



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2017 – 02:42 AM EST

PDB ID : 1AMR
Title : X-RAY CRYSTALLOGRAPHIC STUDY OF PYRIDOXAMINE 5'-PHOSPHATE-TYPE ASPARTATE AMINOTRANSFERASES FROM ESCHERICHIA COLI IN THREE FORMS
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Deposited on : unknown
Resolution : 2.10 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

<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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

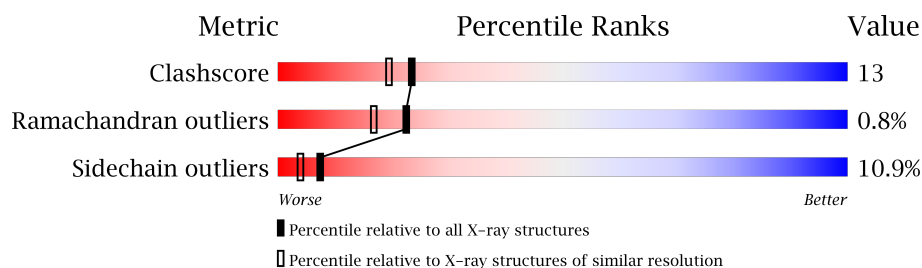
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)

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	396	

2 Entry composition [i](#)

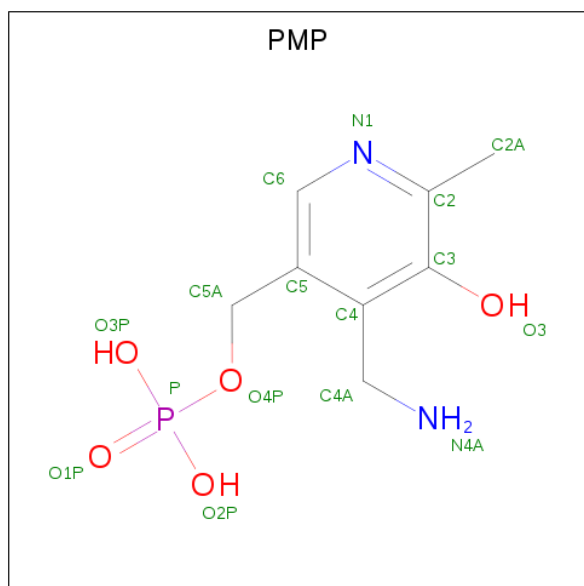
There are 4 unique types of molecules in this entry. The entry contains 3357 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ASPARTATE AMINOTRANSFERASE.

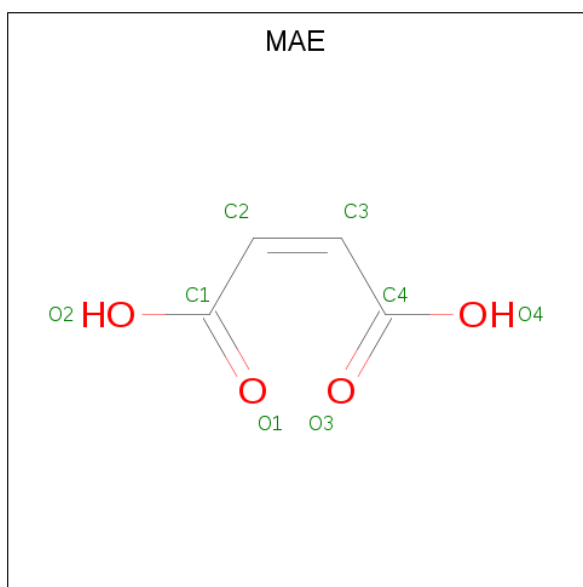
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	396	3069	1936	536	584	13	0	0	0

- Molecule 2 is 4'-DEOXY-4'-AMINOPYRIDOXAL-5'-PHOSPHATE (three-letter code: PMP) (formula: C₈H₁₃N₂O₅P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	16	8	2	5	1	0	0

- Molecule 3 is MALEIC ACID (three-letter code: MAE) (formula: C₄H₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	264	Total	O	0	0
			264	264		

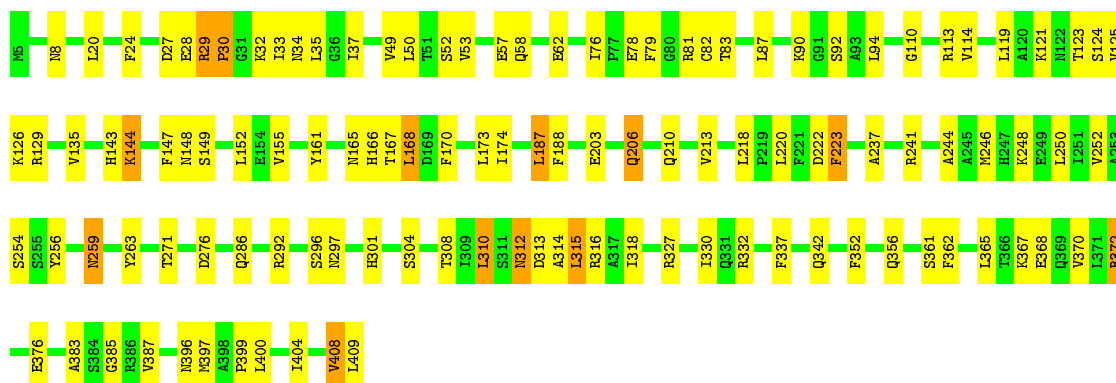
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

Note EDS was not executed.

