

wwPDB X-ray Structure Validation Summary Report (i)

Nov 3, 2023 – 05:43 AM EDT

PDB ID : 3W6Y

Title: Structure of Trypanosoma cruzi dihydroorotate dehydrogenase in complex with

TT2-2-199

Authors: Inaoka, D.K.; Iida, M.; Tabuchi, T.; Lee, N.; Hashimoto, S.; Matsuoka, S.;

Kuranaga, T.; Shiba, T.; Sakamoto, K.; Suzuki, S.; Balogun, E.O.; Nara, T.;

Aoki, T.; Inoue, M.; Honma, T.; Tanaka, A.; Harada, S.; Kita, K.

Deposited on : 2013-02-27

Resolution : 2.68 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS: 2.36

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) : 2.36

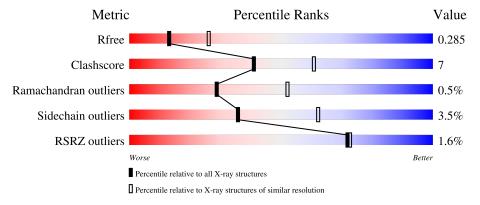


1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.68 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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	313	80%	19%	
1	В	313	85%	15%	

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	405	-	-	-	X
3	GOL	A	410	-	-	-	X
3	GOL	A	411	-	-	-	X
3	GOL	A	412	-	-	-	X
3	GOL	В	404	-	-	-	X



2 Entry composition (i)

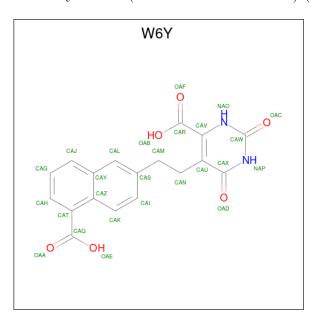
There are 6 unique types of molecules in this entry. The entry contains 5280 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 (fumarate).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	313	Total	С	N	О	S	0	0	0
	11	010	2388	1530	396	444	18	U	0	
1	B	313	Total	С	N	О	S	0	0	0
1	Ъ	313	2388	1530	396	444	18			

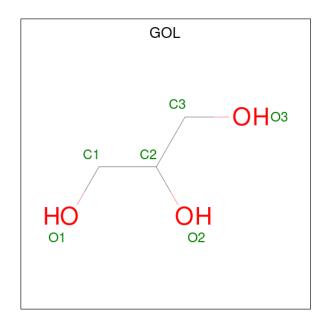
• Molecule 2 is 5-[2-(5-carboxynaphthalen-2-yl)ethyl]-2,6-dioxo-1,2,3,6-tetrahydropyrimidine-4-carboxylic acid (three-letter code: W6Y) (formula: $C_{18}H_{14}N_2O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 26	_		_	0	0
2	В	1	Total 26	_		_	0	0

• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0

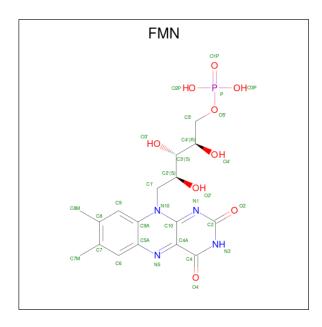
Continued on next page...



Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0
3	В	1	Total C O 6 3 3	0	0

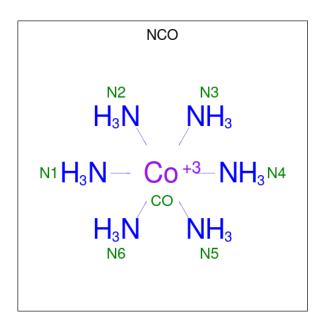
 $\bullet \ \ Molecule\ 4\ is\ FLAVIN\ MONONUCLEOTIDE\ (three-letter\ code:\ FMN)\ (formula:\ C_{17}H_{21}N_4O_9P).$



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
1	٨	1	Total	С	N	О	Р	0	0
4	4 A	1	31	17	4	9	1	U	U
1	D	1	Total	С	N	О	Р	0	0
4	Б	1	31	17	4	9	1	U	0

 \bullet Molecule 5 is COBALT HEXAMMINE(III) (three-letter code: NCO) (formula: ${\rm CoH_{18}N_6)}.$





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 7	Co 1	N 6	0	0

• Molecule 6 is water.

