



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:19 PM GMT

PDB ID : 3QTC  
Title : Crystal structure of the catalytic domain of MmOmeRS, an O-methyl tyrosyl-tRNA synthetase evolved from Methanosarcina mazei PylRS, complexed with O-methyl tyrosine and AMP-PNP  
Authors : Dellas, N.; Takimoto, J.K.; Noel, J.P.; Wang, L.  
Deposited on : 2011-02-22  
Resolution : 1.75 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

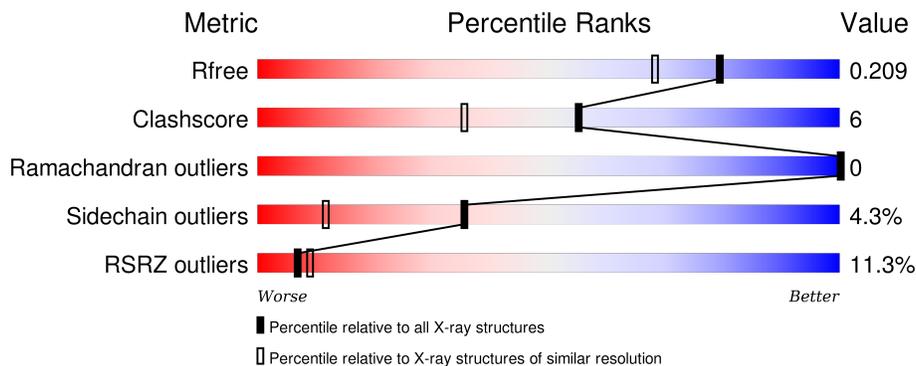
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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))
$R_{free}$	91344	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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. 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  $\leq 5\%$ . 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
1	A	290	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2455 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 Pyrrolysyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	257	2153	1371	372	402	8	0	8	0

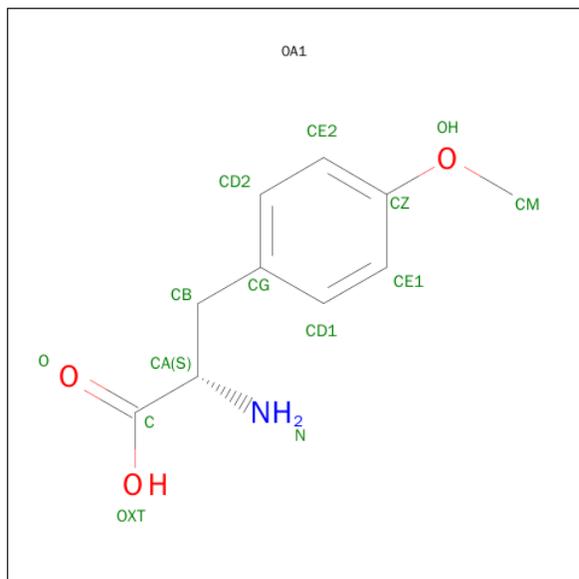
There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	MET	-	EXPRESSION TAG	UNP Q8PWY1
A	166	LYS	-	EXPRESSION TAG	UNP Q8PWY1
A	167	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	168	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	169	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	170	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	171	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	172	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	173	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	174	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	175	GLY	-	EXPRESSION TAG	UNP Q8PWY1
A	176	GLY	-	EXPRESSION TAG	UNP Q8PWY1
A	177	LEU	-	EXPRESSION TAG	UNP Q8PWY1
A	178	VAL	-	EXPRESSION TAG	UNP Q8PWY1
A	179	PRO	-	EXPRESSION TAG	UNP Q8PWY1
A	180	ARG	-	EXPRESSION TAG	UNP Q8PWY1
A	181	GLY	-	EXPRESSION TAG	UNP Q8PWY1
A	182	SER	-	EXPRESSION TAG	UNP Q8PWY1
A	183	HIS	-	EXPRESSION TAG	UNP Q8PWY1
A	184	GLY	-	EXPRESSION TAG	UNP Q8PWY1
A	302	THR	ALA	ENGINEERED MUTATION	UNP Q8PWY1
A	346	VAL	ASN	ENGINEERED MUTATION	UNP Q8PWY1
A	348	TRP	CYS	ENGINEERED MUTATION	UNP Q8PWY1
A	384	PHE	TYR	ENGINEERED MUTATION	UNP Q8PWY1
A	401	LEU	VAL	ENGINEERED MUTATION	UNP Q8PWY1

