



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:48 AM GMT

PDB ID : 2OAT  
Title : ORNITHINE AMINOTRANSFERASE COMPLEXED WITH 5-FLUOROMETHYLOORNITHINE  
Authors : Storici, P.; Schirmer, T.  
Deposited on : 1998-05-07  
Resolution : 1.95 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) : **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

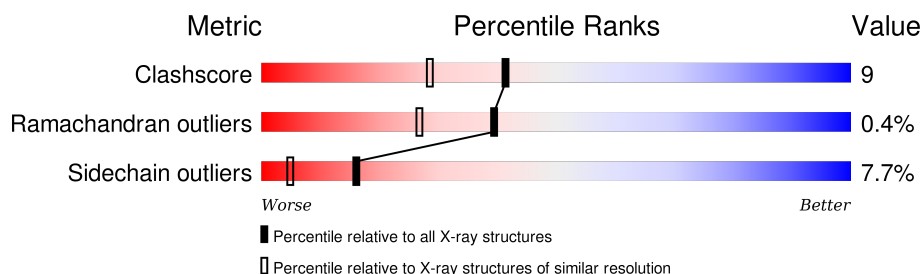
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	439	
1	B	439	
1	C	439	

## 2 Entry composition [i](#)

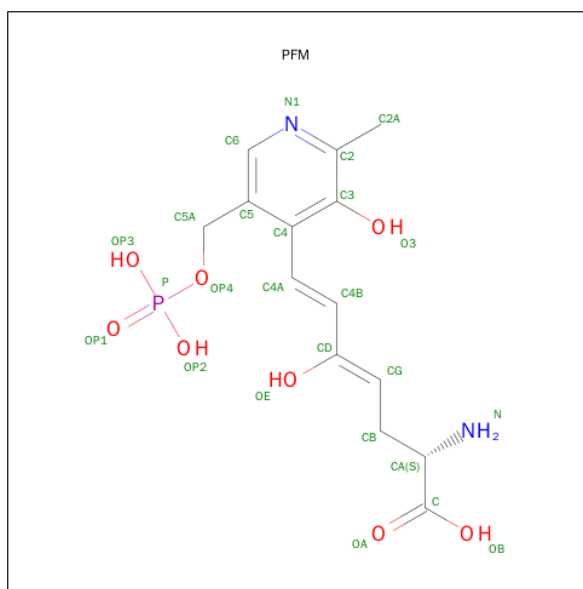
There are 3 unique types of molecules in this entry. The entry contains 10302 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ORNITHINE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	0	0	0
			3161	2030	533	586	12			
1	B	404	Total	C	N	O	S	0	0	0
			3161	2030	533	586	12			
1	C	404	Total	C	N	O	S	0	0	0
			3161	2030	533	586	12			

- Molecule 2 is 1-AMINO-7-(2-METHYL-3-OXIDO-5-((PHOSPHONOXY)METHYL)-4-PYRIDOXAL-5-OXO-6-HEPTENATE (three-letter code: PFM) (formula: C<sub>14</sub>H<sub>19</sub>N<sub>2</sub>O<sub>8</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			25	14	2	8	1		
2	B	1	Total	C	N	O	P	0	0
			25	14	2	8	1		
2	C	1	Total	C	N	O	P	0	0
			25	14	2	8	1		

- Molecule 3 is water.