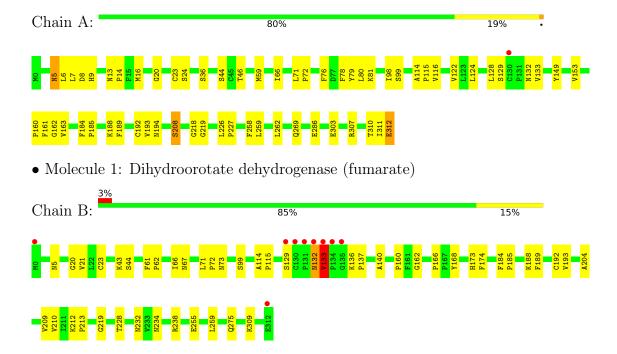
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
6	A	144	Total O 144 144	0	0
6	В	113	Total O 113 113	0	0



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 (fumarate)





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	68.03Å 71.84Å 129.53Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.31 - 2.68	Depositor
rtesolution (A)	39.28 - 2.68	EDS
% Data completeness	97.5 (39.31-2.68)	Depositor
(in resolution range)	97.5 (39.28-2.68)	EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.41 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
D.D.	0.195 , 0.282	Depositor
R, R_{free}	0.201 , 0.285	DCC
R_{free} test set	916 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 39.8	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5280	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 29.90 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4335e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

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: FMN, GOL, W6Y, NCO

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	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.56	0/2440	0.72	0/3305	
1	В	0.55	0/2440	0.73	0/3305	
All	All	0.56	0/4880	0.72	0/6610	

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2388	0	2391	39	0
1	В	2388	0	2391	35	0
2	A	26	0	12	1	0
2	В	26	0	12	1	0
3	A	66	0	88	1	0
3	В	60	0	80	1	0
4	A	31	0	19	2	0
4	В	31	0	19	2	0
5	A	7	0	0	0	0
6	A	144	0	0	2	0
6	В	113	0	0	2	0
All	All	5280	0	5012	71	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 7.

The worst 5 of 71 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{array}{c} { m Clash} \\ { m overlap} \ ({ m \AA}) \end{array}$
1:A:311:ILE:HG22	1:A:312:GLU:HG3	1.70	0.73
1:B:132:ASN:HB2	1:B:133:VAL:HG13	1.70	0.72
1:A:7:LEU:O	1:A:9:HIS:HD2	1.73	0.70
1:A:71:LEU:HD22	2:A:401:W6Y:H5	1.80	0.64
1:A:13:ASN:ND2	1:A:286:GLU:OE1	2.32	0.63

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	entiles
1	A	311/313 (99%)	297 (96%)	13 (4%)	1 (0%)	41	64
1	В	311/313 (99%)	294 (94%)	15 (5%)	2 (1%)	25	47
All	All	$622/626 \ (99\%)$	591 (95%)	28 (4%)	3 (0%)	29	52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	133	VAL
1	В	23	CYS
1	A	23	CYS

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	$258/258 \; (100\%)$	246 (95%)	12 (5%)	26 50		
1	В	258/258 (100%)	252 (98%)	6 (2%)	50 76		
All	All	$516/516 \; (100\%)$	498 (96%)	18 (4%)	36 62		

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	73	ASN
1	В	133	VAL
1	В	132	ASN
1	A	208	SER
1	В	67	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	\mathbf{Type}
1	В	87	HIS
1	В	132	ASN
1	В	275	GLN
1	В	215	GLN
1	В	234	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)