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

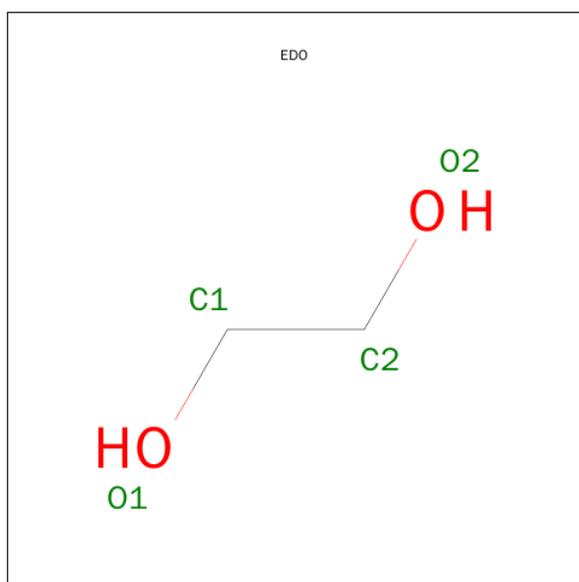
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0

- Molecule 3 is O-METHYL-L-TYROSINE (three-letter code: OA1) (formula:  $C_{10}H_{13}NO_3$ ).



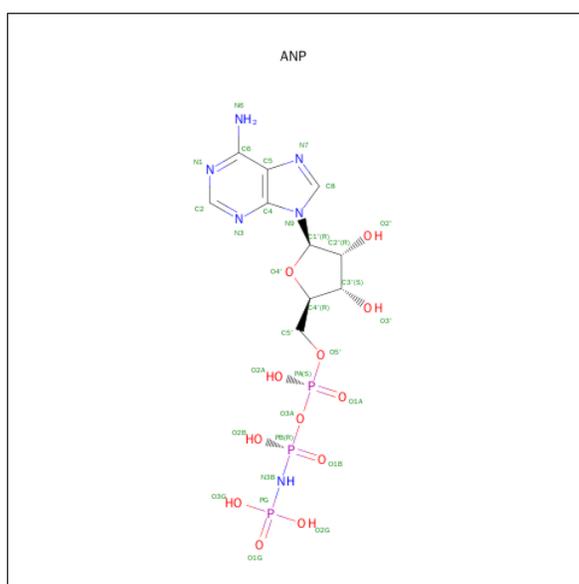
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 14 10 1 3	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula:  $C_{10}H_{17}N_6O_{12}P_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O P 31 10 6 12 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	235	Total O 235 235	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.81Å 104.81Å 71.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.30 – 1.75 42.30 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (42.30-1.75) 99.8 (42.30-1.75)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 1.75Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.183 , 0.212 0.183 , 0.209	Depositor DCC
$R_{free}$ test set	2268 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.8	Xtrriage
Anisotropy	0.005	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 44.1	EDS
Estimated twinning fraction	0.033 for h,-h-k,-l	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Outliers	0 of 44961 reflections	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2455	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 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: 0A1, MG, ANP, EDO

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	0.56	1/2206 (0.0%)	0.61	0/2966

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	444	GLU	CD-OE2	-5.90	1.19	1.25

There are no bond angle outliers.

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	A	2153	0	2170	28	0
2	A	2	0	0	0	0
3	A	14	0	12	0	0
4	A	20	0	30	0	0
5	A	31	0	13	0	0
6	A	235	0	0	5	0
All	All	2455	0	2225	28	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 6.

