

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

#### Apr 28, 2024 – 08:37 am BST

PDB ID : 2JHN

Title : 3-methyladenine dna-glycosylase from Archaeoglobus fulgidus

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Deposited on : 2007-02-22

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 (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36.2

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)

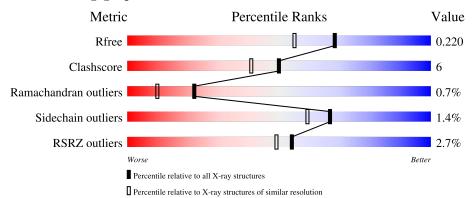
Validation Pipeline (wwPDB-VP) : 2.36.2

## 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	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	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	A	295	88%	10%			
1	В	295	92%	7% •			

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
2	MBO	В	1296	_	-	X	_



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5493 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.

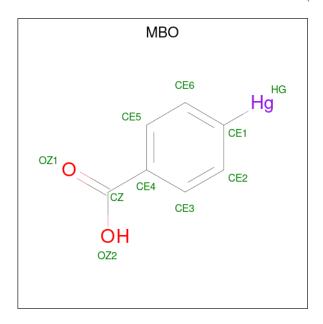
• Molecule 1 is a protein called 3-METHYLADENINE DNA-GLYCOSYLASE.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	293	Total 2459	C 1587	N 426	O 436	S 10	0	6	0
1	В	291	Total 2441	C 1580	N 418	O 434	S 9	0	7	0

There are 2 discrepancies between the modelled and reference sequences:

	Chain	Residue	Residue   Modelled   Actual		Comment	Reference	
	A 229 ILE		MET	engineered mutation	UNP O28163		
Ī	B 229 ILE		MET	engineered mutation	UNP O28163		

• Molecule 2 is MERCURIBENZOIC ACID (three-letter code: MBO) (formula: C<sub>7</sub>H<sub>5</sub>HgO<sub>2</sub>).



Mol	Chain	Residues	A	<b>A</b> tor	ms		ZeroOcc	AltConf
2	٨	1	Total	С	Hg	О	0	0
2	A	1	10	7	1	2	U	0



Mol	Chain	Residues	A	tor	ns		ZeroOcc	AltConf
2	В	1	Total	C 7	Hg 1	0	0	0

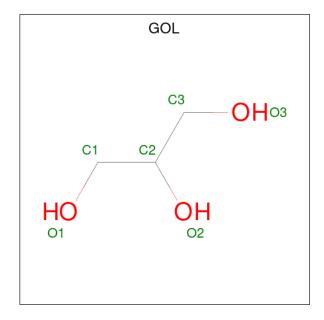
• Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Hg 1 1	0	0
3	В	1	Total Hg 1 1	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Na 2 2	0	0
4	В	2	Total Na 2 2	0	0

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).

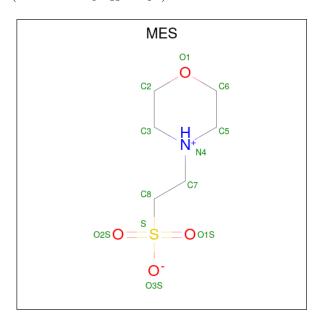


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0



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

• Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	Δ	1	Total C N O S	0	0
0	71	1	12 6 1 4 1	0	Ü
6	R	1	Total C N O S	0	0
0	D	1	12 6 1 4 1		
6	R	1	Total C N O S	0	0
U	D	1	12 6 1 4 1		U
6	R	1	Total C N O S	0	0
U	D	1	12 6 1 4 1	0	U

• Molecule 7 is water.

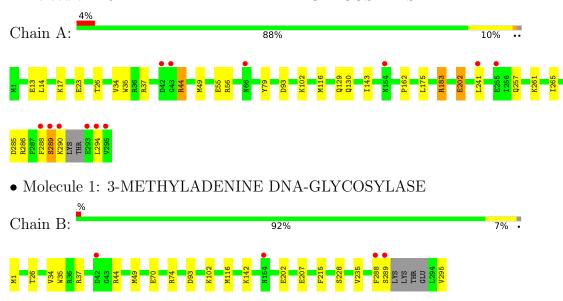
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	204	Total O 204 204	0	0
7	В	291	Total O 291 291	0	0



# 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: 3-METHYLADENINE DNA-GLYCOSYLASE





## 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	69.49Å 49.97Å 105.80Å	D: t	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $107.43^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	12.00 - 1.80	Depositor	
Resolution (A)	19.95 - 1.80	EDS	
% Data completeness	98.4 (12.00-1.80)	Depositor	
(in resolution range)	98.4 (19.95-1.80)	EDS	
$R_{merge}$	0.08	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.87 (at 1.80Å)	Xtriage	
Refinement program	REFMAC 5.2.0019	Depositor	
Ρ. Р.	0.185 , 0.223	Depositor	
$R, R_{free}$	0.184 , $0.220$	DCC	
$R_{free}$ test set	3212  reflections  (5.06%)	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	17.6	Xtriage	
Anisotropy	0.300	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 54.8	EDS	
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.32$	Xtriage	
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage	
$F_o, F_c$ correlation	0.96	EDS	
Total number of atoms	5493	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	19.0	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 52.59 % 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 4.7558e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<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: MES, HG, GOL, NA, MBO

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).

