

wwPDB X-ray Structure Validation Summary Report (i)

Sep 4, 2023 – 08:30 PM EDT

PDB ID : 3U15

Title: Structure of hDMX with Dimer Inducing Indolyl Hydantoin RO-2443

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Deposited on : 2011-09-29

Resolution : 1.80 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

EDS: 2.35

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

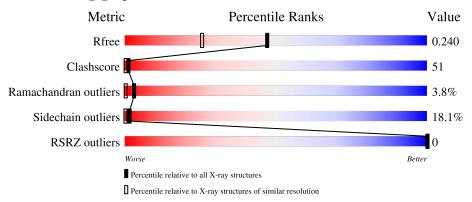
Validation Pipeline (wwPDB-VP) : 2.35

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 1.80 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	Similar resolution
Metric	$(\# { m Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length		Quality of chain	1		
1	A	100	32%	41%	8%	•	18%
1	В	100	23%	47%	12%		18%
1	С	100	29%	42%	9%	•	18%
1	D	100	19%	45%	16%		19%

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	SO4	A	112	-	-	X	-



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2896 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 Protein Mdm4.

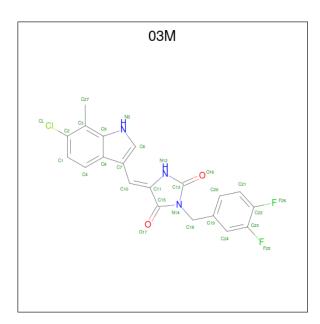
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace			
1	٨	82	Total	С	N	О	S	0	0	0
1	A	02	658	424	112	116	6	0	U	
1	B	82	Total	С	N	О	S	0	0	0
1	Ъ	02	658	424	112	116	6	0		
1	С	82	Total	С	N	О	S	0	0	0
1		02	658	424	112	116	6	0	U	
1	D	Ω1	Total	С	N	О	S	0	0	0
1	. В	D 81	651	419	111	115	6	0		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	GLY	-	expression tag	UNP O15151
A	13	PRO	-	expression tag	UNP O15151
A	17	SER	CYS	engineered mutation	UNP O15151
В	12	GLY	-	expression tag	UNP O15151
В	13	PRO	_	expression tag	UNP O15151
В	17	SER	CYS	engineered mutation	UNP O15151
С	12	GLY	_	expression tag	UNP O15151
С	13	PRO	-	expression tag	UNP O15151
С	17	SER	CYS	engineered mutation	UNP O15151
D	12	GLY	-	expression tag	UNP O15151
D	13	PRO	-	expression tag	UNP O15151
D	17	SER	CYS	engineered mutation	UNP O15151

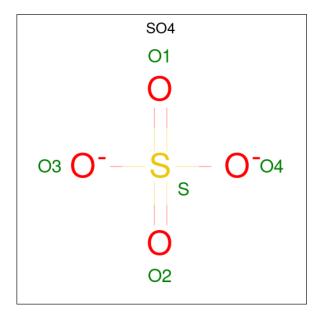
• Molecule 2 is (5Z)-5-[(6-chloro-7-methyl-1H-indol-3-yl)methylidene]-3-(3,4-difluorobenzyl)i midazolidine-2,4-dione (three-letter code: 03M) (formula: $C_{20}H_{14}ClF_2N_3O_2$).





Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	
2	A	1		C		F	N	0	0	0
			28 Total	$\frac{20}{C}$	$\frac{1}{\text{Cl}}$	$\frac{2}{F}$	<u>о</u> N	$\frac{2}{\Omega}$		
2	В	1	28	20	1	2	3	2	0	0
2	С	1	Total	С	Cl	F	N	О	0	0
		1	28	20	1	2	3	2	Ü	Ü
$\frac{1}{2}$	D	1	Total	С	Cl	F	N	O	0	0
		_	28	20	1	2	3	2		

 \bullet Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: $\mathrm{O_4S}).$





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

\bullet Molecule 4 is water.