• Molecule 1: ASPARTATE AMINOTRANSFERASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	157.60 Å 85.70 Å 78.90 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR, TOM, TOM/FRODO	Depositor
R, R_{free}	0.194 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3357	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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: PMP, MAE

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	0/3130	0.72	1/4240 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	250	LEU	CA-CB-CG	5.19	127.23	115.30

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	3069	0	3018	77	0
2	A	16	0	11	1	0
3	A	8	0	2	0	0
4	A	264	0	0	22	0
All	All	3357	0	3031	78	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 13.

All (78) 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:252:VAL:HG13	1:A:271:THR:HB	1.59	0.85
1:A:318:ILE:HG22	4:A:642:HOH:O	1.83	0.78
1:A:286:GLN:HG2	4:A:510:HOH:O	1.84	0.76
1:A:135:VAL:HG11	1:A:144:LYS:HE2	1.71	0.71
1:A:52:SER:HB3	4:A:642:HOH:O	1.93	0.69
1:A:94:LEU:HD11	1:A:244:ALA:HB1	1.76	0.68
1:A:356:GLN:NE2	1:A:361:SER:HA	2.09	0.67
1:A:301:HIS:HD2	4:A:481:HOH:O	1.77	0.66
1:A:206:GLN:HG3	4:A:503:HOH:O	1.96	0.65
1:A:121:LYS:HE3	4:A:428:HOH:O	1.98	0.64
1:A:29:ARG:O	1:A:32:LYS:HG3	1.98	0.62
1:A:313:ASP:HB2	4:A:588:HOH:O	1.98	0.62
1:A:210:GLN:O	1:A:213:VAL:HG22	2.01	0.61
1:A:123:THR:HG22	1:A:124:SER:N	2.16	0.60
1:A:35:LEU:HD21	1:A:400:LEU:HD11	1.83	0.59
2:A:413:PMP:N4A	2:A:413:PMP:O3	2.35	0.59
1:A:312:ASN:ND2	1:A:315:LEU:H	1.99	0.59
1:A:126:LYS:HE3	4:A:559:HOH:O	2.02	0.58
1:A:58:GLN:O	1:A:62:GLU:HG2	2.03	0.57
1:A:33:ILE:HG22	1:A:35:LEU:HD13	1.86	0.57
1:A:187:LEU:HD11	1:A:222:ASP:HB2	1.86	0.57
1:A:79:PHE:O	1:A:83:THR:HG23	2.06	0.56
1:A:327:ARG:HG3	4:A:623:HOH:O	2.06	0.56
1:A:123:THR:CG2	1:A:125:VAL:HG23	2.36	0.55
1:A:312:ASN:HD21	1:A:314:ALA:HB3	1.71	0.55
1:A:82:CYS:HB3	1:A:310:LEU:HD23	1.89	0.55
1:A:143:HIS:HB2	1:A:144:LYS:HE3	1.88	0.55
1:A:27:ASP:O	1:A:32:LYS:HD3	2.06	0.55
1:A:57:GLU:OE2	1:A:301:HIS:HE1	1.91	0.54
1:A:123:THR:HG21	1:A:125:VAL:HG23	1.90	0.53
1:A:29:ARG:HG3	1:A:29:ARG:O	2.09	0.53
1:A:385:GLY:HA3	4:A:523:HOH:O	2.07	0.53
1:A:304:SER:O	1:A:308:THR:HG23	2.09	0.53
1:A:312:ASN:HD22	1:A:315:LEU:H	1.57	0.51
1:A:37:ILE:HG13	4:A:658:HOH:O	2.09	0.51
1:A:83:THR:HB	4:A:532:HOH:O	2.09	0.51
1:A:155:VAL:HG23	4:A:643:HOH:O	2.09	0.51
1:A:372:ARG:HG2	1:A:408:VAL:HG22	1.93	0.50
1:A:223:PHE:O	1:A:254:SER:HA	2.11	0.50
1:A:397:MET:CE	1:A:397:MET:HA	2.42	0.49
1:A:404:ILE:O	1:A:409:LEU:HD13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ASN:N	4:A:643:HOH:O	2.46	0.48
1:A:397:MET:HE3	1:A:400:LEU:HD13	1.95	0.48
1:A:119:LEU:O	1:A:123:THR:HB	2.14	0.48
1:A:123:THR:CG2	1:A:124:SER:N	2.77	0.47
1:A:370:VAL:HG21	1:A:383:ALA:HA	1.96	0.47
1:A:83:THR:HG22	1:A:256:TYR:OH	2.15	0.46
1:A:397:MET:HA	1:A:397:MET:HE3	1.98	0.46
1:A:368:GLU:HB2	4:A:564:HOH:O	2.15	0.46
1:A:170:PHE:O	1:A:174:ILE:HG12	2.16	0.46
1:A:396:ASN:O	1:A:399:PRO:HD2	2.16	0.44
1:A:24:PHE:CZ	1:A:34:ASN:HB2	2.52	0.44
1:A:256:TYR:HA	1:A:259:ASN:HD21	1.82	0.44
1:A:8:ASN:HB2	4:A:528:HOH:O	2.17	0.44
1:A:330:ILE:HD12	4:A:665:HOH:O	2.18	0.44
1:A:337:PHE:HD1	1:A:397:MET:HE1	1.83	0.43
1:A:147:PHE:HB2	4:A:643:HOH:O	2.16	0.43
1:A:161:TYR:CE1	1:A:166:HIS:HA	2.53	0.43
1:A:187:LEU:HD12	1:A:188:PHE:N	2.34	0.43
1:A:110:GLY:O	1:A:114:VAL:HG13	2.18	0.43
1:A:167:THR:CG2	1:A:168:LEU:N	2.81	0.43
1:A:76:ILE:O	1:A:79:PHE:HB3	2.19	0.43
1:A:332:ARG:NH1	4:A:678:HOH:O	2.51	0.43
1:A:332:ARG:NH1	4:A:488:HOH:O	2.51	0.42
1:A:292:ARG:HA	1:A:296:SER:HA	2.00	0.42
1:A:29:ARG:HA	1:A:30:PRO:HD2	1.60	0.42
1:A:352:PHE:HB2	4:A:624:HOH:O	2.18	0.42
1:A:123:THR:HG22	1:A:124:SER:H	1.83	0.42
1:A:168:LEU:HD21	1:A:173:LEU:HD12	2.01	0.42
1:A:223:PHE:HA	1:A:223:PHE:HD1	1.77	0.42
1:A:332:ARG:HD2	1:A:332:ARG:HA	1.77	0.41
1:A:113:ARG:NH2	1:A:149:SER:HB3	2.35	0.41
1:A:87:LEU:O	1:A:241:ARG:HD3	2.21	0.41
1:A:237:ALA:O	1:A:241:ARG:HG3	2.20	0.41
1:A:50:LEU:HB2	1:A:53:VAL:HG23	2.03	0.41
1:A:330:ILE:CD1	4:A:665:HOH:O	2.69	0.41
1:A:123:THR:CG2	1:A:124:SER:H	2.35	0.40
1:A:356:GLN:HE22	1:A:361:SER:HA	1.85	0.40

