



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:27 PM GMT

PDB ID : 1P3D
Title : Crystal Structure of UDP-N-acetylmuramic acid:L-alanine ligase (MurC) in Complex with UMA and ANP.
Authors : Mol, C.D.; Brooun, A.; Dougan, D.R.; Hilgers, M.T.; Tari, L.W.; Wijnands, R.A.; Knuth, M.W.; McRee, D.E.; Swanson, R.V.
Deposited on : 2003-04-17
Resolution : 1.70 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

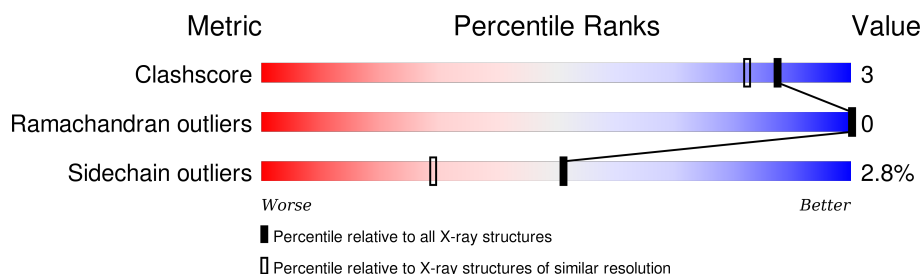
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)

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 ≥ 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	475	
1	B	475	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8054 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 UDP-N-acetylmuramate--alanine ligase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	Se	0	7	0
			3568	2250	623	678	3	14			
1	B	460	Total	C	N	O	S	Se	0	3	0
			3531	2223	617	674	3	14			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	15	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	31	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	110	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	115	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	135	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	138	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	187	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	194	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	199	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	209	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	228	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	236	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	371	MSE	MET	MODIFIED RESIDUE	UNP P45066
A	400	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	1	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	15	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	31	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	110	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	115	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	135	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	138	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	187	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	194	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	199	MSE	MET	MODIFIED RESIDUE	UNP P45066

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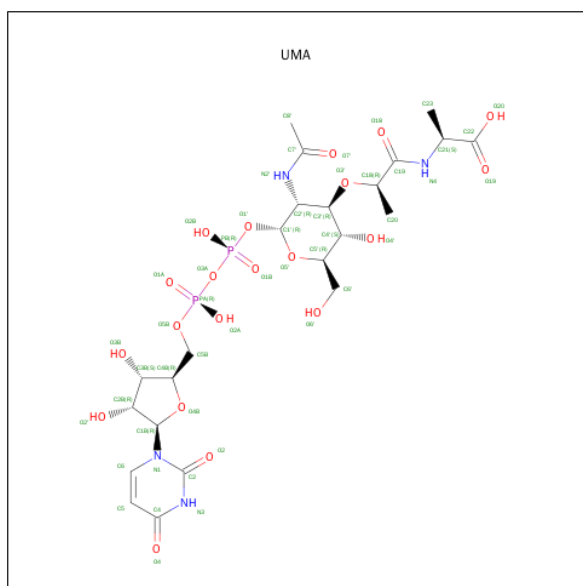
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Chain	Residue	Modelled	Actual	Comment	Reference
B	209	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	228	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	236	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	371	MSE	MET	MODIFIED RESIDUE	UNP P45066
B	400	MSE	MET	MODIFIED RESIDUE	UNP P45066

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mn 2 2	0	0
2	A	2	Total Mn 2 2	0	0

- Molecule 3 is URIDINE-5'-DIPHOSPHATE-N-ACETYLMURAMOYL-L-ALANINE (three-letter code: UMA) (formula: C₂₃H₃₆N₄O₂₀P₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 49 23 4 20 2	0	0
3	B	1	Total C N O P 49 23 4 20 2	0	0

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



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

- Molecule 5 is water.

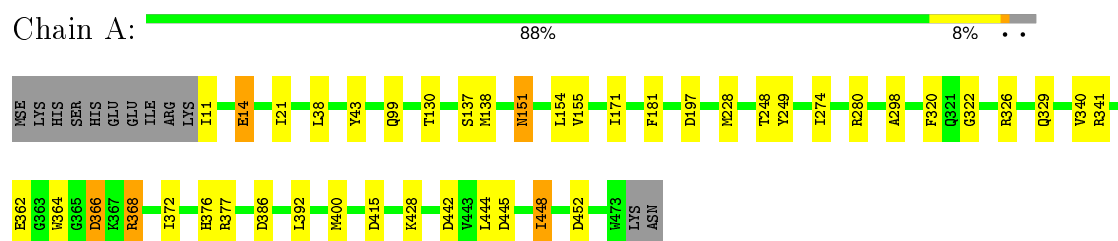
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	397	Total O 397 397	0	0
5	B	394	Total O 394 394	0	0

