



# wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 10:28 PM GMT

PDB ID : 4JMC  
Title : Enduracididine biosynthesis enzyme MppR complexed with pyruvate  
Authors : Silvaggi, N.R.  
Deposited on : 2013-03-13  
Resolution : 1.72 Å(reported)

This is a wwPDB validation summary 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 <http://wwpdb.org/ValidationPDFNotes.html>

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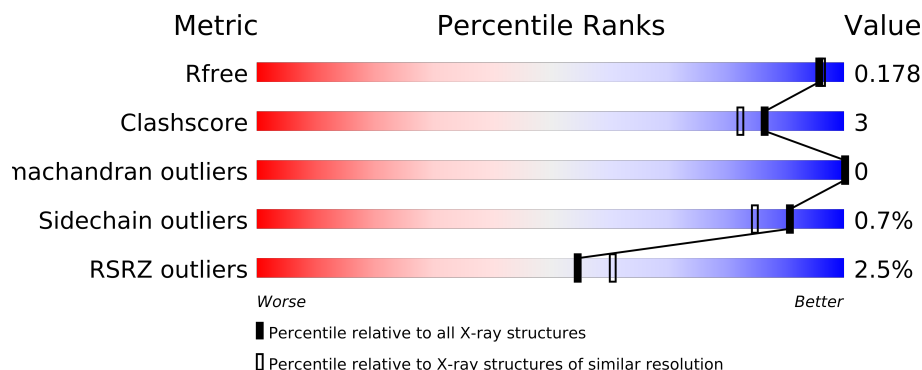
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance



The reported resolution of this entry is 1.72 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))
$R_{free}$	66092	2979 (1.74-1.70)
Clashscore	79885	3506 (1.74-1.70)
Ramachandran outliers	78287	3449 (1.74-1.70)
Sidechain outliers	78261	3449 (1.74-1.70)
RSRZ outliers	66119	2979 (1.74-1.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	302	
1	B	302	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	PYR	B	402[B]	X	-

## 2 Entry composition i

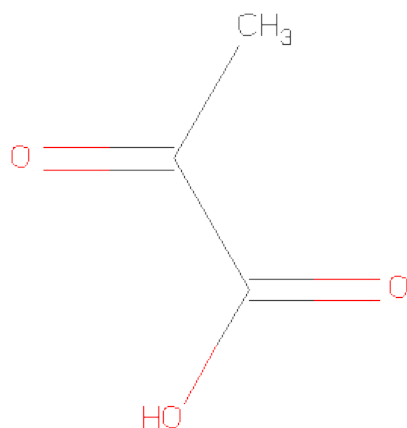
There are 3 unique types of molecules in this entry. The entry contains 8255 atoms, of which 3762 are hydrogens and 0 are deuterium.

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 Putative uncharacterized protein mppR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	257	Total	C	H	N	O	S	0	7	0
			3817	1255	1849	334	367	12			
1	B	258	Total	C	H	N	O	S	0	13	0
			3926	1283	1913	347	372	11			

- Molecule 2 is PYRUVIC ACID (three-letter code: PYR) (formula:  $C_3H_4O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			5	3	2		
2	B	1	Total	C	O	0	0
			5	3	2		
2	B	1	Total	C	O	0	1
			6	3	3		

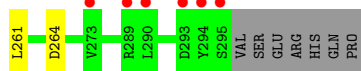
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	224	Total 224	O 224	0	0
3	B	272	Total 272	O 272	0	0

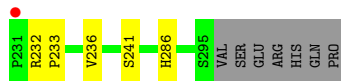
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- Molecule 1: Putative uncharacterized protein mppR

Age Group	Percentage
18-24	10%
25-34	85%
35-44	3%
45-54	2%
55-64	1%
65-74	1%
75-84	1%
85+	1%



Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.32Å 110.32Å 87.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.33 – 1.72 33.40 – 1.72	Depositor EDS
% Data completeness (in resolution range)	99.2 (32.33-1.72) 99.1 (33.40-1.72)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 1.72Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1069)	Depositor
R, $R_{free}$	0.157 , 0.178 0.156 , 0.178	Depositor DCC
$R_{free}$ test set	3299 reflections (5.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 38.8	EDS
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 65138 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8255	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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