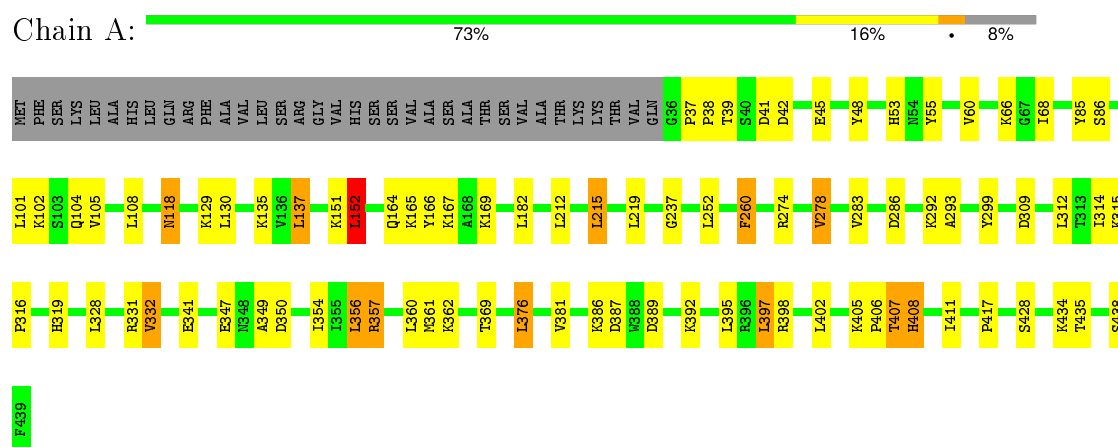
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	236	Total 236	O 236	2	0
3	B	250	Total 250	O 250	0	0
3	C	258	Total 258	O 258	1	0

### 3 Residue-property plots

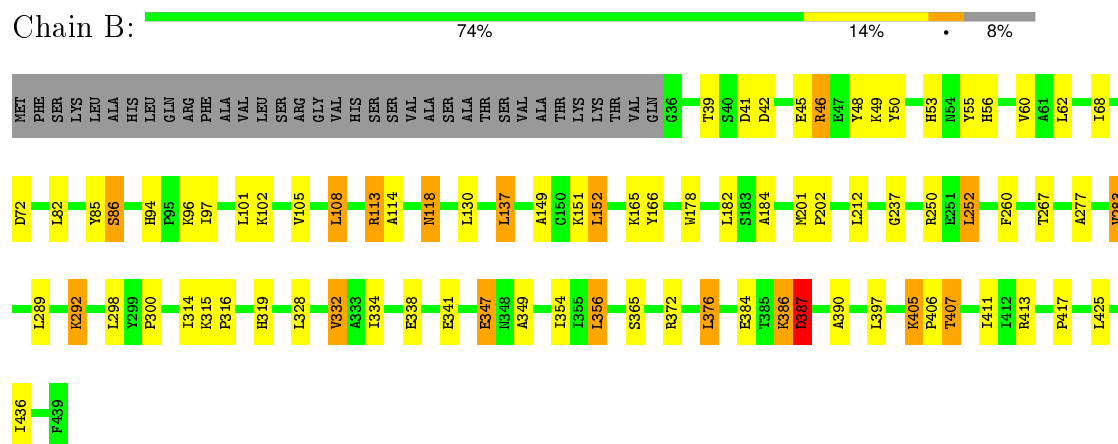
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

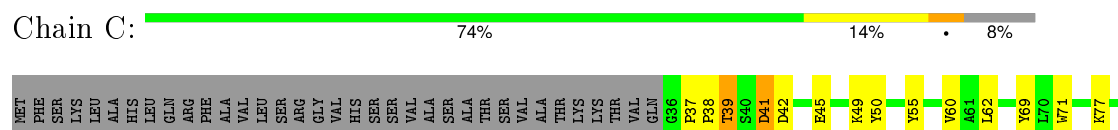
#### • Molecule 1: ORNITHINE AMINOTRANSFERASE



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K292	L298	I314	K315	P316	P327	L328	R331	V332	V339	E347	N348	A349	L352	L356	R357	L360	L376	T385	K386	L397	K405	P406	T407	H408	I411	I412	R413	D423	E424	L425	I429	K434	T435	S438	F439
Y85	S86	K96	I97	L101	Q104	V105	L108	R113	N118	E125	K129	L130	L137	A149	L152	K169	L182	D195	M201	P202	L212	P213	A214	L215	L219	P231	R250	E251	L252	P260	L265	R271	R284	L289	

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.28Å 115.28Å 186.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.60 – 1.95	Depositor
% Data completeness (in resolution range)	97.0 (19.60-1.95)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
Refinement program	REFMAC, X-PLOR	Depositor
R, $R_{free}$	0.204 , 0.232	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10302	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

## 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: PFM

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	0.62	0/3235	0.98	6/4393 (0.1%)
1	B	0.64	0/3235	1.02	8/4393 (0.2%)
1	C	0.65	0/3235	1.04	11/4393 (0.3%)
All	All	0.64	0/9705	1.02	25/13179 (0.2%)

There are no bond length outliers.

