

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2022 – 12:01 AM EST

PDB ID	:	4N9L
Title	:	crystal structure of beta-lactamse PenP_E166S in complex with meropenem
Authors	:	Pan, X.; Wong, W.; Zhao, Y.
Deposited on		
Resolution	:	2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see references (1)) were used in the production of this report:

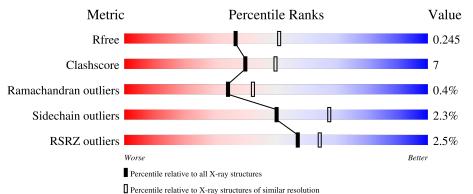
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.26
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

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 2.30 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	5042(2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	А	268	3% 82%	12%	•••
1	В	268	2% 8 1%	13%	•••



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4470 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 Beta-lactamase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	В	256	Total 2052	C 1296	N 350	O 403	${ m S} { m 3}$	0	10	0
1	А	256	Total 2052	C 1296	N 350	O 403	$\frac{S}{3}$	0	10	0

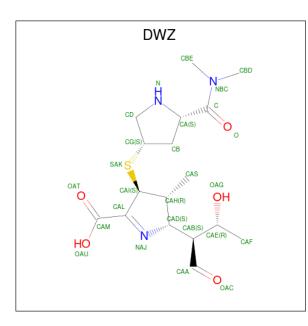
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	23	GLY	-	expression tag	UNP P00808
В	24	PRO	-	expression tag	UNP P00808
В	25	MET	-	expression tag	UNP P00808
В	166	SER	GLU	engineered mutation	UNP P00808
А	23	GLY	-	expression tag	UNP P00808
А	24	PRO	-	expression tag	UNP P00808
А	25	MET	-	expression tag	UNP P00808
А	166	SER	GLU	engineered mutation	UNP P00808

• Molecule 2 is $(2S,3R,4S)-4-\{[(3S,5S)-5-(dimethylcarbamoyl)pyrrolidin-3-yl]sulfanyl\}-2-[(2S,3R)-3-hydroxy-1-oxobutan-2-yl]-3-methyl-3,4-dihydro-2H-pyrrole-5-carboxylic acid (three-letter code: DWZ) (formula: C₁₇H₂₇N₃O₅S).$







Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	В	1	Total	С	Ν	0	S	0	0
		1	26	17	3	5	1	0	0
0	٨	1	Total	С	Ν	Ο	S	0	0
	A		26	17	3	5	1		0

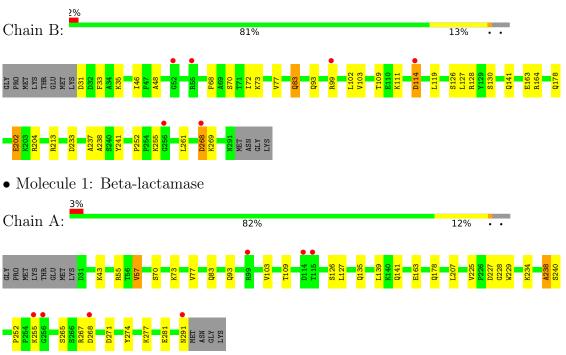
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	161	Total O 161 161	0	0
3	А	153	Total O 153 153	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: Beta-lactamase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	43.26Å 90.96Å 66.20Å	Depositor
a, b, c, α , β , γ	90.00° 104.24° 90.00°	Depositor
Resolution (Å)	37.10 - 2.30	Depositor
Resolution (A)	37.10 - 2.30	EDS
% Data completeness	99.9 (37.10-2.30)	Depositor
(in resolution range)	99.9 (37.10-2.30)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$11.67 (at 2.29 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
D D.	0.180 , 0.242	Depositor
R, R_{free}	0.188 , 0.245	DCC
R_{free} test set	1131 reflections (5.11%)	wwPDB-VP
Wilson B-factor $(Å^2)$	13.7	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.37, 40.2	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4470	wwPDB-VP
Average B, all atoms $(Å^2)$	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.75% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: DWZ

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	Bo	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.90	6/2112~(0.3%)	0.96	10/2859~(0.3%)	
1	В	0.88	5/2112~(0.2%)	1.00	10/2859~(0.3%)	
All	All	0.89	11/4224~(0.3%)	0.98	20/5718~(0.3%)	

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	#Planarity outliers
1	А	0	1
1	В	0	2
All	All	0	3

