

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 14, 2023 – 04:28 pm BST

PDB ID Title		8AMY High-resolution crystal structure of the Mu8.1 conotoxin from Conus Mucrona-
11010	•	tus
Authors	:	Mueller, E.; Hackney, C.M.; Ellgaard, L.; Morth, J.P.
Deposited on		
Resolution	:	1.67  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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

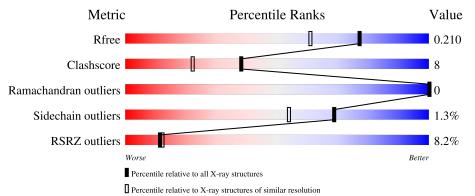
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA)	::	2.35 1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (2001) Parkinson et al. (1996)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.35

# 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 1.67 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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	
			8%	
1	А	89	83%	12% •



#### 8AMY

# 2 Entry composition (i)

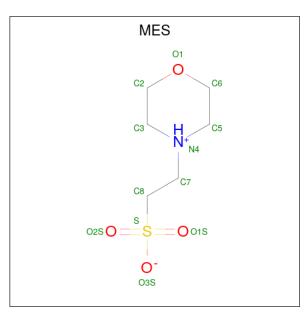
There are 8 unique types of molecules in this entry. The entry contains 1496 atoms, of which 679 are hydrogens and 0 are deuteriums.

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 Mu8.1 conotoxin.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
1	А	85	Total 1373	С 445	Н 665	N 118	0 133	S 12	0	5	0

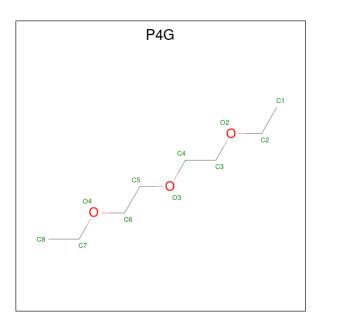
• Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



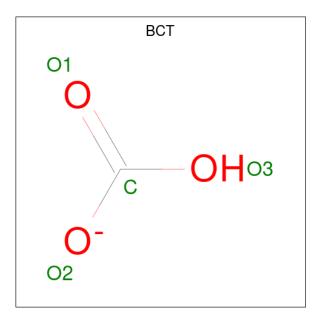
Mol	Chain	Residues		A	ton	ıs			ZeroOcc	AltConf
2	А	1	Total 25	С 6	Н 13	N 1	0 4	S 1	0	0

• Molecule 3 is 1-ETHOXY-2-(2-ETHOXYETHOXY)ETHANE (three-letter code: P4G) (formula:  $C_8H_{18}O_3$ ).



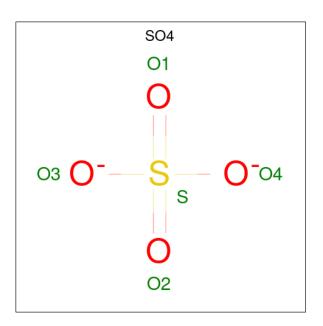


Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
3	А	1	Total 11	C 8	0 3	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{H} & \text{O} \\ 5 & 1 & 1 & 3 \end{array}$	0	0





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
5	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	TotalZn11	0	0

• Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	Total Na 1 1	0	0

• Molecule 8 is water.

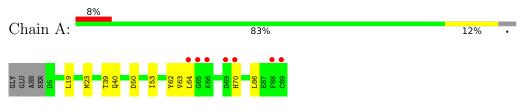
M	ol	Chain	Residues	Atoms	ZeroOcc	AltConf
8		А	70	Total         O           70         70	0	0



## 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: Mu8.1 conotoxin





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants	52.86Å 52.86Å 137.43Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	34.62 - 1.67	Depositor
Resolution (A)	34.62 - 1.67	EDS
% Data completeness	98.2 (34.62-1.67)	Depositor
(in resolution range)	98.9(34.62 - 1.67)	EDS
R <sub>merge</sub>	0.07	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.23 (at 1.67 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
D D.	0.169 , $0.200$	Depositor
$R, R_{free}$	0.175 , $0.210$	DCC
$R_{free}$ test set	584 reflections $(5.01\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	30.3	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.39, $58.6$	EDS
L-test for twinning <sup>2</sup>	$ \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	0.97	EDS
Total number of atoms	1496	wwPDB-VP
Average B, all atoms $(Å^2)$	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.14% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: MES, ZN, P4G, SO4, NA, BCT

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	Bond lengths		nd angles
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.70	0/735	0.81	1/994~(0.1%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	50	ASP	CB-CG-OD1	5.03	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

## 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	708	665	654	8	0
2	А	12	13	13	1	0
3	А	11	0	18	4	0
4	А	4	1	1	0	0
5	А	10	0	0	0	0
6	А	1	0	0	0	0
7	А	1	0	0	0	0
8	А	70	0	0	0	0
All	All	817	679	686	11	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 8.