26 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	Trino	Chain	Dag	T inle	Bo	ond leng	ths	В	ond ang	gles
IVIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	403	-	5,5,5	0.33	0	5,5,5	0.26	0
3	GOL	В	410	-	5,5,5	0.33	0	5,5,5	0.18	0
2	W6Y	A	401	-	27,28,28	2.24	5 (18%)	37,40,40	1.66	7 (18%)
3	GOL	В	407	-	5,5,5	0.66	0	5,5,5	0.71	0
3	GOL	В	411	-	5,5,5	0.49	0	5,5,5	0.24	0
3	GOL	A	402	-	5,5,5	0.33	0	5,5,5	0.39	0
3	GOL	A	410	-	5,5,5	0.33	0	5,5,5	0.17	0
3	GOL	A	407	-	5,5,5	0.20	0	5,5,5	0.43	0
3	GOL	В	406	-	5,5,5	0.60	0	5,5,5	0.52	0
2	W6Y	В	401	-	27,28,28	2.23	5 (18%)	37,40,40	1.65	8 (21%)
3	GOL	A	412	-	5,5,5	0.41	0	5,5,5	0.22	0
3	GOL	В	404	-	5,5,5	0.18	0	5,5,5	0.51	0
3	GOL	A	411	-	5,5,5	0.50	0	5,5,5	0.58	0
3	GOL	В	405	-	5,5,5	0.32	0	5,5,5	0.21	0
5	NCO	A	414	-	6,6,6	0.93	0	-		
3	GOL	A	404	_	5,5,5	0.33	0	5, 5, 5	0.34	0
3	GOL	A	408	-	5,5,5	0.46	0	5, 5, 5	0.50	0
4	FMN	A	413	_	33,33,33	1.44	4 (12%)	48,50,50	1.32	7 (14%)
3	GOL	В	402	-	5,5,5	0.49	0	5,5,5	0.36	0
3	GOL	В	409	-	5,5,5	0.54	0	5,5,5	0.39	0
4	FMN	В	412	-	33,33,33	1.56	5 (15%)	48,50,50	1.21	6 (12%)
3	GOL	В	408	-	5,5,5	0.46	0	5,5,5	0.60	0
3	GOL	A	409	-	5,5,5	0.46	0	5,5,5	0.45	0
3	GOL	A	405	-	5,5,5	0.48	0	5,5,5	0.54	0
3	GOL	A	406	-	5,5,5	0.40	0	5,5,5	0.35	0
3	GOL	В	403	-	5,5,5	0.28	0	5,5,5	0.30	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
3	GOL	A	403	-	-	2/4/4/4	-
3	GOL	В	410	-	-	0/4/4/4	-
2	W6Y	A	401	-	-	7/13/13/13	0/3/3/3
3	GOL	В	407	-	-	0/4/4/4	-
3	GOL	В	411	-	-	1/4/4/4	-
3	GOL	A	402	_	-	0/4/4/4	-
3	GOL	A	410	_	-	2/4/4/4	_
3	GOL	A	407	-	-	0/4/4/4	-
3	GOL	В	406	_	-	0/4/4/4	-
2	W6Y	В	401	-	-	1/13/13/13	0/3/3/3
3	GOL	A	412	_	-	4/4/4/4	-
3	GOL	В	404	-	-	2/4/4/4	-
3	GOL	A	411	-	-	0/4/4/4	-
3	GOL	В	405	_	-	0/4/4/4	-
3	GOL	A	404	_	-	2/4/4/4	-
3	GOL	A	408	-	-	4/4/4/4	-
4	FMN	A	413	-	-	4/18/18/18	0/3/3/3
3	GOL	В	402	-	-	2/4/4/4	-
3	GOL	В	409	-	-	4/4/4/4	-
4	FMN	В	412	-	-	2/18/18/18	0/3/3/3
3	GOL	В	408	-	-	4/4/4/4	-
3	GOL	A	409	-	-	2/4/4/4	-
3	GOL	A	405	-	-	0/4/4/4	-
3	GOL	A	406	-	-	0/4/4/4	-
3	GOL	В	403	-	-	3/4/4/4	-

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
2	В	401	W6Y	CAT-CAQ	-6.95	1.39	1.50
2	A	401	W6Y	CAT-CAQ	-6.82	1.39	1.50
4	В	412	FMN	C9A-C5A	5.68	1.50	1.41
4	A	413	FMN	C9A-C5A	5.20	1.49	1.41
2	A	401	W6Y	CAV-CAR	-5.16	1.40	1.48

