Full wwPDB Geometry-Only Validation Report (i)

May 22, 2020 – 01:41 pm BST

PDB ID	:	5KSC
Title	:	E166A/R274N/R276N Toho-1 Beta-lactamase aztreonam acyl-enzyme intermediate
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Deposited on	:	2016-07-08
Resolution	:	2.10 Å(reported)

This is a Full wwPDB Geometry-Only 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:

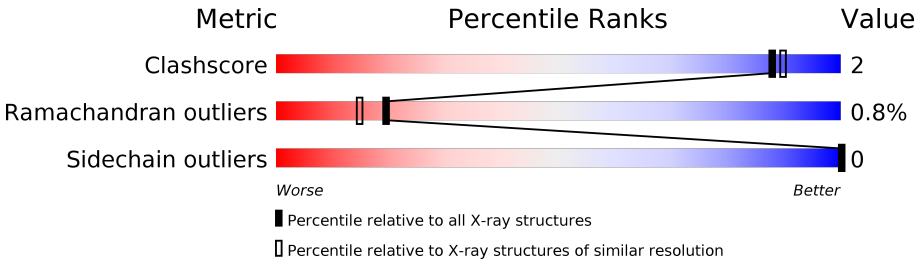
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
NEUTRON DIFFRACTION

The reported resolution of this entry is 2.10 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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 on 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	261	95% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2071 atoms, of which 0 are hydrogens and 48 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.

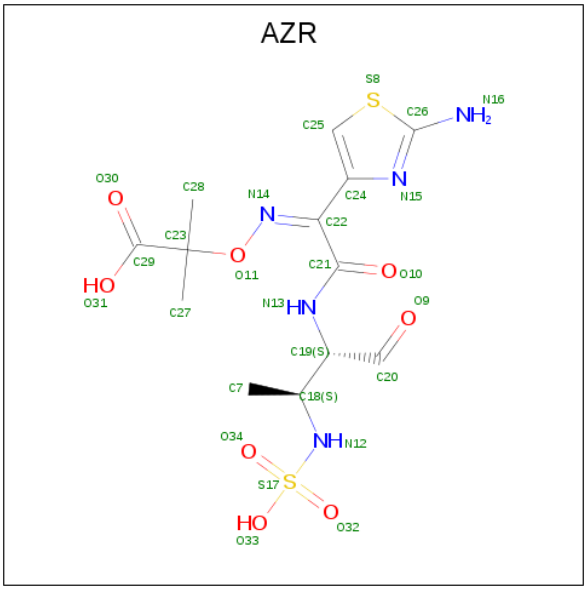
- Molecule 1 is a protein called Beta-lactamase Toho-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			1966	1224	350	386	6			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	ALA	GLU	engineered mutation	UNP Q47066
A	271	ASN	ARG	engineered mutation	UNP Q47066
A	273	ASN	ARG	engineered mutation	UNP Q47066

- Molecule 2 is 2-({[(1Z)-1-(2-amino-1,3-thiazol-4-yl)-2-oxo-2-{[(2S,3S)-1-oxo-3-(sulfoamino)butan-2-yl]amino}ethylidene]amino}oxy)-2-methylpropanoic acid (three-letter code: AZR) (formula: $C_{13}H_{19}N_5O_8S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			28	13	5	8	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	D	O		
3	A	29	77	48	29	0	0

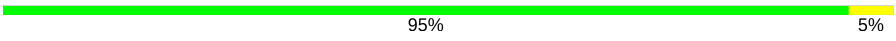
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

Note EDS was not executed.

- Molecule 1: Beta-lactamase Toho-1

Chain A:



4 Model quality

4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AZR, DOD

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	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.24	0/1996	0.40	0/2710

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

4.2 Too-close contacts

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	1966	0	1978	8	0
2	A	28	0	17	2	0
3	A	77	0	0	2	0
All	All	2071	0	1995	8	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 2.

All (8) 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:129:SER:OG	2:A:301:AZR:N12	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:ASP:OD2	3:A:401:DOD:O	2.23	0.52
1:A:202:GLN:OE1	1:A:202:GLN:N	2.46	0.49
1:A:79:VAL:HG21	1:A:137:LEU:HD22	1.86	0.47
1:A:280:ALA:O	1:A:284:THR:OG1	2.23	0.47
1:A:176:PRO:O	1:A:179:THR:OG1	2.27	0.45
1:A:129:SER:HG	2:A:301:AZR:HN12	1.54	0.42
1:A:93:ARG:NH2	3:A:414:DOD:O	2.53	0.40

There are no symmetry-related clashes.

4.3 Torsion angles (i)

4.3.1 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	259/261 (99%)	248 (96%)	9 (4%)	2 (1%)	19 15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	219	SER
1	A	102	VAL

4.3.2 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	208/209 (100%)	208 (100%)	0	100 100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

4.3.3 RNA

There are no RNA molecules in this entry.

4.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates

There are no carbohydrates in this entry.