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	413	ARG	CD-NE-CZ	11.92	140.29	123.60
1	C	113	ARG	NE-CZ-NH1	-6.95	116.83	120.30
1	C	413	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	B	252	LEU	CA-CB-CG	6.53	130.33	115.30
1	B	413	ARG	NE-CZ-NH1	6.26	123.43	120.30

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	A	3161	0	3165	57	0
1	B	3161	0	3165	58	0
1	C	3161	0	3165	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	25	0	15	2	0
2	B	25	0	14	1	0
2	C	25	0	16	3	0
3	A	236	0	0	4	0
3	B	250	0	0	14	0
3	C	258	0	0	7	0
All	All	10302	0	9540	163	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 9.

The worst 5 of 163 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:309:ASP:HB3	3:A:659:HOH:O	1.65	0.95
1:C:101:LEU:O	1:C:105:VAL:HG23	1.68	0.92
1:C:250:ARG:HD2	3:C:649:HOH:O	1.69	0.91
1:C:407:THR:HB	3:C:669:HOH:O	1.71	0.90
1:B:101:LEU:HD12	1:B:328:LEU:HD11	1.55	0.88

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	402/439 (92%)	387 (96%)	13 (3%)	2 (0%)	34	21
1	B	402/439 (92%)	388 (96%)	13 (3%)	1 (0%)	52	43
1	C	402/439 (92%)	382 (95%)	18 (4%)	2 (0%)	34	21
All	All	1206/1317 (92%)	1157 (96%)	44 (4%)	5 (0%)	39	27

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	408	HIS
1	A	408	HIS
1	A	292	LYS
1	C	292	LYS
1	B	292	LYS

### 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	337/366 (92%)	311 (92%)	26 (8%)	16	5
1	B	337/366 (92%)	310 (92%)	27 (8%)	15	4
1	C	337/366 (92%)	312 (93%)	25 (7%)	17	5
All	All	1011/1098 (92%)	933 (92%)	78 (8%)	16	5

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	182	LEU
1	B	354	ILE
1	C	376	LEU
1	B	212	LEU
1	B	283	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	53	HIS
1	B	118	ASN
1	C	118	ASN
1	A	400	ASN
1	B	400	ASN

### 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 ⓘ

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	PFM	A	440	-	21,25,25	2.82	2 (9%)	24,35,35	1.41	2 (8%)
2	PFM	B	440	-	21,25,25	2.73	2 (9%)	24,35,35	1.43	4 (16%)
2	PFM	C	440	-	21,25,25	3.71	7 (33%)	24,35,35	2.53	2 (8%)

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	PFM	A	440	-	-	1/14/20/20	0/1/1/1
2	PFM	B	440	-	-	0/14/20/20	0/1/1/1
2	PFM	C	440	-	-	0/14/20/20	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	440	PFM	C4B-CD	-13.42	1.33	1.45
2	A	440	PFM	C4B-CD	-9.81	1.36	1.45
2	B	440	PFM	C4B-CD	-9.45	1.37	1.45
2	C	440	PFM	C4-C4A	-7.33	1.34	1.47
2	A	440	PFM	C4-C4A	-6.71	1.35	1.47

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	440	PFM	OE-CD-CG	-9.26	112.36	121.08
2	A	440	PFM	OE-CD-CG	-2.80	118.44	121.08
2	B	440	PFM	OP2-P-OP4	-2.69	98.81	106.56
2	B	440	PFM	C4B-CD-CG	-2.55	118.87	122.48
2	B	440	PFM	OP3-P-OP1	2.57	118.85	110.58

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	440	PFM	CD-CG-CB-CA

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	440	PFM	2	0
2	B	440	PFM	1	0
2	C	440	PFM	3	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 will therefore be empty.

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

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

### 6.3 Carbohydrates ⓘ

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

### 6.4 Ligands ⓘ

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

### 6.5 Other polymers ⓘ

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