All (11) 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:23[B]:MET:SD	1:A:62[B]:TYR:OH	2.16	1.03
3:A:502:P4G:H52	3:A:502:P4G:H83	1.75	0.69
1:A:39:THR:HG22	3:A:502:P4G:H22	1.80	0.63
1:A:23[B]:MET:SD	1:A:62[B]:TYR:CZ	2.99	0.54
1:A:23[B]:MET:SD	1:A:62[B]:TYR:CE1	3.05	0.49
3:A:502:P4G:H52	3:A:502:P4G:C8	2.39	0.48
1:A:53:ILE:CD1	1:A:86:LEU:HD11	2.46	0.46
1:A:63:VAL:HG12	1:A:64:LEU:HD12	2.00	0.43
1:A:40:GLN:HG2	3:A:502:P4G:H41	2.01	0.42
1:A:19:LEU:O	1:A:23[B]:MET:HG3	2.20	0.41

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	Perce	ntiles
1	А	88/89~(99%)	85~(97%)	3~(3%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	83/81 (102%)	82~(99%)	1 (1%)	71 57	

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	70	HIS

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

#### 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)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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 Lin		Link	Bo	ond leng	ths	Bond angles			
10101	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
5	SO4	А	504	-	4,4,4	0.38	0	6,6,6	0.46	0
5	SO4	А	505	-	4,4,4	0.28	0	6,6,6	0.28	0
4	BCT	А	503	-	2,3,3	1.38	0	2,3,3	<mark>3.69</mark>	1 (50%)
3	P4G	А	502	-	10,10,10	0.41	0	9,9,9	0.33	0
2	MES	А	501	-	12,12,12	1.54	1 (8%)	14,16,16	<mark>3.79</mark>	7 (50%)



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	P4G	А	502	-	-	7/8/8/8	-
2	MES	А	501	-	-	6/6/14/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	501	MES	C8-S	-3.76	1.72	1.77

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	А	501	MES	O2S-S-C8	9.90	118.84	106.92
2	А	501	MES	C2-C3-N4	6.67	120.21	110.10
4	А	503	BCT	O2-C-O1	4.84	132.09	119.55
2	А	501	MES	O1-C6-C5	3.54	119.59	111.80
2	А	501	MES	O3S-S-O2S	-3.30	103.22	111.27
2	А	501	MES	O3S-S-C8	2.78	110.27	105.77
2	А	501	MES	C5-N4-C3	2.32	114.06	108.83
2	А	501	MES	C6-O1-C2	2.08	116.85	109.89

There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
2	А	501	MES	C8-C7-N4-C5
2	А	501	MES	N4-C7-C8-S
3	А	502	P4G	C5-C6-O4-C7
3	А	502	P4G	O2-C3-C4-O3
2	А	501	MES	C8-C7-N4-C3
3	А	502	P4G	C3-C4-O3-C5
2	А	501	MES	C7-C8-S-O1S
2	А	501	MES	C7-C8-S-O2S
3	А	502	P4G	C1-C2-O2-C3
2	А	501	MES	C7-C8-S-O3S
3	А	502	P4G	C8-C7-O4-C6
3	А	502	P4G	C6-C5-O3-C4
3	А	502	P4G	O3-C5-C6-O4

All (13) torsion outliers are listed below:



There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	502	P4G	4	0
2	А	501	MES	1	0

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 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	<RSRZ $>$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	85/89~(95%)	0.52	7 (8%) 11 12	23, 33, 71, 130	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	66	LYS	4.1
1	А	70	HIS	3.6
1	А	88	PHE	3.2
1	А	89	CYS	3.2
1	А	69	ASP	2.6
1	А	65	GLY	2.6
1	А	64	LEU	2.1

## 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	$B-factors(Å^2)$	Q < 0.9
2	MES	А	501	12/12	0.70	0.22	$31,\!50,\!89,\!119$	0

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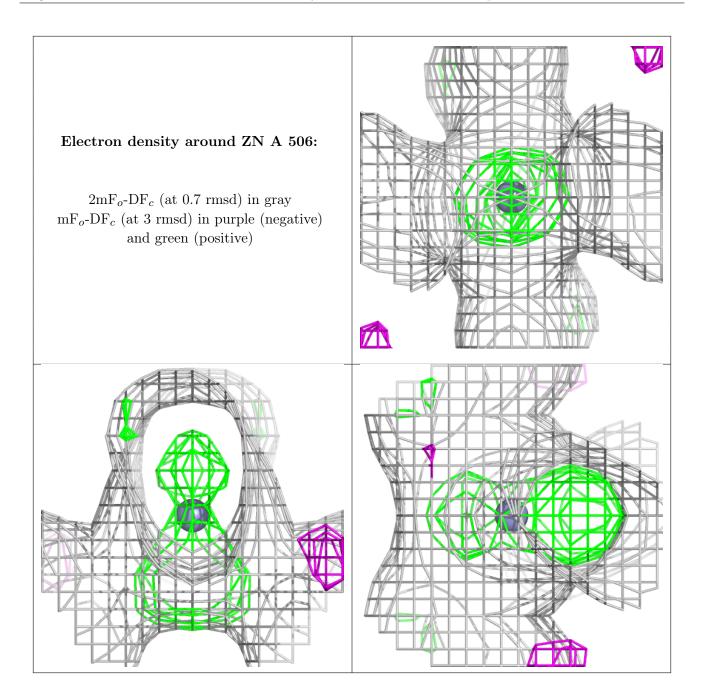


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	P4G	А	502	11/11	0.79	0.36	$20,\!41,\!48,\!49$	11
7	NA	А	507	1/1	0.83	0.30	73,73,73,73	0
4	BCT	А	503	4/4	0.95	0.18	53,61,69,69	0
5	SO4	А	505	5/5	0.96	0.11	53,53,60,66	5
6	ZN	А	506	1/1	0.99	0.10	34,34,34,34	1
5	SO4	А	504	5/5	0.99	0.15	28,29,30,36	0

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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.