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	0.44	0/2060	0.61	0/2815
1	B	0.49	0/2128	0.65	0/2907
All	All	0.47	0/4188	0.63	0/5722

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	98	TRP	Peptide

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1968	1849	0	5	0
1	B	2013	1913	0	15	0
2	A	5	0	3	0	0
2	B	11	0	6	3	0
3	A	224	0	0	2	0
3	B	272	0	0	4	0
All	All	4493	3762	9	20	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

The worst 5 of 20 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:165:ARG:NH2	3:B:579:HOH:O	1.97	0.89
1:A:50:MET:HE1	1:A:147[B]:MET:HG3	1.59	0.85
1:B:223:GLU:O	3:B:755:HOH:O	2.07	0.72
1:A:174:SER:HG	1:A:181:ARG:H	1.47	0.63
1:B:192[B]:ARG:CD	2:B:402[B]:PYR:O3	2.49	0.60

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	260/302 (86%)	259 (100%)	1 (0%)	0	100	100
1	B	267/302 (88%)	266 (100%)	1 (0%)	0	100	100
All	All	527/604 (87%)	525 (100%)	2 (0%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	208/239 (87%)	206 (99%)	2 (1%)	85	75
1	B	217/239 (91%)	216 (100%)	1 (0%)	94	89
All	All	425/478 (89%)	422 (99%)	3 (1%)	91	85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	GLU
1	A	261	LEU
1	B	223	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	GLN
1	A	157	GLN
1	A	206	GLN
1	B	142	GLN
1	B	152	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

3 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	$\# Z  > 2$
2	PYR	A	401	1	3,4,5	6.69	2 (66%)	2,4,6	2.32	1 (50%)
2	PYR	B	401	1	3,4,5	6.37	2 (66%)	2,4,6	2.40	1 (50%)
2	PYR	B	402[B]	-	5,5,5	3.37	3 (60%)	6,6,6	2.82	3 (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
2	PYR	A	401	1	-	0/1/2/4	0/0/0/0
2	PYR	B	401	1	-	0/1/2/4	0/0/0/0
2	PYR	B	402[B]	-	-	2/4/4/4	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	PYR	C2-C1	-11.15	1.40	1.51
2	B	401	PYR	C2-C1	-10.75	1.40	1.51
2	B	402[B]	PYR	C2-C1	-6.34	1.38	1.53
2	A	401	PYR	O1-C1	2.96	1.31	1.23
2	B	402[B]	PYR	O1-C1	2.86	1.31	1.22

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	402[B]	PYR	O2-C1-C2	4.71	124.75	114.37
2	B	402[B]	PYR	C3-C2-C1	3.83	126.39	117.47
2	B	401	PYR	O2-C1-O1	-3.39	117.32	123.71
2	A	401	PYR	O2-C1-O1	-3.19	117.70	123.71
2	B	402[B]	PYR	O2-C1-O1	-2.62	117.41	123.62

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	402[B]	PYR	O1-C1-C2-C3
2	B	402[B]	PYR	O2-C1-C2-C3

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	257/302 (85%)	0.06	10 (3%) 37 42	13, 28, 49, 80	0
1	B	258/302 (85%)	-0.06	3 (1%) 75 82	11, 22, 38, 53	0
All	All	515/604 (85%)	0.00	13 (2%) 54 60	11, 24, 44, 80	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	295	SER	4.7
1	A	294	TYR	4.3
1	A	225	VAL	4.2
1	A	290	LEU	4.1
1	A	293	ASP	3.0

### 6.2 Non-standard residues in protein, DNA, RNA chains

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

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PYR	A	401	5/6	0.14	1.18	21,22,28,34	0
2	PYR	B	402[B]	6/6	0.15	1.06	19,31,32,35	0
2	PYR	B	401	5/6	0.09	-0.39	18,20,26,29	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.