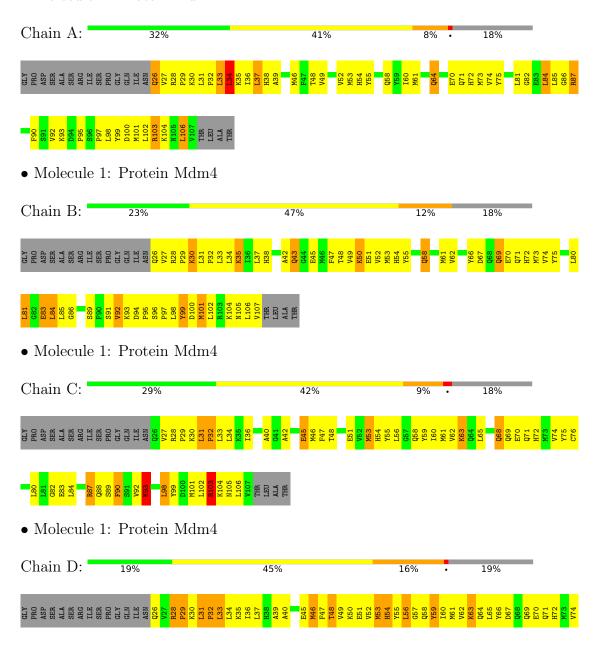
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	43	Total O 43 43	0	0
4	В	34	Total O 34 34	0	0
4	С	37	Total O 37 37	0	0
4	D	35	Total O 35 35	0	0



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: Protein Mdm4









4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 31	Depositor	
Cell constants	73.03Å 73.03Å 68.77Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	36.50 - 1.80	Depositor	
recsolution (11)	32.25 - 1.75	EDS	
% Data completeness	99.5 (36.50-1.80)	Depositor	
(in resolution range)	99.7 (32.25-1.75)	EDS	
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	3.72 (at 1.75Å)	Xtriage	
Refinement program	REFMAC 5.6.0117	Depositor	
R, R_{free}	0.184 , 0.238	Depositor	
$\Pi,\ \Pi_{free}$	0.191 , 0.240	DCC	
R_{free} test set	2075 reflections $(5.03%)$	wwPDB-VP	
Wilson B-factor (Å ²)	22.8	Xtriage	
Anisotropy	0.099	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 55.2	EDS	
L-test for twinning ²	$< L >=0.39, < L^2>=0.21$	Xtriage	
	0.469 for -h,-k,l		
Estimated twinning fraction	0.477 for h,-h-k,-l	Xtriage	
	0.470 for -k,-h,-l		
	0.256 for H, K, L		
Reported twinning fraction	0.249 for -K, -H, -L	Depositor	
Reported twinning fraction	0.247 for -h,-k,l	Depositor	
	0.248 for K, H, -L		
Outliers	0 of 41271 reflections	Xtriage	
F_o, F_c correlation	0.95	EDS	
Total number of atoms	2896	wwPDB-VP	
Average B, all atoms (Å ²)	30.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.88% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: SO4, 03M

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		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.90	0/671	1.16	2/902 (0.2%)	
1	В	0.81	0/671	1.03	0/902	
1	С	0.85	0/671	0.99	1/902 (0.1%)	
1	D	0.84	0/664	1.14	4/892 (0.4%)	
All	All	0.85	0/2677	1.08	7/3598 (0.2%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1
1	С	0	1
1	D	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	A	34	LEU	CA-CB-CG	8.27	134.31	115.30
1	A	28	ARG	NE-CZ-NH1	7.27	123.93	120.30
1	D	103	ARG	NE-CZ-NH2	6.17	123.39	120.30
1	С	103	ARG	NE-CZ-NH2	5.64	123.12	120.30
1	D	28	ARG	NE-CZ-NH1	5.50	123.05	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	В	106	LEU	Peptide
1	С	93	LYS	Peptide
1	D	93	LYS	Peptide

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	658	0	674	66	0
1	В	658	0	674	94	0
1	С	658	0	674	66	0
1	D	651	0	665	65	0
2	A	28	0	14	2	0
2	В	28	0	14	4	0
2	С	28	0	14	2	0
2	D	28	0	14	3	0
3	A	5	0	0	4	0
3	D	5	0	0	1	0
4	A	43	0	0	2	0
4	В	34	0	0	3	0
4	С	37	0	0	3	0
4	D	35	0	0	5	0
All	All	2896	0	2743	278	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 51.