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
2	A	401	W6Y	CAU-CAX-NAP	6.07	120.23	115.69
2	В	401	W6Y	CAU-CAX-NAP	5.24	119.60	115.69

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type	Atoms	${f Z}$	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
2	В	401	W6Y	CAX-NAP-CAW	-3.59	121.17	126.34
2	A	401	W6Y	CAX-NAP-CAW	-3.49	121.31	126.34
2	В	401	W6Y	OAB-CAR-CAV	3.47	122.47	116.76

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	W6Y	CAS-CAM-CAN-CAU
2	A	401	W6Y	OAB-CAR-CAV-NAO
2	В	401	W6Y	OAB-CAR-CAV-NAO
3	A	404	GOL	O1-C1-C2-C3
3	A	408	GOL	O1-C1-C2-C3

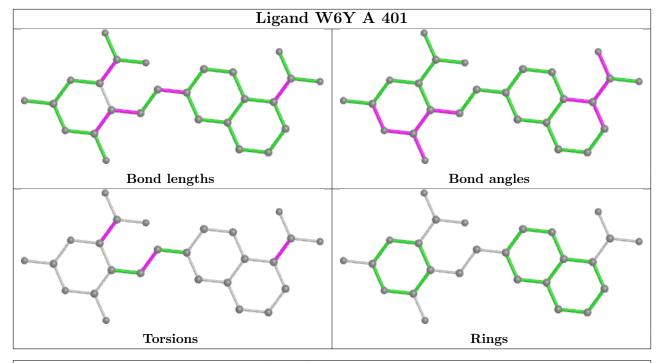
There are no ring outliers.

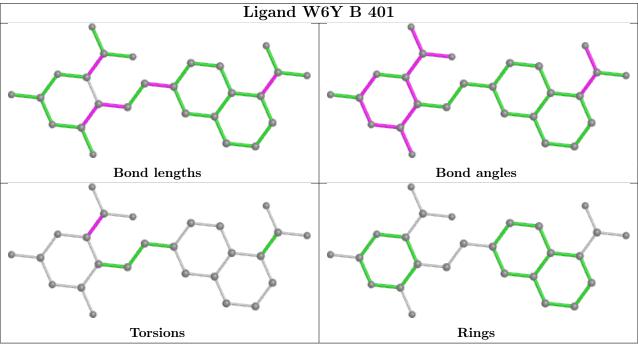
6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	W6Y	1	0
3	В	411	GOL	1	0
2	В	401	W6Y	1	0
3	A	411	GOL	1	0
4	A	413	FMN	2	0
4	В	412	FMN	2	0

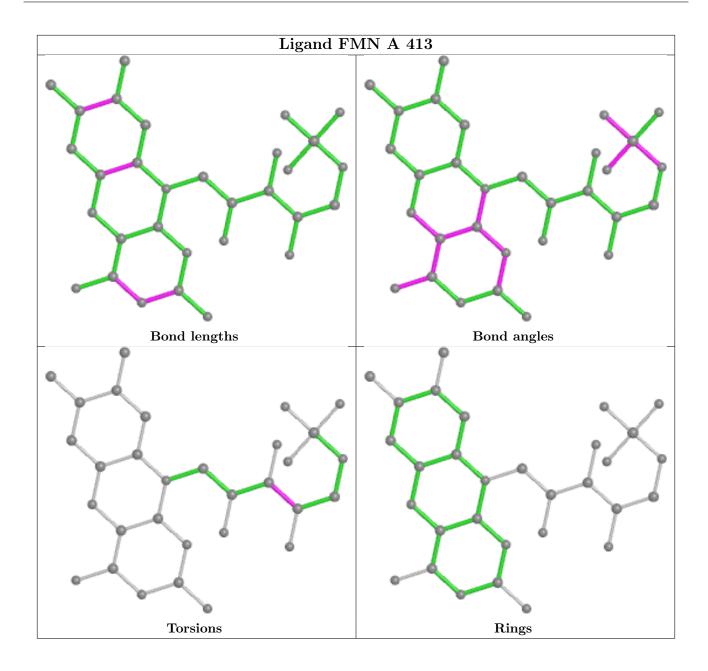
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