Mal Chair		Bond lengths		Bond angles	
Mol   Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.69	0/2509	0.68	0/3368
1	В	0.81	0/2491	0.69	0/3348
All	All	0.75	0/5000	0.69	0/6716

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	2459	0	2469	32	0
1	В	2441	0	2452	14	0
2	A	10	0	4	3	0
2	В	10	0	4	10	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	A	2	0	0	0	0
4	В	2	0	0	0	0
5	A	12	0	16	0	0
5	В	12	0	16	0	0
6	A	12	0	13	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	В	36	0	39	2	0
7	A	204	0	0	7	0
7	В	291	0	0	2	0
All	All	5493	0	5013	58	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 58 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
2:B:1296:MBO:HE5	2:B:1296:MBO:CE6	2.06	1.23
2:B:1296:MBO:HE6	2:B:1296:MBO:CE1	2.07	1.22
2:B:1296:MBO:HE6	2:B:1296:MBO:CE5	2.06	1.22
2:B:1296:MBO:HE5	2:B:1296:MBO:CE4	2.06	1.20
2:B:1296:MBO:HE5	2:B:1296:MBO:CE5	0.97	1.06

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	$295/295\ (100\%)$	288 (98%)	4 (1%)	3 (1%)	15 5
1	В	$294/295\ (100\%)$	291 (99%)	2 (1%)	1 (0%)	41 27
All	All	589/590 (100%)	579 (98%)	6 (1%)	4 (1%)	22 10

All (4) Ramachandran outliers are listed below:

Mo	l	Chain	Res	Type
1		A	289	SER



Mol	Chain	Res	Type
1	A	294	LEU
1	A	26	THR
1	В	26	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	A	252/248 (102%)	247 (98%)	5 (2%)	55 44
1	В	251/248 (101%)	248 (99%)	3 (1%)	71 65
All	All	503/496 (101%)	495 (98%)	8 (2%)	67 54

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	295	VAL
1	В	44	ARG
1	A	241	LEU
1	A	202	GLU
1	В	1	MET

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

Mol	Chain	Res	Type
1	A	257	GLN
1	В	130	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)

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 for Mogul analysis.

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	Во	ond leng	ths	В	ond ang	gles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MBO	В	1296	1	7,10,10	0.79	0	11,13,13	1.18	0
6	MES	В	1303	-	12,12,12	1.50	1 (8%)	14,16,16	1.17	1 (7%)
5	GOL	A	1300	-	5,5,5	0.36	0	5,5,5	0.53	0
2	MBO	A	1296	1	7,10,10	0.77	0	11,13,13	1.14	0
6	MES	A	1301	-	12,12,12	1.61	2 (16%)	14,16,16	1.51	1 (7%)
5	GOL	В	1300	-	5,5,5	0.65	0	5,5,5	1.00	0
6	MES	В	1302	-	12,12,12	1.85	3 (25%)	14,16,16	1.67	2 (14%)
6	MES	В	1301	-	12,12,12	1.44	2 (16%)	14,16,16	1.08	1 (7%)
5	GOL	В	1304	-	5,5,5	0.46	0	5,5,5	0.34	0
5	GOL	A	1302	-	5,5,5	0.42	0	5,5,5	0.39	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
2	MBO	В	1296	1	-	4/4/4/4	0/1/1/1
6	MES	В	1303	-	-	4/6/14/14	0/1/1/1
5	GOL	A	1300	-	-	1/4/4/4	-
2	MBO	A	1296	1	=	0/4/4/4	0/1/1/1



Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Type	Chain	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
6	MES	A	1301	-	-	5/6/14/14	0/1/1/1
5	GOL	В	1300	-	-	2/4/4/4	-
6	MES	В	1302	-	-	0/6/14/14	0/1/1/1
6	MES	В	1301	_	-	0/6/14/14	0/1/1/1
5	GOL	В	1304	_	-	0/4/4/4	-
5	GOL	A	1302	-	-	4/4/4/4	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
6	A	1301	MES	C8-S	4.40	1.83	1.77
6	В	1303	MES	C8-S	4.14	1.83	1.77
6	В	1302	MES	C8-S	4.07	1.83	1.77
6	В	1301	MES	C8-S	3.58	1.82	1.77
6	В	1302	MES	O2S-S	3.46	1.55	1.45