The worst 5 of 278 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:70:GLU:HG2	1:A:73:MET:CG	1.77	1.14
1:C:27:VAL:HG11	1:C:106:LEU:HD13	1.33	1.11
1:A:60:ILE:HD13	1:A:74:VAL:HG21	1.39	1.05
1:A:70:GLU:HG2	1:A:73:MET:HG2	1.39	1.03
1:B:31:LEU:HA	1:B:34:LEU:HB3	1.43	1.00

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	Perce	ntiles
1	A	80/100 (80%)	67 (84%)	13 (16%)	0	100	100
1	В	80/100 (80%)	70 (88%)	10 (12%)	0	100	100
1	С	80/100 (80%)	67 (84%)	8 (10%)	5 (6%)	1	0
1	D	79/100 (79%)	59 (75%)	13 (16%)	7 (9%)	1	0
All	All	319/400 (80%)	263 (82%)	44 (14%)	12 (4%)	3	0

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	76	CYS
1	С	70	GLU
1	D	32	PRO
1	D	33	LEU
1	D	59	TYR

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	72/86 (84%)	60 (83%)	12 (17%)	2 0
1	В	72/86 (84%)	59 (82%)	13 (18%)	1 0
1	C	72/86 (84%)	60 (83%)	12 (17%)	2 0
1	D	71/86 (83%)	56 (79%)	15 (21%)	1 0
All	All	287/344 (83%)	235 (82%)	52 (18%)	1 0



5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	68	GLN
1	С	98	LEU
1	D	84	LEU
1	С	83	GLU
1	С	90	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	72	HIS
1	D	69	GLN
1	С	64	GLN
1	D	68	GLN
1	С	58	GLN

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	Mol Type Chain		Res Link		Вс	Bond lengths			Bond angles		
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
3	SO4	D	2	-	4,4,4	0.35	0	6,6,6	0.78	0	
2	03M	В	1	-	29,31,31	2.19	7 (24%)	37,46,46	3.93	14 (37%)	
3	SO4	A	112	-	4,4,4	0.72	0	6,6,6	1.08	1 (16%)	
2	03M	С	1	-	29,31,31	1.98	5 (17%)	37,46,46	3.52	15 (40%)	
2	03M	A	1	-	29,31,31	1.90	5 (17%)	37,46,46	3.87	14 (37%)	
2	03M	D	1	-	29,31,31	2.13	7 (24%)	37,46,46	4.06	11 (29%)	

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	03M	A	1	-	-	0/6/24/24	0/4/4/4
2	03M	D	1	-	-	0/6/24/24	0/4/4/4
2	03M	В	1	-	-	0/6/24/24	0/4/4/4
2	03M	С	1	-	-	0/6/24/24	0/4/4/4

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	Ideal(Å)
2	D	1	03M	C10-C11	8.29	1.51	1.34
2	В	1	03M	C10-C11	7.50	1.50	1.34
2	С	1	03M	C10-C11	6.00	1.46	1.34
2	A	1	03M	C10-C11	5.43	1.45	1.34
2	В	1	03M	O17-C15	4.65	1.32	1.23

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	1	03M	C11-N12-C13	-15.06	101.09	111.47
2	A	1	03M	C11-N12-C13	-14.90	101.20	111.47
2	D	1	03M	C11-N12-C13	-14.19	101.69	111.47
2	С	1	03M	C11-N12-C13	-13.31	102.30	111.47
2	D	1	03M	C11-C15-N14	11.10	112.36	105.72

There are no chirality outliers.

There are no torsion outliers.