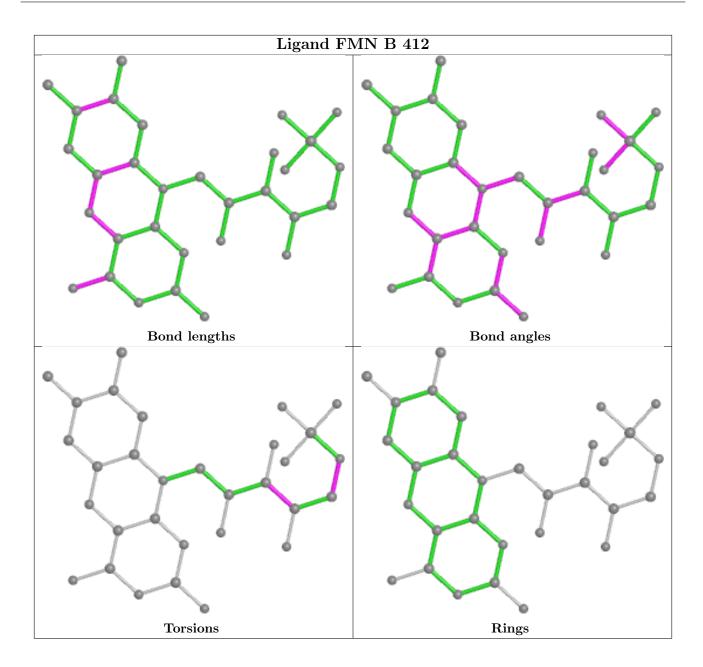












5.7 Other polymers (i)

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 $>$	$\# \mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	313/313 (100%)	-0.13	1 (0%) 94 95	11, 20, 38, 54	0
1	В	313/313 (100%)	-0.02	9 (2%) 51 51	10, 20, 39, 103	0
All	All	626/626 (100%)	-0.07	10 (1%) 72 73	10, 20, 39, 103	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	131	PRO	9.1
1	В	132	ASN	6.7
1	В	130	CYS	4.5
1	В	134	PRO	4.0
1	В	135	GLY	3.5

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)

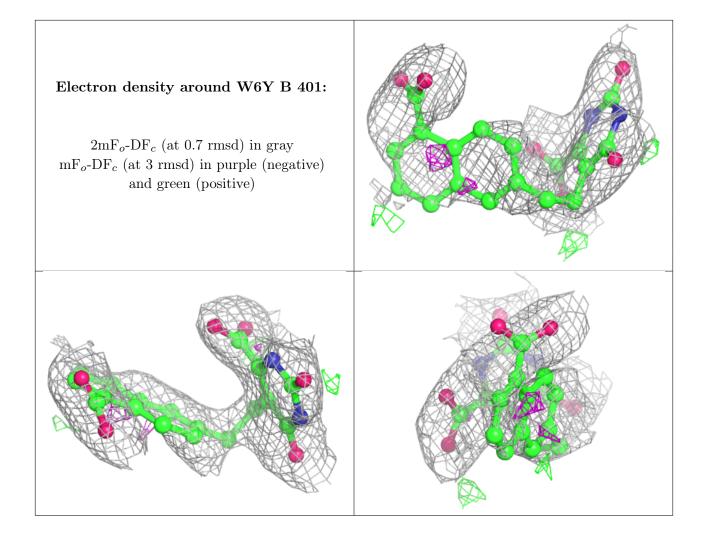
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
3	GOL	A	411	6/6	0.57	0.48	52,60,60,62	0
3	GOL	A	410	6/6	0.65	0.42	70,75,76,77	0
3	GOL	В	402	6/6	0.66	0.31	49,52,53,54	0
3	GOL	A	405	6/6	0.67	0.44	44,50,53,57	0
3	GOL	В	411	6/6	0.70	0.33	57,61,62,63	0
3	GOL	В	404	6/6	0.71	0.43	49,51,53,56	0
3	GOL	В	405	6/6	0.74	0.36	64,66,67,68	0
3	GOL	В	406	6/6	0.75	0.37	41,47,48,50	0
3	GOL	A	412	6/6	0.76	0.50	66,68,70,71	0
3	GOL	В	410	6/6	0.79	0.36	54,58,60,61	0
3	GOL	В	409	6/6	0.79	0.28	37,40,43,44	0
3	GOL	В	408	6/6	0.81	0.30	37,38,39,40	0
2	W6Y	В	401	26/26	0.83	0.27	25,36,47,49	0
3	GOL	A	404	6/6	0.84	0.24	40,44,45,48	0
3	GOL	В	407	6/6	0.86	0.26	30,33,33,34	0
3	GOL	A	406	6/6	0.87	0.22	42,45,47,48	0
3	GOL	A	409	6/6	0.87	0.20	36,38,38,40	0
3	GOL	В	403	6/6	0.88	0.24	33,35,36,38	0
2	W6Y	A	401	26/26	0.89	0.19	32,40,57,63	0
3	GOL	A	408	6/6	0.89	0.39	33,34,34,34	0
3	GOL	A	402	6/6	0.91	0.28	23,24,26,26	0
3	GOL	A	403	6/6	0.91	0.19	30,32,33,35	0
3	GOL	A	407	6/6	0.94	0.11	28,29,30,31	0
4	FMN	В	412	31/31	0.94	0.16	13,16,17,17	0
4	FMN	A	413	31/31	0.95	0.16	13,17,19,19	0
5	NCO	A	414	7/7	0.98	0.14	10,10,10,11	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.

