

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

#### Apr 29, 2024 – 01:20 am BST

PDB ID	:	4AZS
Title	:	High resolution (2.2 A) crystal structure of WbdD.
Authors	:	Hagelueken, G.; Huang, H.; Naismith, J.H.
Deposited on	:	2012-06-26
Resolution	:	2.15 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:

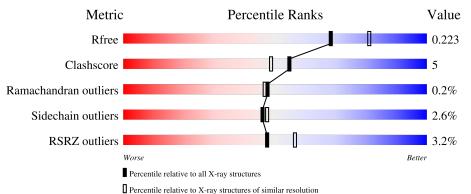
MolProbity		4.02b-467
5		
Mogul	:	1.8.4, CSD as $541be(2020)$
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

# 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 2.15 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	1479(2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	٨	560	2%					
1	A	569	68%	9%	•	22%		

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
4	SO4	А	1480	-	-	Х	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	А	1481	-	-	Х	-
4	SO4	А	1484	-	-	Х	-
4	SO4	А	1485	-	-	Х	-

Continued from previous page...



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3936 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 METHYLTRANSFERASE WBDD.

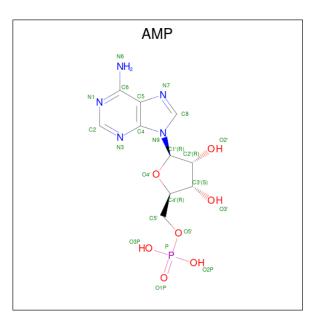
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	442	Total	С	Ν	0	$\mathbf{S}$	0	7	0
T	11	112	3640	2346	619	665	10	0	•	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	-12	MET	-	expression tag	UNP Q47592
А	-11	HIS	-	expression tag	UNP Q47592
А	-10	HIS	-	expression tag	UNP Q47592
А	-9	HIS	-	expression tag	UNP Q47592
A	-8	HIS	-	expression tag	UNP Q47592
А	-7	HIS	-	expression tag	UNP Q47592
A	-6	HIS	-	expression tag	UNP Q47592
А	-5	GLU	-	expression tag	UNP Q47592
A	-4	ASN	-	expression tag	UNP Q47592
А	-3	LEU	-	expression tag	UNP Q47592
A	-2	TYR	-	expression tag	UNP Q47592
А	-1	PHE	-	expression tag	UNP Q47592
A	0	GLN	-	expression tag	UNP Q47592
А	168	PHE	LEU	conflict	UNP Q47592
А	273	TYR	HIS	conflict	UNP Q47592
А	440	VAL	ALA	conflict	UNP Q47592
А	480	VAL	GLY	conflict	UNP Q47592

There are 17 discrepancies between the modelled and reference sequences:

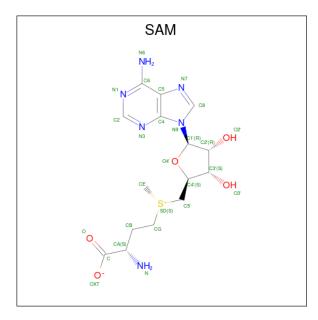
• Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula:  $C_{10}H_{14}N_5O_7P$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	А	1	Total	С	Ν	0	Р	0	0
	11	Ĩ	23	10	5	7	1	0	0

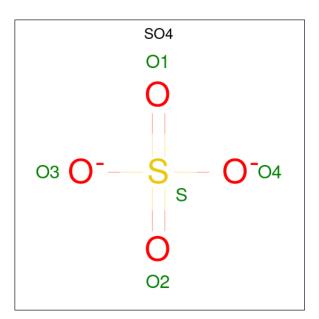
• Molecule 3 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula:  $C_{15}H_{22}N_6O_5S$ ).