4.6 Ligand geometry

1 ligand is 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	AZR	A	301	1	20,28,28	4.51	13 (65%)	18,41,41	3.40	6 (33%)

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	AZR	A	301	1	-	8/22/35/35	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	AZR	C25-S8	-11.17	1.53	1.70
2	A	301	AZR	O32-S17	8.19	1.51	1.42
2	A	301	AZR	O34-S17	8.09	1.51	1.42
2	A	301	AZR	C24-N15	6.35	1.57	1.37
2	A	301	AZR	C18-N12	-5.94	1.42	1.47
2	A	301	AZR	C21-N13	4.03	1.42	1.34
2	A	301	AZR	S17-N12	3.82	1.64	1.59
2	A	301	AZR	C19-N13	-3.11	1.42	1.46
2	A	301	AZR	O11-C23	-2.75	1.41	1.46
2	A	301	AZR	O11-N14	-2.53	1.37	1.42
2	A	301	AZR	C26-N16	2.37	1.42	1.35
2	A	301	AZR	C24-C22	2.34	1.51	1.48
2	A	301	AZR	C19-C18	-2.22	1.51	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	301	AZR	N16-C26-N15	11.51	138.08	123.19
2	A	301	AZR	O11-N14-C22	4.50	118.86	111.87
2	A	301	AZR	O34-S17-O32	-3.82	111.14	120.16
2	A	301	AZR	C22-C21-N13	3.37	119.98	114.38
2	A	301	AZR	C24-C25-S8	-3.21	107.85	111.79
2	A	301	AZR	C23-O11-N14	2.18	112.27	110.33

There are no chirality outliers.

All (8) torsion outliers are listed below:

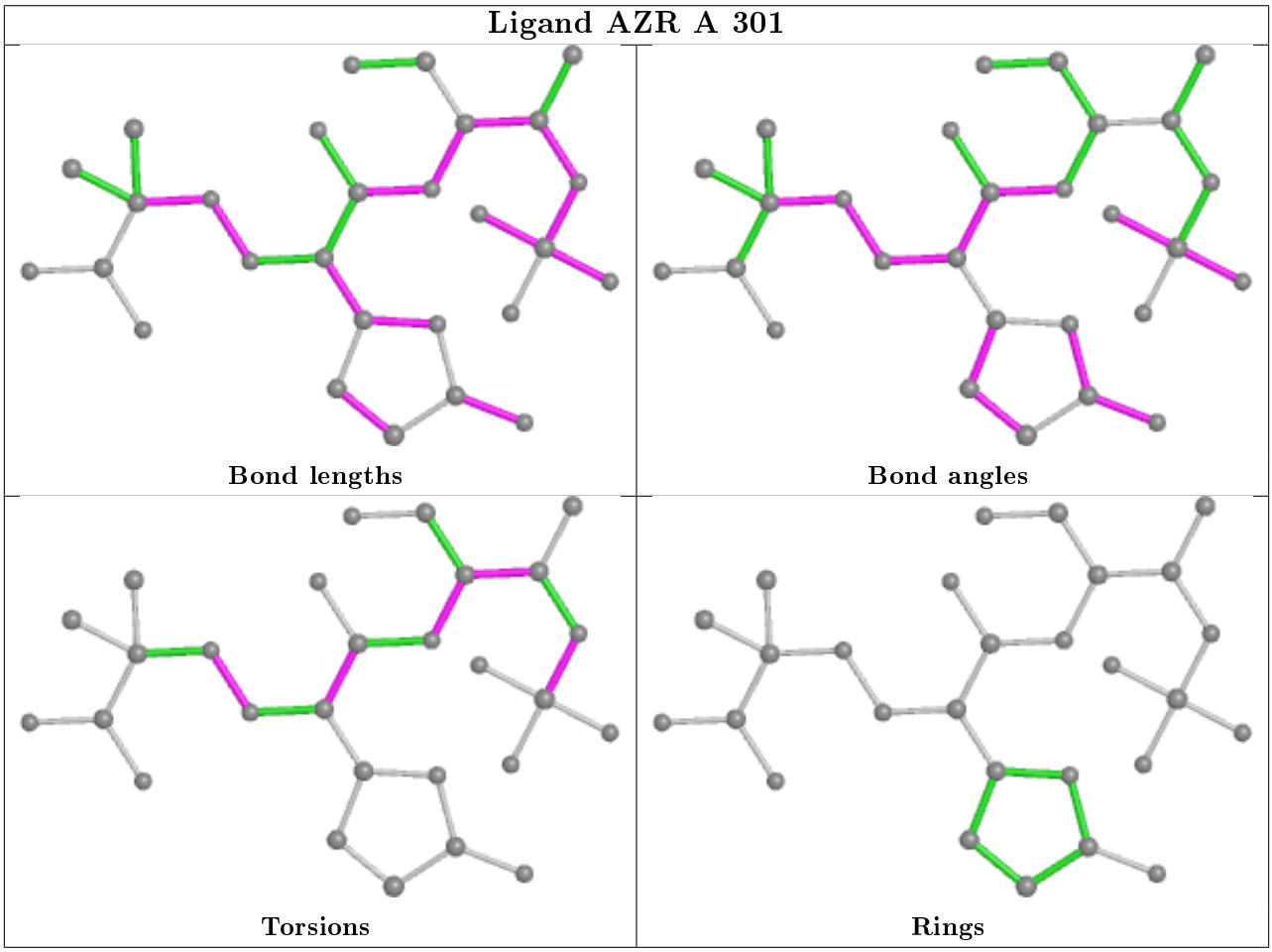
Mol	Chain	Res	Type	Atoms
2	A	301	AZR	C22-N14-O11-C23
2	A	301	AZR	C18-N12-S17-O34
2	A	301	AZR	C7-C18-C19-N13
2	A	301	AZR	C7-C18-C19-C20
2	A	301	AZR	N12-C18-C19-N13
2	A	301	AZR	C20-C19-N13-C21
2	A	301	AZR	O10-C21-C22-N14
2	A	301	AZR	N13-C21-C22-N14

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	AZR	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.



4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.