



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 04:36 PM EDT

PDB ID : 6NMB  
Title : Tranexamic Acid is an Active Site Inhibitor of Urokinase Plasminogen Activator  
Authors : Law, R.H.P.; Wu, G.  
Deposited on : 2019-01-10  
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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (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

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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](#)

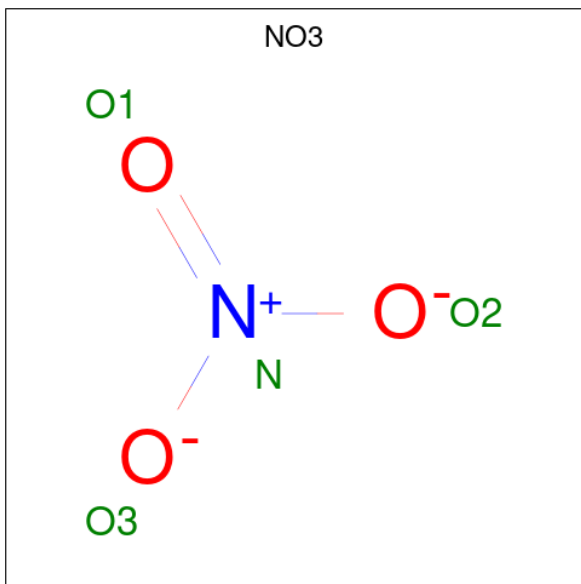
There are 4 unique types of molecules in this entry. The entry contains 8028 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Urokinase-type plasminogen activator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	251	Total 1912	C 1212	N 319	O 364	S 17	0	0	0
1	B	254	Total 1936	C 1225	N 327	O 367	S 17	0	0	0
1	C	253	Total 1915	C 1212	N 322	O 364	S 17	0	0	0
1	D	251	Total 1903	C 1205	N 319	O 362	S 17	0	0	0

- Molecule 2 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>).



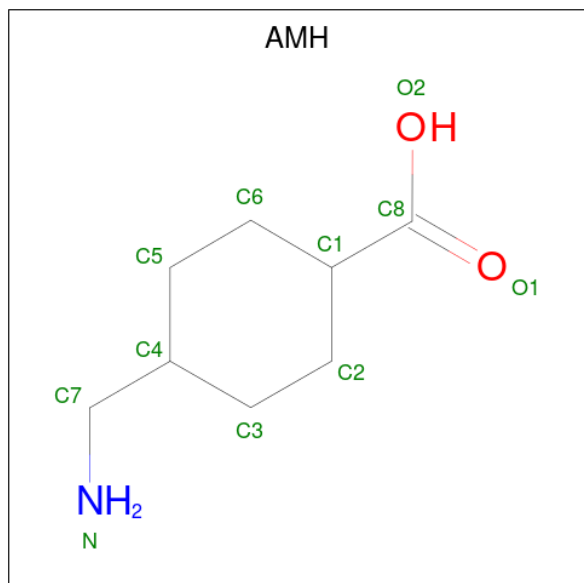
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	N	O		
2	A	1	Total 4	N 1	O 3	0	0
2	B	1	Total 4	N 1	O 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	N	O	0	0
			4	1	3		
2	D	1	Total	N	O	0	0
			4	1	3		

- Molecule 3 is TRANS-4-AMINOMETHYLCYCLOHEXANE-1-CARBOXYLIC ACID (three-letter code: AMH) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	8	1	2		
3	B	1	Total	C	N	O	0	0
			11	8	1	2		
3	C	1	Total	C	N	O	0	0
			11	8	1	2		
3	D	1	Total	C	N	O	0	0
			11	8	1	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	85	Total	O	0	0
			85	85		
4	B	81	Total	O	0	1
			82	82		
4	C	68	Total	O	0	0
			68	68		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	D	67	Total	O	0	0
			67	67		

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, $\alpha$ , $\beta$ , $\gamma$	73.04Å 65.45Å 111.14Å 90.00° 97.42° 90.00°	Depositor
Resolution (Å)	48.56 – 2.30	Depositor
% Data completeness (in resolution range)	90.0 (48.56-2.30)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.76 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.14_3260, PHENIX 1.14_3260	Depositor
R, $R_{free}$	0.221 , 0.271	Depositor
Wilson B-factor (Å <sup>2</sup> )	18.7	Xtrriage
Anisotropy	0.940	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8028	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	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 56.76 % 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 2.6127e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

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### 4.2 Too-close contacts [i](#)

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### 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 monosaccharides in this entry.

### 4.6 Ligand geometry [i](#)

8 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	AMH	D	302	-	11,11,11	1.37	2 (18%)	13,14,14	1.44	1 (7%)
2	NO3	C	301	-	1,3,3	0.55	0	0,3,3	-	-
3	AMH	A	302	-	11,11,11	1.14	0	13,14,14	1.41	2 (15%)
2	NO3	D	301	-	1,3,3	0.57	0	0,3,3	-	-
3	AMH	C	302	-	11,11,11	1.21	1 (9%)	13,14,14	1.81	5 (38%)
2	NO3	B	301	-	1,3,3	0.45	0	0,3,3	-	-
2	NO3	A	301	-	1,3,3	0.47	0	0,3,3	-	-
3	AMH	B	302	-	11,11,11	1.11	1 (9%)	13,14,14	1.99	5 (38%)

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
3	AMH	C	302	-	-	1/6/16/16	0/1/1/1
3	AMH	D	302	-	-	0/6/16/16	1/1/1/1
3	AMH	B	302	-	-	0/6/16/16	0/1/1/1
3	AMH	A	302	-	-	3/6/16/16	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	302	AMH	C1-C8	2.39	1.55	1.51
3	B	302	AMH	C6-C1	2.20	1.58	1.53
3	D	302	AMH	C6-C1	2.10	1.58	1.53
3	C	302	AMH	C1-C8	2.03	1.55	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	302	AMH	C6-C1-C2	4.37	119.20	109.97
3	B	302	AMH	O1-C8-C1	-3.02	115.54	122.93
3	C	302	AMH	C5-C4-C3	2.95	116.54	109.33
3	A	302	AMH	O1-C8-C1	-2.87	115.91	122.93
3	D	302	AMH	O1-C8-C1	-2.66	116.42	122.93
3	A	302	AMH	C5-C4-C3	2.63	115.77	109.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	302	AMH	C3-C4-C7	-2.47	106.22	111.47
3	B	302	AMH	C2-C3-C4	-2.46	108.35	112.42
3	B	302	AMH	C5-C6-C1	2.30	115.04	111.18
3	B	302	AMH	C6-C1-C8	2.24	115.68	111.32
3	C	302	AMH	C5-C6-C1	2.22	114.90	111.18
3	C	302	AMH	C2-C3-C4	2.16	116.00	112.42
3	C	302	AMH	C6-C5-C4	2.12	115.92	112.42

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	AMH	C3-C4-C7-N
3	A	302	AMH	C5-C4-C7-N
3	C	302	AMH	C3-C4-C7-N
3	A	302	AMH	C6-C1-C8-O1

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	302	AMH	C1-C2-C3-C4-C5-C6

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 [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.