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	238	ALA	C-N	14.78	1.68	1.34
1	В	83[A]	GLN	C-N	12.82	1.63	1.34
1	В	83[B]	GLN	C-N	12.82	1.63	1.34
1	В	252	PRO	C-N	10.46	1.54	1.34
1	А	252	PRO	C-N	9.77	1.52	1.34
1	А	83[A]	GLN	C-N	8.63	1.53	1.34
1	А	83[B]	GLN	C-N	8.63	1.53	1.34
1	А	57	VAL	C-N	7.25	1.50	1.34
1	В	238	ALA	C-N	6.95	1.50	1.34
1	В	114	ASP	CB-CG	6.18	1.64	1.51
1	А	109	THR	CB-OG1	-5.75	1.31	1.43

All (11) bond length outliers are listed below:

All (20) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	83[A]	GLN	O-C-N	-15.41	98.05	122.70
1	В	83[B]	GLN	O-C-N	-15.41	98.05	122.70
1	А	238	ALA	O-C-N	-14.38	99.69	122.70
1	А	83[A]	GLN	O-C-N	-8.77	108.67	122.70
1	А	83[B]	GLN	O-C-N	-8.77	108.67	122.70
1	В	83[A]	GLN	CA-C-N	7.79	134.35	117.20
1	В	83[B]	GLN	CA-C-N	7.79	134.35	117.20
1	А	267	ARG	NE-CZ-NH2	-7.07	116.77	120.30
1	А	83[A]	GLN	CA-C-N	5.96	130.31	117.20
1	А	83[B]	GLN	CA-C-N	5.96	130.31	117.20
1	В	109	THR	OG1-CB-CG2	5.65	123.00	110.00
1	В	204	ARG	NE-CZ-NH2	-5.65	117.48	120.30
1	А	83[A]	GLN	C-N-CA	5.56	135.60	121.70
1	А	83[B]	GLN	C-N-CA	5.56	135.60	121.70
1	В	204	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	А	271	ASP	CB-CG-OD1	5.24	123.01	118.30
1	В	128	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	В	83[A]	GLN	C-N-CA	5.15	134.57	121.70
1	В	83[B]	GLN	C-N-CA	5.15	134.57	121.70
1	А	267	ARG	NE-CZ-NH1	5.05	122.83	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	57	VAL	Mainchain
1	В	83[A]	GLN	Mainchain
1	В	83[B]	GLN	Mainchain

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	2052	0	2105	22	0
1	В	2052	0	2105	35	0
2	А	26	0	26	8	0
2	В	26	0	25	6	0
3	А	153	0	0	5	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	В	161	0	0	11	0
All	All	4470	0	4261	59	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.

All (59) 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:238:ALA:C	1:A:240:SER:N	1.68	1.45
1:B:70:SER:OG	2:B:400:DWZ:HAA	1.14	1.31
1:B:31:ASP:N	3:B:609:HOH:O	1.96	0.97
1:A:70:SER:OG	2:A:400:DWZ:HAA	1.62	0.96
1:A:291:ASN:O	3:A:650:HOH:O	1.85	0.92
1:B:70:SER:HG	2:B:400:DWZ:HAA	0.97	0.80
1:A:70:SER:CB	2:A:400:DWZ:HAA	2.15	0.77
1:B:99:ARG:HD3	3:B:524:HOH:O	1.87	0.74
1:A:70:SER:CB	2:A:400:DWZ:CAA	2.69	0.70
1:B:70:SER:CB	2:B:400:DWZ:HAA	2.19	0.70
1:B:70:SER:CB	2:B:400:DWZ:CAA	2.70	0.70
1:A:77[B]:VAL:HG21	1:A:127:LEU:HD11	1.74	0.69
1:B:77[B]:VAL:HG21	1:B:127:LEU:HD11	1.74	0.68
1:A:238:ALA:O	1:A:240:SER:N	2.25	0.68
1:B:99:ARG:CD	3:B:524:HOH:O	2.41	0.67
1:B:99:ARG:CG	1:B:102:LEU:HD12	2.24	0.67
1:B:119:LEU:HD21	1:B:141[A]:GLN:HG3	1.80	0.63
1:B:33:PHE:CE1	1:B:46[A]:ILE:CD1	2.82	0.63
1:B:99:ARG:HG3	1:B:102:LEU:HD12	1.82	0.61
1:A:141[A]:GLN:HG2	3:A:607:HOH:O	2.02	0.59
2:A:400:DWZ:CAA	2:A:400:DWZ:CAL	2.77	0.59
1:B:268:ASP:HB3	3:B:612:HOH:O	2.01	0.59
1:B:93:GLN:NE2	3:B:594:HOH:O	2.36	0.59
1:B:268:ASP:CB	3:B:612:HOH:O	2.50	0.58
1:A:277:LYS:HE3	1:A:281:GLU:OE2	2.07	0.55
1:B:99:ARG:HD2	3:B:627:HOH:O	2.07	0.54
1:B:33:PHE:CE1	1:B:46[A]:ILE:HD13	2.42	0.54
1:B:99:ARG:NE	3:B:524:HOH:O	2.41	0.53
1:B:99:ARG:HG2	1:B:102:LEU:HD12	1.91	0.52
1:B:31:ASP:CG	3:B:586:HOH:O	2.49	0.51
1:A:135:GLN:HE21	1:A:139[B]:LEU:HD11	1.73	0.51
1:A:274:TYR:OH	2:A:400:DWZ:HB	2.11	0.50