The worst 5 of 28 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:275[B]:ARG:HG3	1:A:410:GLU:HG2	1.62	0.81
1:A:217:ARG:HH11	1:A:217:ARG:HG2	1.48	0.78
1:A:275[B]:ARG:HD2	1:A:410:GLU:OE1	1.89	0.72
1:A:203[A]:ASN:HD21	1:A:205:LYS:HG2	1.54	0.72
1:A:275[B]:ARG:HG3	1:A:410:GLU:CG	2.21	0.70

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	Percentiles
1	A	259/290 (89%)	256 (99%)	3 (1%)	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	A	240/259 (93%)	228 (95%)	12 (5%)	30 8

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	282	THR
1	A	293	LYS
1	A	302[B]	THR
1	A	252	ARG
1	A	302[A]	THR

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	287	GLN
1	A	304	ASN
1	A	349	GLN
1	A	368	ASN
1	A	392	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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
5	ANP	A	810	2	27,33,33	2.15	9 (33%)	30,52,52	2.17	7 (23%)
3	0A1	A	811	-	11,14,14	0.53	0	12,18,18	0.92	0
4	EDO	A	812	-	3,3,3	0.54	0	2,2,2	0.05	0
4	EDO	A	813	-	3,3,3	0.48	0	2,2,2	0.51	0
4	EDO	A	814	-	3,3,3	0.41	0	2,2,2	0.43	0
4	EDO	A	815	-	3,3,3	0.54	0	2,2,2	0.34	0
4	EDO	A	817	-	3,3,3	0.42	0	2,2,2	0.41	0

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
5	ANP	A	810	2	-	1/12/38/38	0/3/3/3
3	0A1	A	811	-	-	0/6/10/10	0/1/1/1
4	EDO	A	812	-	-	0/1/1/1	0/0/0/0
4	EDO	A	813	-	-	0/1/1/1	0/0/0/0
4	EDO	A	814	-	-	0/1/1/1	0/0/0/0
4	EDO	A	815	-	-	0/1/1/1	0/0/0/0
4	EDO	A	817	-	-	0/1/1/1	0/0/0/0

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	810	ANP	PG-O3G	-2.50	1.49	1.56
5	A	810	ANP	PB-O2B	-2.23	1.50	1.56
5	A	810	ANP	PB-O3A	2.21	1.61	1.59
5	A	810	ANP	O4'-C1'	2.78	1.44	1.41
5	A	810	ANP	C5-C4	3.26	1.47	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	810	ANP	N3-C2-N1	-8.11	122.68	128.89
5	A	810	ANP	O1G-PG-N3B	-3.84	106.00	111.90
5	A	810	ANP	C2'-C1'-N9	-2.73	110.12	114.29
5	A	810	ANP	O1B-PB-N3B	-2.17	108.56	111.90
5	A	810	ANP	O3G-PG-O2G	2.08	113.75	107.58

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	810	ANP	O1B-PB-N3B-PG

There are no ring outliers.

No monomer is involved in short contacts.

## 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<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	257/290 (88%)	0.54	29 (11%) <b>7</b> <b>9</b>	17, 27, 46, 57	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	385	GLY	8.4
1	A	213	GLY	8.3
1	A	281	ASP	7.3
1	A	334	ASP	7.1
1	A	282	THR	6.6

### 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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	0A1	A	811	14/14	0.91	0.12	1.01	30,34,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	A	813	4/4	0.87	0.15	0.97	54,55,56,56	0
4	EDO	A	817	4/4	0.93	0.12	0.94	42,43,44,45	0
4	EDO	A	814	4/4	0.96	0.11	0.46	34,36,37,39	0
4	EDO	A	815	4/4	0.95	0.11	0.46	26,30,30,30	0
4	EDO	A	812	4/4	0.96	0.08	0.06	40,41,42,44	0
2	MG	A	801	1/1	0.99	0.07	-1.07	32,32,32,32	0
5	ANP	A	810	31/31	0.98	0.06	-1.09	19,23,27,29	0
2	MG	A	800	1/1	0.99	0.05	-	24,24,24,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.