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	394/396 (100%)	375 (95%)	16 (4%)	3 (1%)	22 17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	PRO
1	A	92	SER
1	A	263	TYR

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	320/320 (100%)	285 (89%)	35 (11%)	7 4

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LEU
1	A	28	GLU
1	A	29	ARG
1	A	49	VAL
1	A	78	GLU
1	A	81	ARG
1	A	90	LYS
1	A	129	ARG

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Mol	Chain	Res	Type
1	A	144	LYS
1	A	152	LEU
1	A	165	ASN
1	A	168	LEU
1	A	187	LEU
1	A	203	GLU
1	A	206	GLN
1	A	218	LEU
1	A	220	LEU
1	A	223	PHE
1	A	246	MET
1	A	248	LYS
1	A	259	ASN
1	A	276	ASP
1	A	297	ASN
1	A	310	LEU
1	A	312	ASN
1	A	315	LEU
1	A	316	ARG
1	A	342	GLN
1	A	362	PHE
1	A	365	LEU
1	A	367	LYS
1	A	372	ARG
1	A	376	GLU
1	A	387	VAL
1	A	408	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	84	GLN
1	A	96	ASN
1	A	166	HIS
1	A	247	HIS
1	A	259	ASN
1	A	286	GLN
1	A	301	HIS
1	A	312	ASN
1	A	328	GLN
1	A	342	GLN

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Mol	Chain	Res	Type
1	A	356	GLN
1	A	357	ASN

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](#)

2 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	PMP	A	413	-	16,16,16	1.89	2 (12%)	20,23,23	1.68	4 (20%)
3	MAE	A	414	-	1,7,7	0.38	0	0,8,8	0.00	-

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	PMP	A	413	-	-	0/8/8/8	0/1/1/1
3	MAE	A	414	-	-	0/0/5/5	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	413	PMP	C3-C2	-5.83	1.36	1.40
2	A	413	PMP	C2A-C2	2.30	1.54	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	413	PMP	O3P-P-O4P	-2.66	99.66	106.73
2	A	413	PMP	O2P-P-O4P	-2.48	100.13	106.73
2	A	413	PMP	C5-C6-N1	-2.18	120.17	123.87
2	A	413	PMP	O4P-P-O1P	4.06	117.85	106.47

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
2	A	413	PMP	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.