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:93:GLN:HG3	3:A:609:HOH:O	2.14	0.48
1:A:77[B]:VAL:HG23	1:A:207:LEU:HD13	1.96	0.48
1:A:70:SER:HB2	2:A:400:DWZ:HAA	1.92	0.47
1:A:73:LYS:HD3	1:A:126:SER:OG	2.15	0.46
1:B:114:ASP:HB2	3:B:505:HOH:O	2.16	0.46
1:B:213:ARG:HD2	3:A:555:HOH:O	2.16	0.45
1:B:202[A]:GLU:HG3	3:B:637:HOH:O	2.17	0.45
1:A:225:VAL:CG1	1:A:229:TRP:HB2	2.46	0.45
1:B:111:LYS:HE3	1:A:227:ASP:O	2.17	0.44
1:B:33:PHE:CD1	1:B:46[A]:ILE:HD12	2.52	0.44
1:A:73:LYS:HB2	1:A:234:LYS:HE3	2.00	0.44
1:B:99:ARG:NH1	1:B:99:ARG:HB3	2.33	0.44
1:B:237:ALA:HB3	2:B:400:DWZ:SAK	2.58	0.43
2:A:400:DWZ:CAA	2:A:400:DWZ:CAI	2.95	0.43
1:B:48:ALA:HB2	1:B:261:LEU:HD13	2.00	0.43
2:A:400:DWZ:HAI	2:A:400:DWZ:HAB	1.67	0.43
1:B:111:LYS:HD3	1:A:228:GLY:HA3	2.00	0.43
2:B:400:DWZ:HASB	2:B:400:DWZ:OAG	2.18	0.43
1:B:68:PHE:CD1	1:B:72:ILE:HB	2.54	0.43
1:B:99:ARG:CZ	1:B:99:ARG:CB	2.97	0.43
1:B:164:ARG:NH2	1:B:178[A]:GLN:HE21	2.17	0.42
1:B:99:ARG:HG3	1:B:102:LEU:CD1	2.50	0.42
1:A:43:LYS:O	1:A:265:SER:HA	2.19	0.42
1:A:55:ARG:NH1	3:A:627:HOH:O	2.52	0.41
1:B:73:LYS:HD3	1:B:126:SER:OG	2.20	0.41
1:B:241:TYR:HA	1:B:269:LYS:O	2.20	0.40

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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	А	264/268~(98%)	255~(97%)	8(3%)	1 (0%)	34 42
1	В	264/268~(98%)	257 (97%)	6~(2%)	1 (0%)	34 42
All	All	528/536~(98%)	512 (97%)	14 (3%)	2~(0%)	34 42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	103	VAL
1	В	103	VAL

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	226/226~(100%)	223~(99%)	3~(1%)	69 82		
1	В	226/226 (100%)	218~(96%)	8 (4%)	36 50		
All	All	452/452~(100%)	441 (98%)	11 (2%)	50 66		

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	35	LYS
1	В	130	SER
1	В	163	GLU
1	В	202[A]	GLU
1	В	202[B]	GLU
1	В	233	ASP
1	В	255	LYS
1	В	268	ASP
1	А	163	GLU
1	А	255	LYS
1	А	268	ASP

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such side chains are listed below:



Mol	Chain	Res	Type
1	В	54	ASN
1	В	82	GLN
1	В	93	GLN
1	А	93	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)

2 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 Trme		Chain Dag		Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
Mol Type Chain	Res	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2		
2	DWZ	В	400	1	22,27,27	1.97	5 (22%)	$13,\!39,\!39$	1.99	3 (23%)
2	DWZ	А	400	1	22,27,27	2.48	6 (27%)	13,39,39	1.97	3 (23%)

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	DWZ	В	400	1	-	9/18/51/51	0/2/2/2



