wwPDB X-ray Structure Validation Summary Report (i)

Oct 2, 2023 – 04:22 PM EDT

PDB ID	:	6NVT
Title	:	Crystal structure of TLA-1 extended spectrum Beta-lactamase
Authors	:	Rudino-Pinera, E.; Cifuentes-Castro, V.H.; Rodriguez-Almazan, C.
Deposited on	:	2019-02-05
Resolution	:	2.20 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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
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)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

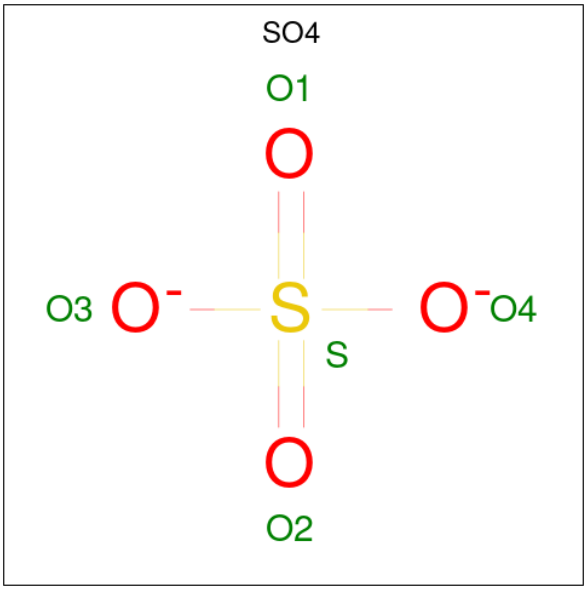
There are 5 unique types of molecules in this entry. The entry contains 10170 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	A	276	Total	C	N	O	S	7	3	0
			2201	1402	371	423	5			
1	B	276	Total	C	N	O	S	9	3	0
			2201	1405	368	423	5			
1	C	276	Total	C	N	O	S	16	5	0
			2213	1412	371	425	5			
1	D	276	Total	C	N	O	S	9	4	0
			2213	1410	369	429	5			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	O	S		0	0
			5	4	1			
2	A	1	Total	O	S		0	0
			5	4	1			

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0

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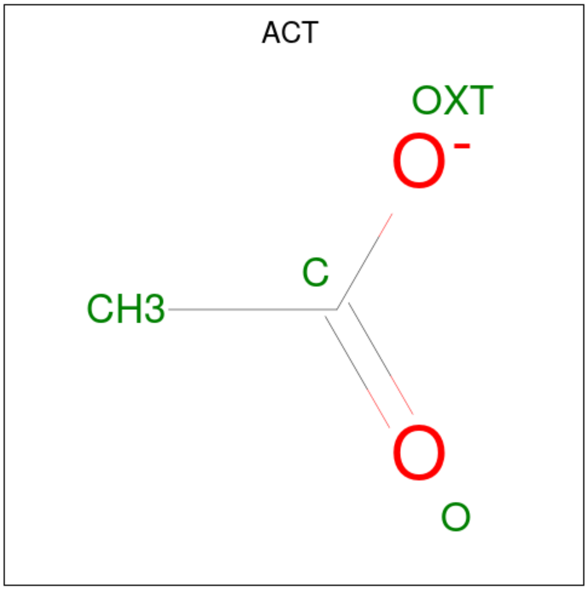
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0
3	C	4	Total Cl 4 4	0	0
3	D	2	Total Cl 2 2	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	254	Total O 254 254	0	0
5	B	263	Total O 263 263	0	0
5	C	256	Total O 256 256	0	0
5	D	263	Total O 263 263	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	99.06Å 99.01Å 99.70Å 90.00° 90.04° 90.00°	Depositor
Resolution (Å)	35.15 – 2.20	Depositor
% Data completeness (in resolution range)	99.9 (35.15-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.181 , 0.208	Depositor
Wilson B-factor (Å^2)	35.4	Xtriage
Anisotropy	0.053	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.007 for l,k,-h 0.009 for -h,-l,-k 0.007 for -h,l,k 0.469 for k,h,-l 0.469 for -k,-h,-l 0.008 for l,h,k 0.007 for k,l,h 0.007 for -l,-h,k 0.007 for -k,-l,h 0.477 for h,-k,-l 0.008 for l,-k,h	Xtriage
Total number of atoms	10170	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.20% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

4 Model quality

4.1 Standard geometry

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles

4.3.1 Protein backbone

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA

MolProbity failed to run properly - this section is therefore empty.

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 monosaccharides in this entry.