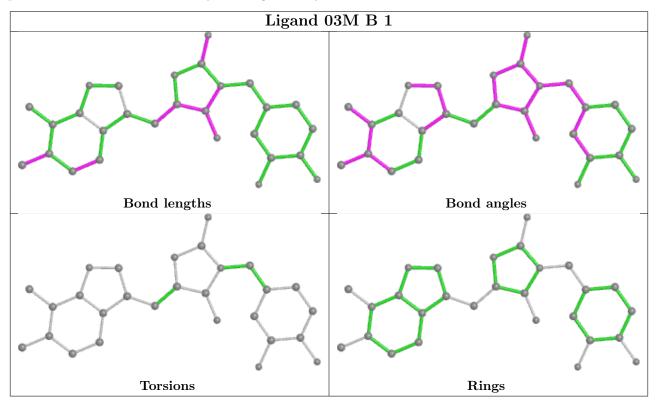
There are no ring outliers.

6 monomers are involved in 16 short contacts:

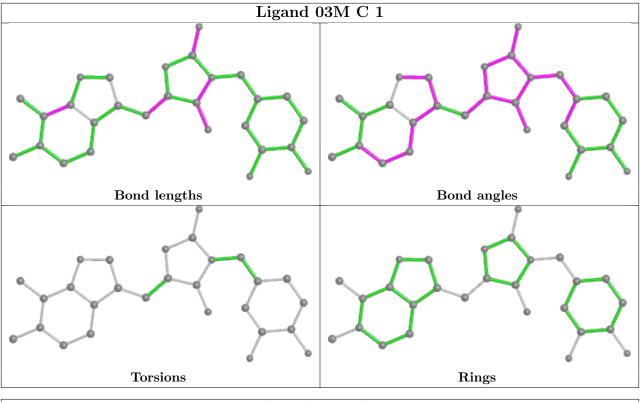


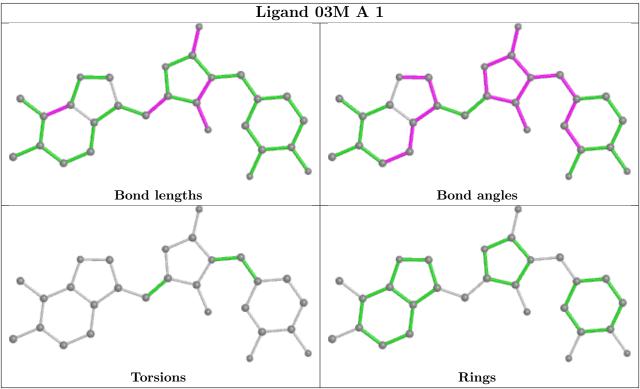
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2	SO4	1	0
2	В	1	03M	4	0
3	A	112	SO4	4	0
2	С	1	03M	2	0
2	A	1	03M	2	0
2	D	1	03M	3	0

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.

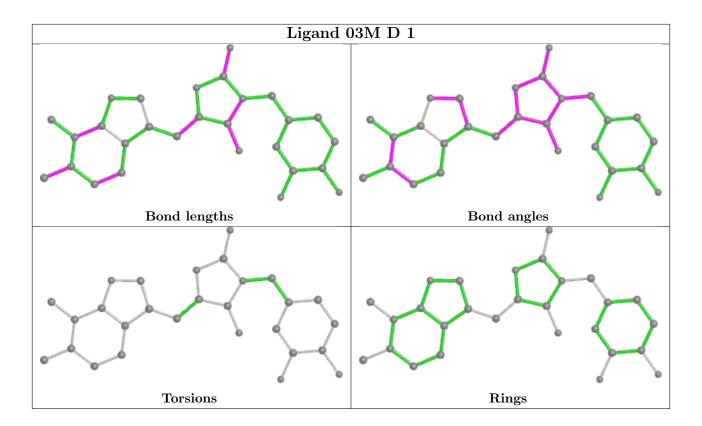












5.7 Other polymers (i)

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 $>$	#	# RSRZ > 2		$OWAB(A^2)$	Q < 0.9
1	A	82/100 (82%)	-0.55	0	100	100	19, 29, 41, 47	0
1	В	82/100 (82%)	-0.56	0	100	100	19, 30, 44, 50	0
1	С	82/100 (82%)	-0.52	0	100	100	22, 31, 37, 44	0
1	D	81/100 (81%)	-0.48	0	100	100	19, 32, 40, 46	0
All	All	327/400 (81%)	-0.53	0	100	100	19, 31, 41, 50	0

There are no RSRZ outliers to report.