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DWZ	А	400	1	-	11/18/51/51	0/2/2/2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
2	А	400	DWZ	CAI-CAH	-5.82	1.51	1.55
2	А	400	DWZ	CAI-SAK	-5.79	1.70	1.84
2	В	400	DWZ	CAI-SAK	-4.65	1.73	1.84
2	А	400	DWZ	CAM-CAL	-4.52	1.45	1.52
2	А	400	DWZ	CG-SAK	-4.19	1.75	1.82
2	В	400	DWZ	CAI-CAH	-4.00	1.52	1.55
2	В	400	DWZ	CG-SAK	-3.89	1.75	1.82
2	А	400	DWZ	CAL-NAJ	-3.55	1.26	1.28
2	В	400	DWZ	CAL-NAJ	-3.48	1.26	1.28
2	В	400	DWZ	CAM-CAL	-3.40	1.46	1.52
2	А	400	DWZ	CAB-CAA	2.24	1.53	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	В	400	DWZ	C-CA-N	5.01	120.81	111.74
2	А	400	DWZ	CAB-CAD-NAJ	-4.03	104.11	111.94
2	В	400	DWZ	CAS-CAH-CAI	3.78	120.04	113.35
2	А	400	DWZ	CA-C-NBC	-3.58	114.30	118.57
2	В	400	DWZ	CAB-CAD-NAJ	-2.41	107.26	111.94
2	А	400	DWZ	CAS-CAH-CAI	2.39	117.57	113.35

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	400	DWZ	O-C-NBC-CBE
2	В	400	DWZ	CA-C-NBC-CBE
2	В	400	DWZ	O-C-NBC-CBD
2	В	400	DWZ	CA-C-NBC-CBD
2	В	400	DWZ	CAH-CAI-SAK-CG
2	В	400	DWZ	CAE-CAB-CAD-CAH
2	В	400	DWZ	CAA-CAB-CAE-CAF
2	А	400	DWZ	O-C-NBC-CBE
2	А	400	DWZ	CA-C-NBC-CBE
2	А	400	DWZ	O-C-NBC-CBD



Mol	Chain	Res	Type	Atoms
2	А	400	DWZ	CA-C-NBC-CBD
2	А	400	DWZ	NBC-C-CA-N
2	А	400	DWZ	O-C-CA-N
2	А	400	DWZ	CD-CG-SAK-CAI
2	А	400	DWZ	CAH-CAI-SAK-CG
2	А	400	DWZ	CAE-CAB-CAD-CAH
2	А	400	DWZ	OAC-CAA-CAB-CAE
2	В	400	DWZ	O-C-CA-N
2	В	400	DWZ	NBC-C-CA-N
2	А	400	DWZ	OAC-CAA-CAB-CAD

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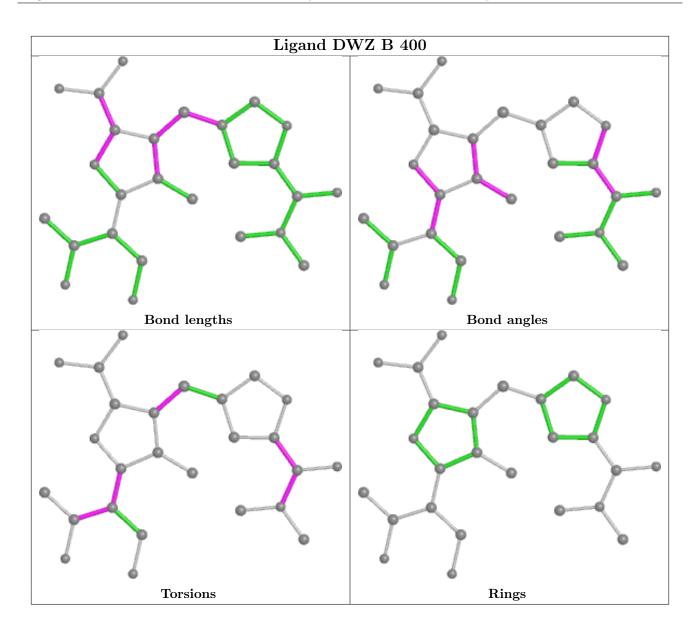
There are no ring outliers.