All (5) bond angle outliers are listed below:

$\mathbf{N}$	[ol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
	6	В	1302	MES	O1S-S-C8	4.48	112.31	106.92
(	6	A	1301	MES	O2S-S-C8	4.09	111.84	106.92
(	6	В	1303	MES	O1S-S-C8	2.72	110.20	106.92
	6	В	1302	MES	O2S-S-C8	2.70	110.17	106.92
(	6	В	1301	MES	O2S-S-C8	2.06	109.40	106.92

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1302	GOL	O1-C1-C2-C3
5	A	1302	GOL	C1-C2-C3-O3
5	В	1300	GOL	C1-C2-C3-O3
6	В	1303	MES	N4-C7-C8-S
6	В	1303	MES	C7-C8-S-O2S

There are no ring outliers.

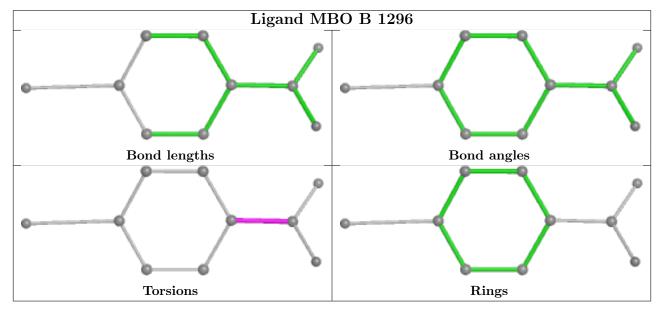
4 monomers are involved in 15 short contacts:

Mol	Chain	$\operatorname{Res}$	Type	Clashes	Symm-Clashes
2	В	1296	MBO	10	0



Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	В	1303	MES	1	0
2	A	1296	MBO	3	0
6	В	1302	MES	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 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	293/295~(99%)	-0.07	12 (4%) 37 31	9, 21, 34, 46	22 (7%)
1	В	291/295~(98%)	-0.35	4 (1%) 75 72	5, 14, 29, 38	24 (8%)
All	All	584/590 (98%)	-0.21	16 (2%) 54 49	5, 17, 33, 46	46 (7%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	295	VAL	6.1
1	A	290	LYS	5.3
1	A	289	SER	5.0
1	A	288	PHE	4.1
1	В	288	PHE	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.

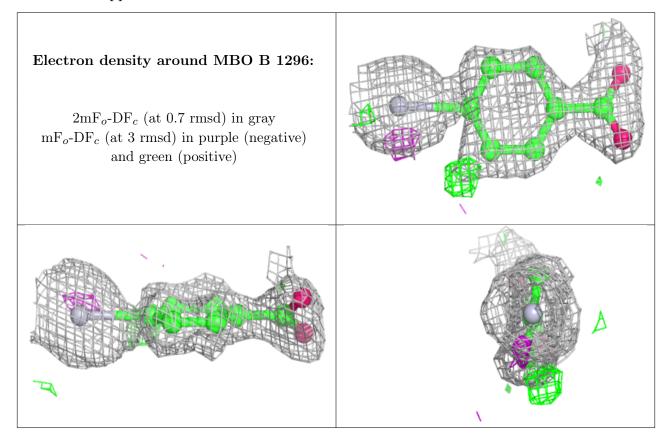
#### 6.4 Ligands (i)

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
6	MES	A	1301	12/12	0.70	0.23	46,47,48,49	12
6	MES	В	1303	12/12	0.78	0.21	37,42,43,43	12
5	GOL	В	1304	6/6	0.79	0.19	21,24,26,26	6
6	MES	В	1302	12/12	0.86	0.21	15,22,27,29	12
5	GOL	В	1300	6/6	0.89	0.12	15,22,28,29	0
5	GOL	A	1300	6/6	0.90	0.15	22,28,32,36	0
5	GOL	A	1302	6/6	0.93	0.09	29,30,31,32	6
6	MES	В	1301	12/12	0.94	0.11	12,20,23,24	12
4	NA	В	1299	1/1	0.96	0.07	20,20,20,20	0
4	NA	A	1299	1/1	0.97	0.05	22,22,22,22	0
3	HG	В	1297	1/1	0.97	0.08	42,42,42,42	1
3	HG	A	1297	1/1	0.98	0.07	44,44,44,44	1
4	NA	A	1298	1/1	0.98	0.10	18,18,18,18	0
2	MBO	A	1296	10/10	1.00	0.07	22,24,27,27	10
2	MBO	В	1296	10/10	1.00	0.07	20,21,25,25	10
4	NA	В	1298	1/1	1.00	0.07	9,9,9,9	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.





# 6.5 Other polymers (i)

There are no such residues in this entry.