3 Residue-property plots

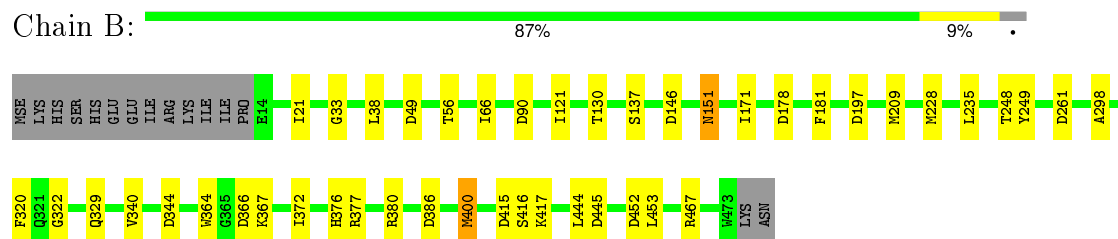
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

- Molecule 1: UDP-N-acetylmuramate--alanine ligase



- Molecule 1: UDP-N-acetylmuramate--alanine ligase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.92Å 87.33Å 86.11Å 90.00° 104.86° 90.00°	Depositor
Resolution (Å)	25.00 – 1.70	Depositor
% Data completeness (in resolution range)	96.5 (25.00-1.70)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.168 , 0.194	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8054	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: UMA, MN, ANP

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	0.36	1/3649 (0.0%)	0.69	7/4917 (0.1%)
1	B	0.34	0/3592	0.70	10/4838 (0.2%)
All	All	0.35	1/7241 (0.0%)	0.70	17/9755 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	368	ARG	CZ-NH2	7.25	1.42	1.33

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	368	ARG	NE-CZ-NH1	-7.67	116.47	120.30
1	B	344	ASP	CB-CG-OD2	6.79	124.41	118.30
1	A	386	ASP	CB-CG-OD2	6.29	123.96	118.30
1	A	415	ASP	CB-CG-OD2	6.11	123.80	118.30
1	B	366	ASP	CB-CG-OD2	5.85	123.57	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	3568	0	3562	16	0
1	B	3531	0	3513	20	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	49	0	33	0	0
3	B	49	0	33	1	0
4	A	31	0	13	0	0
4	B	31	0	13	0	0
5	A	397	0	0	0	0
5	B	394	0	0	3	0
All	All	8054	0	7167	37	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 3.

The worst 5 of 37 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:137:SER:HA	1:A:171[B]:ILE:HD13	1.74	0.68
1:B:400:MSE:HG2	1:B:416:SER:HB3	1.78	0.66
1:A:21:ILE:HD13	1:A:38:LEU:HD13	1.82	0.62
1:B:130:THR:HA	1:B:151:ASN:HD21	1.65	0.61
1:B:121:ILE:HD12	1:B:171[A]:ILE:CD1	2.33	0.57

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	468/475 (98%)	461 (98%)	7 (2%)	0	100	100
1	B	461/475 (97%)	454 (98%)	7 (2%)	0	100	100
All	All	929/950 (98%)	915 (98%)	14 (2%)	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	382/372 (103%)	367 (96%)	15 (4%)	39	16
1	B	375/372 (101%)	369 (98%)	6 (2%)	70	54
All	All	757/744 (102%)	736 (97%)	21 (3%)	51	29

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	362	GLU
1	A	366	ASP
1	B	329	GLN
1	A	341	ARG
1	B	367	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	20	GLN
1	B	376	HIS
1	B	151	ASN
1	A	282	ASN
1	B	61	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	UMA	A	602	-	39,51,51	0.76	1 (2%)	54,76,76	1.42	4 (7%)
4	ANP	A	603	2	27,33,33	1.34	4 (14%)	30,52,52	2.40	6 (20%)
3	UMA	B	1602	2	39,51,51	0.72	1 (2%)	54,76,76	1.36	3 (5%)
4	ANP	B	1603	2	27,33,33	1.53	5 (18%)	30,52,52	2.21	5 (16%)

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	UMA	A	602	-	-	0/34/79/79	0/3/3/3
4	ANP	A	603	2	-	0/12/38/38	0/3/3/3
3	UMA	B	1602	2	-	0/34/79/79	0/3/3/3
4	ANP	B	1603	2	-	0/12/38/38	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1603	ANP	C6-N6	-2.65	1.26	1.34
4	B	1603	ANP	C2-N1	2.18	1.38	1.33
4	A	603	ANP	PB-O1B	2.20	1.48	1.46
4	A	603	ANP	C2-N1	2.45	1.38	1.33
3	B	1602	UMA	C7'-N2'	2.72	1.44	1.34

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	ANP	N3-C2-N1	-11.33	120.22	128.89
4	B	1603	ANP	N3-C2-N1	-9.80	121.39	128.89
4	B	1603	ANP	C1'-N9-C4	-2.92	122.53	126.94
4	A	603	ANP	C4-C5-N7	-2.41	107.26	109.48
4	A	603	ANP	C1'-N9-C4	-2.40	123.31	126.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1602	UMA	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](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.