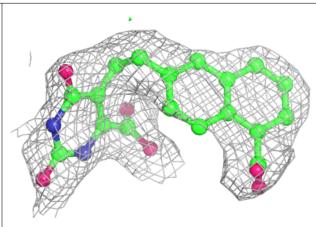


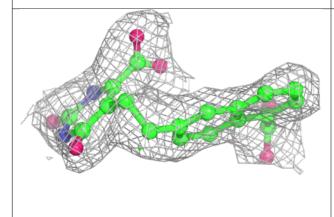


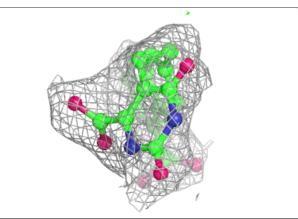


Electron density around W6Y A 401:

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

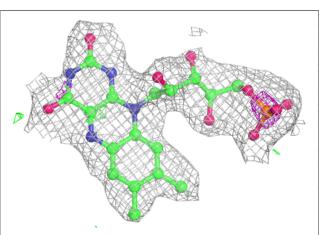


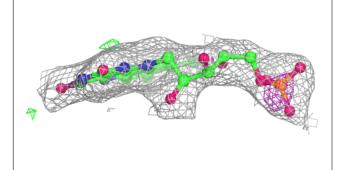


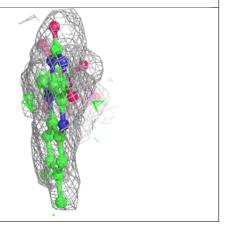


Electron density around FMN B 412:

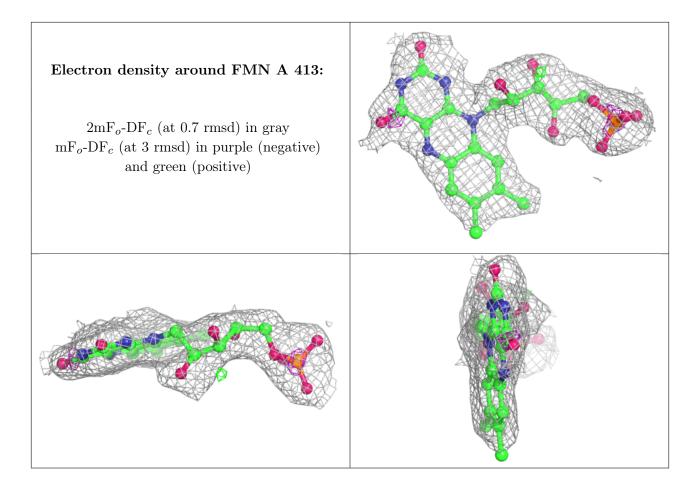
 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)











6.5 Other polymers (i)

There are no such residues in this entry.

