



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 28, 2026 – 05:07 AM EDT

PDB ID : 2A2T / pdb_00002a2t
Title : crystal structure of d(AAATATTT)
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Deposited on : 2005-06-23
Resolution : 3.10 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.

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
3	CAC	E	202	-	X	-	-
3	CAC	E	204	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1823 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.

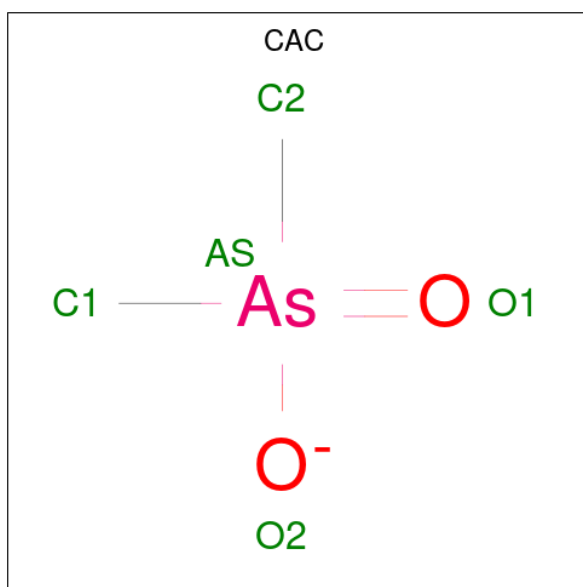
- Molecule 1 is a DNA chain called 5'-D(*AP*AP*AP*TP*AP*TP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	8	161	80	28	46	7	0	0	0
1	G	8	161	80	28	46	7	0	0	0
1	B	8	161	80	28	46	7	0	0	0
1	H	8	161	80	28	46	7	0	0	0
1	C	8	161	80	28	46	7	0	0	0
1	I	8	161	80	28	46	7	0	0	0
1	D	8	161	80	28	46	7	0	0	0
1	J	8	161	80	28	46	7	0	0	0
1	E	8	161	80	28	46	7	0	0	0
1	K	8	161	80	28	46	7	0	0	0
1	F	8	161	80	28	46	7	0	0	0

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Mn	0	0
			1	1		
2	E	5	Total	Mn	0	0
			5	5		

- Molecule 3 is CACODYLATE ION (CCD ID: CAC) (formula: C₂H₆AsO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	As	C	O		
3	E	1	5	1	2	2	0	0
3	E	1	5	1	2	2	0	0
3	E	1	5	1	2	2	0	0
3	E	1	5	1	2	2	0	0
3	E	1	5	1	2	2	0	0
3	E	1	5	1	2	2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			1	1		
4	G	1	Total	O	0	0
			1	1		
4	B	1	Total	O	0	0
			1	1		
4	H	1	Total	O	0	0
			1	1		
4	D	2	Total	O	0	0
			2	2		
4	J	1	Total	O	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	6	Total O 6 6	0	0
4	K	3	Total O 3 3	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	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	147.62Å 24.98Å 82.14Å 90.00° 90.51° 90.00°	Depositor
Resolution (Å)	15.00 – 3.10	Depositor
% Data completeness (in resolution range)	99.4 (15.00-3.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 2.77Å)	Xtrriage
Refinement program	REFMAC 5.2.0016	Depositor
R, R_{free}	0.272 , 0.357	Depositor
Wilson B-factor (Å ²)	49.4	Xtrriage
Anisotropy	0.674	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtrriage
Total number of atoms	1823	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.18 % 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 5.2042e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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

4.2 Too-close contacts [i](#)

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

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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

4.3.2 Protein sidechains [i](#)

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

4.3.3 RNA [i](#)

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

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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
3	CAC	E	206	2	2,4,4	2.94	2 (100%)	4,6,6	1.83	1 (25%)
3	CAC	E	201	2	2,4,4	3.12	2 (100%)	4,6,6	1.16	0
3	CAC	E	202	2	2,4,4	3.01	2 (100%)	4,6,6	2.19	3 (75%)
3	CAC	E	205	2	2,4,4	2.96	2 (100%)	4,6,6	1.77	1 (25%)
3	CAC	E	203	2	2,4,4	2.99	2 (100%)	4,6,6	1.09	0
3	CAC	E	204	2	2,4,4	3.00	2 (100%)	4,6,6	2.31	2 (50%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	201	CAC	AS-C1	3.43	1.98	1.90
3	E	204	CAC	AS-C2	3.21	1.97	1.90
3	E	202	CAC	AS-C2	3.16	1.97	1.90
3	E	205	CAC	AS-C2	3.14	1.97	1.90
3	E	206	CAC	AS-C1	3.07	1.97	1.90

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	204	CAC	O1-AS-C1	-3.69	106.91	111.50
3	E	206	CAC	O1-AS-C2	-2.69	108.15	111.50
3	E	202	CAC	O2-AS-C1	2.55	112.02	105.84
3	E	204	CAC	O2-AS-C1	2.41	111.68	105.84
3	E	202	CAC	O1-AS-C2	-2.33	108.60	111.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues

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.