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	03M	D	1	28/28	0.95	0.09	21,33,45,48	0
2	03M	A	1	28/28	0.96	0.07	23,26,31,36	0
2	03M	С	1	28/28	0.97	0.07	20,27,31,39	0
2	03M	В	1	28/28	0.97	0.07	19,24,30,32	0

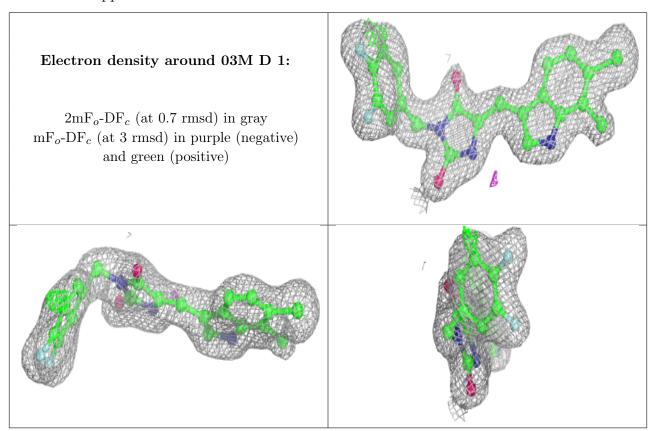
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	SO4	A	112	5/5	0.97	0.07	31,34,35,35	0
3	SO4	D	2	5/5	0.98	0.06	34,35,38,40	0

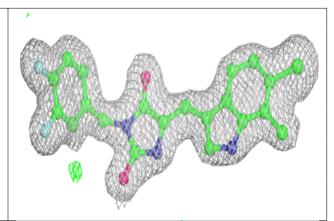
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

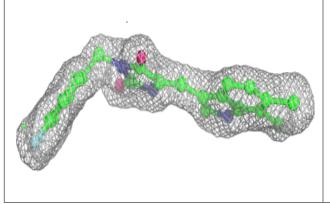


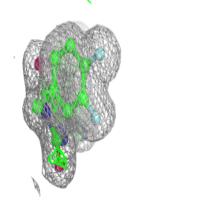


Electron density around 03M A 1:

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

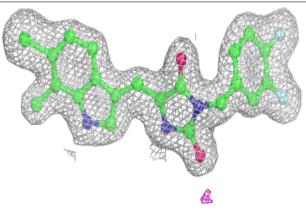


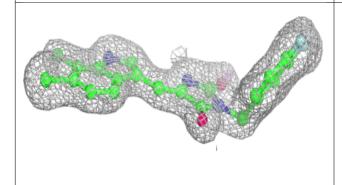


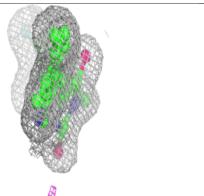


Electron density around 03M C 1:

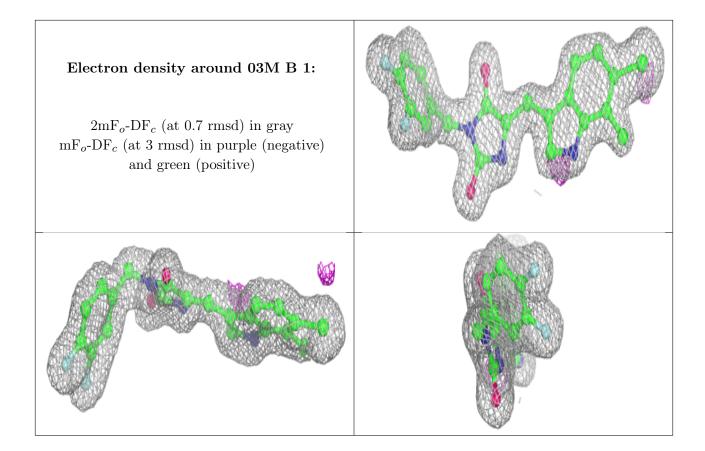
 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)











6.5 Other polymers (i)

There are no such residues in this entry.