Mol	Chain	Residues		Atc	$\mathbf{ms}$			ZeroOcc	AltConf
2	۸	1	Total	С	Ν	0	$\mathbf{S}$	0	0
5	A	1	27	15	6	5	1	0	0

• Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	2	Total Cl 2 2	0	0



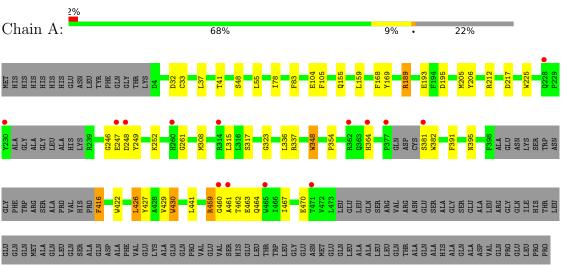
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	189	Total O 189 189	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: METHYLTRANSFERASE WBDD



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants	159.22Å $159.22$ Å $159.22$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	65.00 - 2.15	Depositor
Resolution (A)	65.00 - 2.15	EDS
% Data completeness	$100.0 \ (65.00-2.15)$	Depositor
(in resolution range)	$100.0 \ (65.00-2.15)$	EDS
R <sub>merge</sub>	0.09	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.59 (at 2.14 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
$R, R_{free}$	0.176 , $0.222$	Depositor
10, 10 free	0.183 , $0.223$	DCC
$R_{free}$ test set	1825 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	37.4	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , $42.6$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.48, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3936	wwPDB-VP
Average B, all atoms $(Å^2)$	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.06% 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: SAM, SO4, CL, AMP

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	l Chain B		nd lengths	Bond angles	
Mol Ch	Chain	Chain RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.79	4/3759~(0.1%)	0.81	3/5108~(0.1%)

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 mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	$\ $ ers $\ $ $\#$ Planarity outliers	
1	А	0	2	

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
1	А	430	TRP	CD2-CE2	6.02	1.48	1.41
1	А	225	TRP	CD2-CE2	5.60	1.48	1.41
1	А	348	TRP	CD2-CE2	5.26	1.47	1.41
1	А	422	TRP	CD2-CE2	5.17	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	189	ARG	NE-CZ-NH1	10.01	125.31	120.30
1	А	189	ARG	NE-CZ-NH2	-9.21	115.69	120.30
1	А	195	ASP	CB-CG-OD1	5.95	123.66	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	А	261	GLY	Peptide
1	А	460	GLY	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	А	3640	0	3531	36	1
2	А	23	0	12	1	0
3	А	27	0	22	1	0
4	А	55	0	0	10	1
5	А	2	0	0	0	0
6	А	189	0	0	6	0
All	All	3936	0	3565	38	1

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 5.

The worst 5 of 38 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:168:PHE:HA	4:A:1480:SO4:O4	1.77	0.85
1:A:104[A]:GLU:OE1	4:A:1485:SO4:O4	2.07	0.72
4:A:1481:SO4:O1	6:A:2120:HOH:O	2.08	0.71
1:A:169:TYR:HD1	4:A:1480:SO4:O3	1.74	0.70
1:A:337:ARG:NH2	4:A:1484:SO4:O1	2.24	0.69

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:TYR:N	4:A:1480:SO4:O3[10_555]	2.09	0.11



### 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	Percen	ntiles
1	А	441/569~(78%)	427 (97%)	13 (3%)	1 (0%)	47	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	323	GLY

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	390/486~(80%)	380~(97%)	10 (3%)	46 47

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	459	ARG
1	А	462	THR
1	А	463	GLU
1	А	395	ASN
1	А	416	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:



Mol	Chain	Res	Type
1	А	174	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 15 ligands modelled in this entry, 2 are monoatomic - leaving 13 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	AMP	А	1474	-	$22,\!25,\!25$	0.82	0	$25,\!38,\!38$	1.41	3 (12%)
4	SO4	А	1483	-	4,4,4	0.43	0	$6,\!6,\!6$	0.65	0
4	SO4	А	1480	-	4,4,4	0.22	0	$6,\!6,\!6$	0.42	0
4	SO4	А	1478	-	4,4,4	0.41	0	$6,\!6,\!6$	0.13	0
4	SO4	А	1482	-	4,4,4	0.42	0	$6,\!6,\!6$	0.13	0
4	SO4	А	1485	-	4,4,4	0.58	0	$6,\!6,\!6$	0.56	0
4	SO4	А	1476	-	4,4,4	0.70	0	$6,\!6,\!6$	1.94	2 (33%)
4	SO4	А	1484	-	4,4,4	0.34	0	6,6,6	0.19	0
4	SO4	А	1481	-	4,4,4	0.69	0	$6,\!6,\!6$	0.83	0
4	SO4	А	1486	-	4,4,4	0.47	0	$6,\!6,\!6$	0.45	0
4	SO4	А	1477	-	4,4,4	0.52	0	$6,\!6,\!6$	0.55	0
4	SO4	А	1479	-	4,4,4	0.37	0	$6,\!6,\!6$	0.39	0
3	SAM	А	1475	-	24,29,29	1.33	4 (16%)	23,42,42	1.59	4 (17%)



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.

Ν	Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	2	AMP	А	1474	-	-	6/6/26/26	0/3/3/3
	3	SAM	А	1475	-	-	2/12/33/33	0/3/3/3

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	1475	SAM	O4'-C1'	3.53	1.46	1.41
3	А	1475	SAM	C2-N3	2.87	1.36	1.32
3	А	1475	SAM	OXT-C	-2.12	1.23	1.30
3	А	1475	SAM	CE-SD	-2.04	1.66	1.78

All (4) bond length outliers are listed below:

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	1475	SAM	N3-C2-N1	-3.81	122.72	128.68
4	А	1476	SO4	O3-S-O2	-3.74	89.79	109.31
2	А	1474	AMP	N3-C2-N1	-3.29	123.54	128.68
2	А	1474	AMP	C1'-N9-C4	-2.96	121.44	126.64
3	А	1475	SAM	N6-C6-N1	2.86	124.52	118.57

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	1474	AMP	C5'-O5'-P-O2P
2	А	1474	AMP	C5'-O5'-P-O3P
2	А	1474	AMP	O4'-C4'-C5'-O5'
2	А	1474	AMP	C3'-C4'-C5'-O5'
2	А	1474	AMP	C5'-O5'-P-O1P

There are no ring outliers.

6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	1474	AMP	1	0
4	А	1480	SO4	3	1
4	А	1485	SO4	3	0

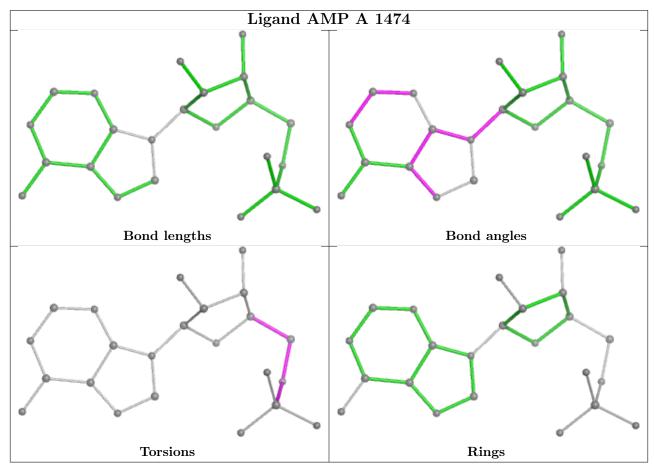
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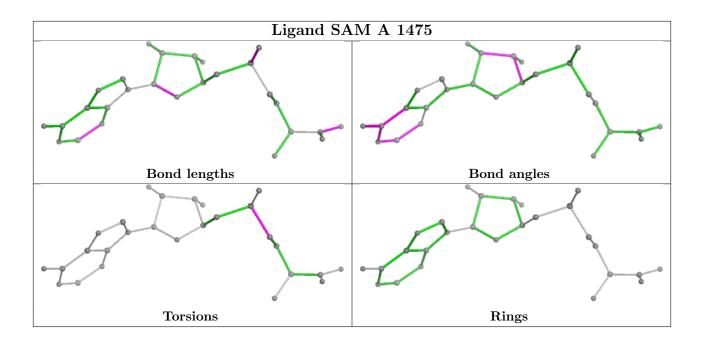
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	1484	SO4	2	0
4	А	1481	SO4	2	0
3	А	1475	SAM	1	0

