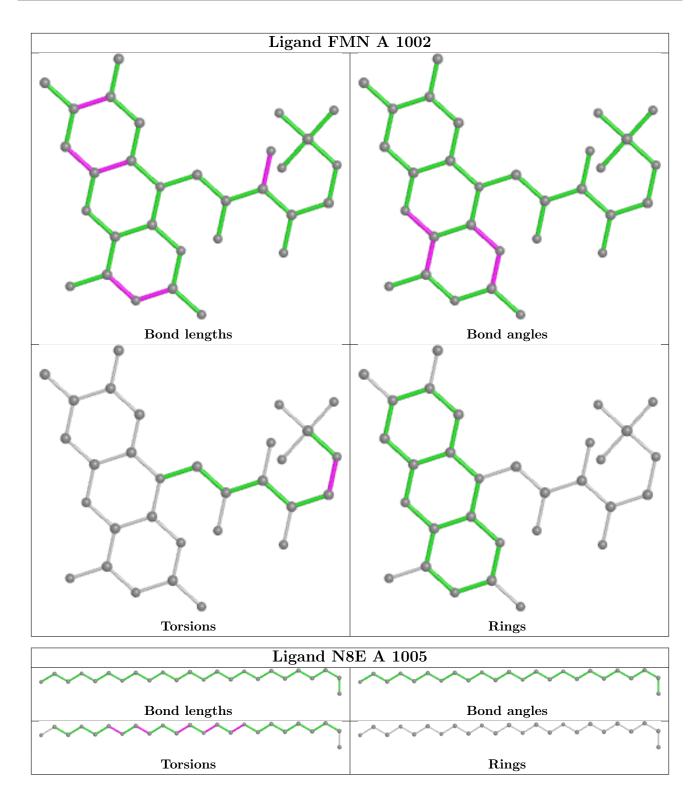
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











### 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,  $95^{th}$  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> <math>#</math>RSRZ&gt;2</rsrz>		$OWAB(Å^2)$	Q<0.9	
1	А	371/443~(83%)	0.40	37 (9%) 7	6	19, 32, 53, 79	2 (0%)

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	184[A]	CYS	14.8
1	А	414	PHE	6.6
1	А	158	PHE	6.2
1	А	175[A]	CYS	6.1
1	А	566	HIS	5.0

### 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
6	N8E	А	1005	24/24	0.60	0.37	86,92,94,94	0
6	N8E	А	1004	24/24	0.93	0.19	39,43,63,63	0

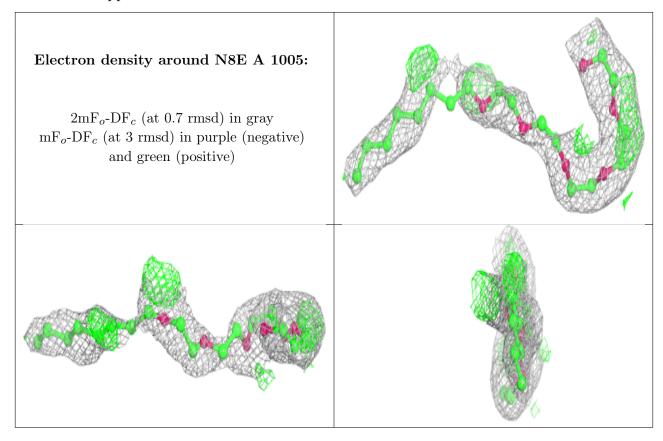
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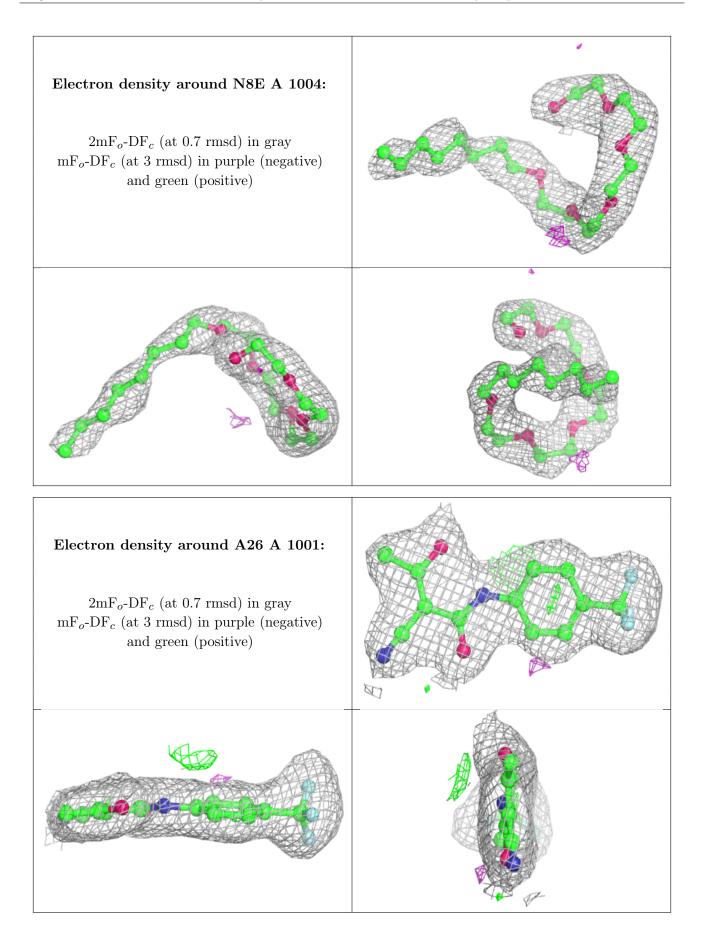
001000	Continuada fronte proceso de pago									
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9		
2	SO4	А	1006	5/5	0.95	0.31	30,30,30,30	5		
3	A26	А	1001	19/19	0.96	0.15	19,25,33,33	0		
4	FMN	А	1002	31/31	0.98	0.20	18,21,24,24	0		
5	ORO	А	1003	11/11	0.98	0.13	19,23,25,26	0		

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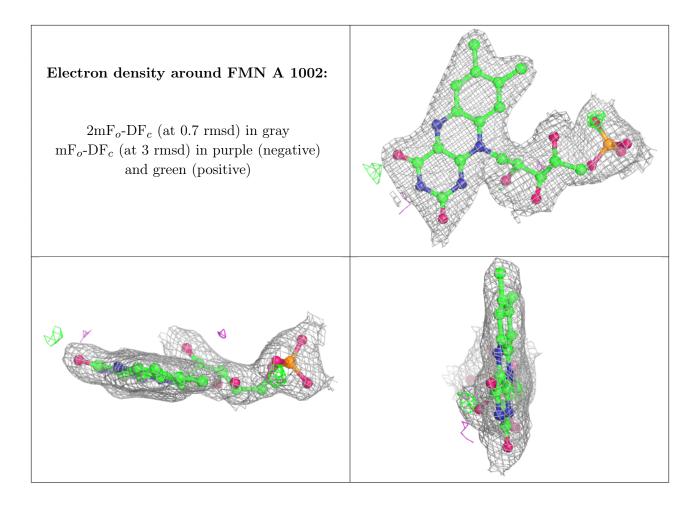
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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











### 6.5 Other polymers (i)

There are no such residues in this entry.