4.6 Ligand geometry

Of 75 ligands modelled in this entry, 8 are monoatomic - leaving 67 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	SO4	D	303	-	4,4,4	0.15	0	6,6,6	0.14	0
4	ACT	A	317	-	3,3,3	0.95	0	3,3,3	1.14	0
4	ACT	C	318	-	3,3,3	0.75	0	3,3,3	1.85	1 (33%)
4	ACT	C	319	-	3,3,3	0.95	0	3,3,3	0.95	0
4	ACT	A	316	-	3,3,3	0.76	0	3,3,3	1.43	0
4	ACT	A	320	-	3,3,3	0.93	0	3,3,3	1.32	1 (33%)
2	SO4	A	307	-	4,4,4	0.45	0	6,6,6	0.54	0
4	ACT	B	314	-	3,3,3	0.83	0	3,3,3	1.79	1 (33%)
4	ACT	A	309	-	3,3,3	0.60	0	3,3,3	1.10	0
2	SO4	C	303	-	4,4,4	0.21	0	6,6,6	0.26	0
4	ACT	B	313	-	3,3,3	1.07	0	3,3,3	0.90	0
2	SO4	C	310	-	4,4,4	0.38	0	6,6,6	0.73	0
2	SO4	C	302	-	4,4,4	0.18	0	6,6,6	0.16	0
2	SO4	A	302	-	4,4,4	0.21	0	6,6,6	0.18	0
2	SO4	C	301	-	4,4,4	0.15	0	6,6,6	0.20	0
2	SO4	A	305	-	4,4,4	0.26	0	6,6,6	0.17	0
2	SO4	A	301	-	4,4,4	0.07	0	6,6,6	0.19	0
2	SO4	C	308	-	4,4,4	0.64	0	6,6,6	0.68	0
2	SO4	A	304	-	4,4,4	0.14	0	6,6,6	0.29	0
4	ACT	A	310	-	3,3,3	1.30	1 (33%)	3,3,3	1.43	1 (33%)
4	ACT	A	313	-	3,3,3	0.73	0	3,3,3	1.06	0
4	ACT	A	315	-	3,3,3	0.96	0	3,3,3	1.45	0
2	SO4	B	306	-	4,4,4	0.14	0	6,6,6	0.22	0
4	ACT	C	321	-	3,3,3	0.84	0	3,3,3	1.69	1 (33%)
4	ACT	D	311	-	3,3,3	1.09	0	3,3,3	0.82	0
2	SO4	B	303	-	4,4,4	0.17	0	6,6,6	0.09	0
2	SO4	D	306	-	4,4,4	0.39	0	6,6,6	0.35	0
2	SO4	C	309	-	4,4,4	0.39	0	6,6,6	0.67	0
2	SO4	B	301	-	4,4,4	0.14	0	6,6,6	0.17	0
4	ACT	D	312	-	3,3,3	0.93	0	3,3,3	1.27	0
4	ACT	A	319	-	3,3,3	0.97	0	3,3,3	1.96	2 (66%)
2	SO4	A	303	-	4,4,4	0.16	0	6,6,6	0.14	0
4	ACT	A	318	-	3,3,3	0.69	0	3,3,3	1.46	0
4	ACT	D	320	-	3,3,3	1.11	0	3,3,3	1.43	1 (33%)
2	SO4	C	306	-	4,4,4	0.13	0	6,6,6	0.16	0
4	ACT	C	317	-	3,3,3	0.91	0	3,3,3	1.79	2 (66%)
4	ACT	D	317	-	3,3,3	1.02	0	3,3,3	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	ACT	A	312	-	3,3,3	1.22	0	3,3,3	1.80	1 (33%)
4	ACT	A	314	-	3,3,3	0.77	0	3,3,3	1.70	1 (33%)
2	SO4	B	305	-	4,4,4	0.15	0	6,6,6	0.19	0
2	SO4	D	302	-	4,4,4	0.15	0	6,6,6	0.19	0
2	SO4	D	305	-	4,4,4	0.11	0	6,6,6	0.21	0
4	ACT	B	311	-	3,3,3	1.24	1 (33%)	3,3,3	0.36	0
2	SO4	B	304	-	4,4,4	0.15	0	6,6,6	0.13	0
2	SO4	D	304	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	A	306	-	4,4,4	0.37	0	6,6,6	0.42	0
4	ACT	B	310	-	3,3,3	1.07	0	3,3,3	1.54	1 (33%)
4	ACT	C	315	-	3,3,3	1.19	1 (33%)	3,3,3	0.98	0
4	ACT	D	309	-	3,3,3	0.77	0	3,3,3	0.85	0
2	SO4	C	307	-	4,4,4	0.18	0	6,6,6	0.06	0
4	ACT	D	310	-	3,3,3	1.00	0	3,3,3	1.69	1 (33%)
4	ACT	C	320	-	3,3,3	0.87	0	3,3,3	0.75	0
4	ACT	B	312	-	3,3,3	1.07	0	3,3,3	1.08	0
4	ACT	D	314	-	3,3,3	1.01	0	3,3,3	1.50	1 (33%)
2	SO4	D	301	-	4,4,4	0.21	0	6,6,6	0.19	0
4	ACT	C	316	-	3,3,3	1.01	0	3,3,3	1.80	1 (33%)
2	SO4	C	305	-	4,4,4	0.18	0	6,6,6	0.13	0
4	ACT	D	319	-	3,3,3	1.01	0	3,3,3	1.04	0
2	SO4	C	304	-	4,4,4	0.17	0	6,6,6	0.09	0
4	ACT	B	309	-	3,3,3	0.88	0	3,3,3	1.48	1 (33%)
4	ACT	D	313	-	3,3,3	0.99	0	3,3,3	0.94	0
4	ACT	D	316	-	3,3,3	0.87	0	3,3,3	2.04	2 (66%)
4	ACT	A	311	-	3,3,3	0.96	0	3,3,3	0.71	0
2	SO4	B	302	-	4,4,4	0.16	0	6,6,6	0.11	0
4	ACT	D	315	-	3,3,3	1.08	0	3,3,3	1.88	2 (66%)
2	SO4	B	307	-	4,4,4	0.15	0	6,6,6	0.14	0
4	ACT	D	318	-	3,3,3	1.06	0	3,3,3	1.13	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	310	ACT	OXT-C	-2.15	1.20	1.30
4	B	311	ACT	OXT-C	-2.12	1.20	1.30
4	C	315	ACT	OXT-C	-2.07	1.20	1.30

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	319	ACT	OXT-C-O	-2.57	112.59	122.05
4	A	312	ACT	OXT-C-O	-2.52	112.75	122.05
4	B	314	ACT	OXT-C-CH3	2.47	125.39	115.18
4	C	318	ACT	OXT-C-CH3	2.47	125.37	115.18
4	D	314	ACT	OXT-C-O	-2.46	113.00	122.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	312	ACT	0	1

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.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.