2 monomers are involved in 14 short contacts:

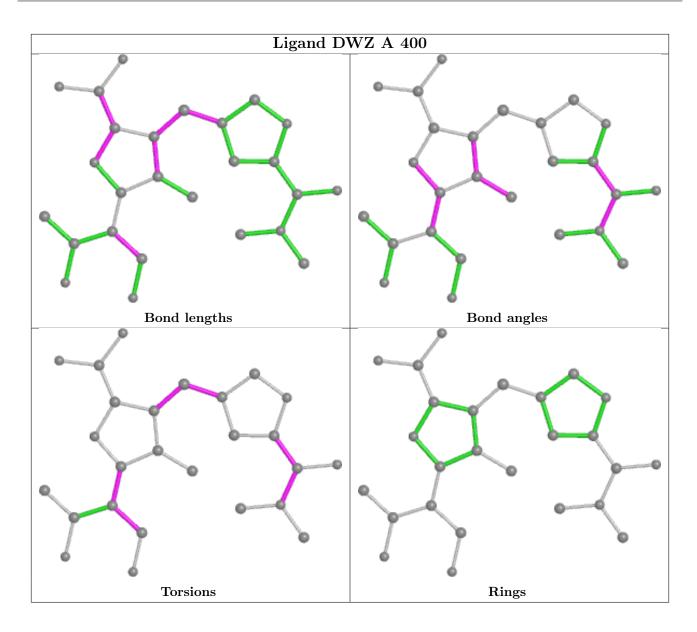
I	Mol	Chain	Res	Type	Clashes	Symm-Clashes
	2	В	400	DWZ	6	0
	2	А	400	DWZ	8	0

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 sufficient must be 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	А	1
1	В	1

All chain breaks are listed below:



Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	А	238:ALA	С	240:SER	Ν	1.68
1	В	83:GLN	С	86:LYS	Ν	1.63



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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	256/268~(95%)	-0.06	7 (2%) 54 62	6, 11, 30, 62	0
1	В	256/268~(95%)	-0.15	6 (2%) 60 67	5, 10, 26, 46	0
All	All	512/536~(95%)	-0.11	13 (2%) 57 64	5, 11, 28, 62	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	255	LYS	4.8
1	А	256	GLY	4.7
1	А	114	ASP	3.0
1	В	52	GLY	2.7
1	В	99	ARG	2.6
1	В	268	ASP	2.6
1	В	55	ARG	2.4
1	А	99	ARG	2.4
1	В	114	ASP	2.4
1	А	291	ASN	2.3
1	В	256	GLY	2.1
1	А	115	THR	2.0
1	А	268	ASP	2.0

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.

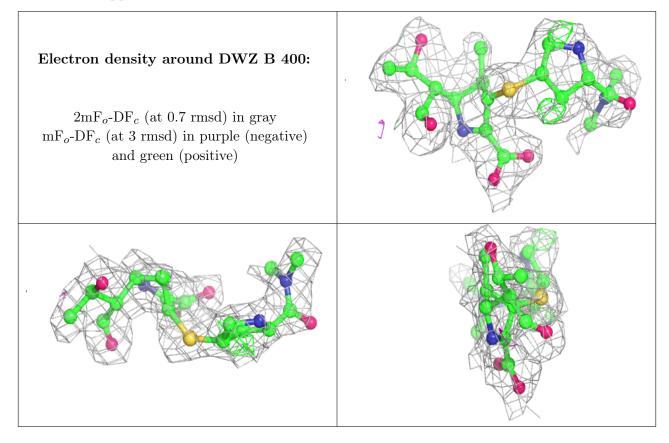


6.4 Ligands (i)

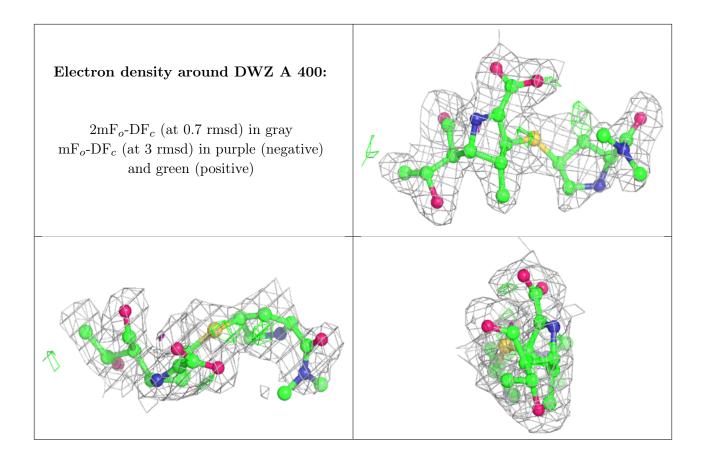
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
2	DWZ	В	400	26/26	0.90	0.17	$13,\!27,\!47,\!47$	0
2	DWZ	А	400	26/26	0.91	0.17	11,23,47,51	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.