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 similar 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		$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	442/569~(77%)	0.08	14 (3%) 47 5	56	23, 39, 80, 102	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	228	GLN	6.0
1	А	461	ALA	5.3
1	А	381	SER	3.7
1	А	377	PRO	3.5
1	А	465	TRP	3.1

### 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
4	SO4	А	1477	5/5	0.75	0.27	73,79,90,98	0
4	SO4	А	1478	5/5	0.84	0.33	83,90,102,108	0

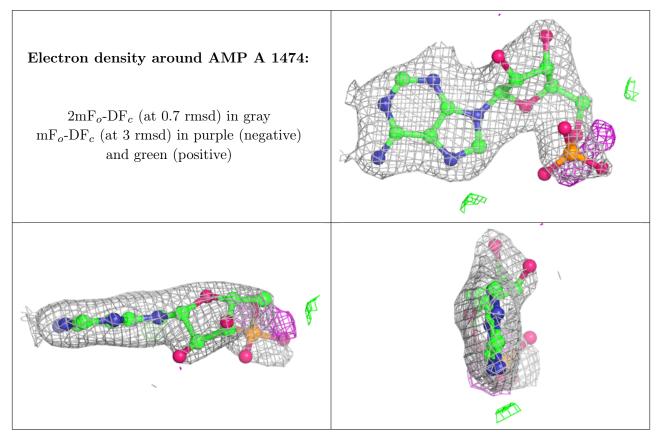
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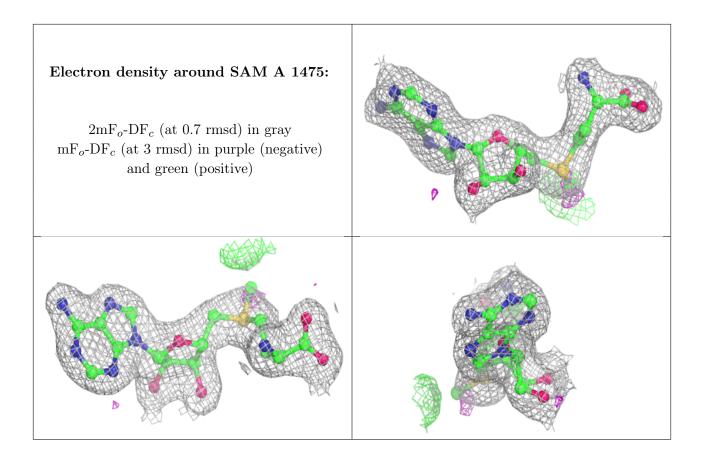
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	SO4	А	1482	5/5	0.87	0.30	93,95,100,103	0
4	SO4	А	1485	5/5	0.88	0.41	59,70,79,92	0
4	SO4	А	1486	5/5	0.89	0.19	55,77,88,93	0
4	SO4	А	1484	5/5	0.93	0.23	78,85,92,96	0
2	AMP	А	1474	23/23	0.94	0.20	38,52,94,100	0
4	SO4	А	1481	5/5	0.95	0.24	31,41,65,67	0
4	SO4	А	1483	5/5	0.96	0.12	$63,\!66,\!76,\!77$	0
4	SO4	А	1479	5/5	0.96	0.08	61,75,85,87	0
3	SAM	А	1475	27/27	0.97	0.11	24,27,30,47	0
5	CL	А	1488	1/1	0.97	0.17	43,43,43,43	1
4	SO4	А	1480	5/5	0.99	0.28	17,22,23,24	5
4	SO4	А	1476	5/5	0.99	0.16	31,32,36,41	0
5	CL	А	1487	1/1	1.00	0.11	31,31,31,31	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.

