



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:24 am GMT

PDB ID : 1B65  
Title : Structure of l-aminopeptidase d-ala-esterase/amidase from ochrobactrum anthropi, a prototype for the serine aminopeptidases, reveals a new variant among the ntn hydrolase fold  
Authors : Bompard-Gilles, C.; Villeret, V.; Davies, G.J.; Fanuel, L.; Joris, B.; Frere, J.M.; Van Beeumen, J.  
Deposited on : 1999-01-20  
Resolution : 1.82 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  
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) : recalc28949

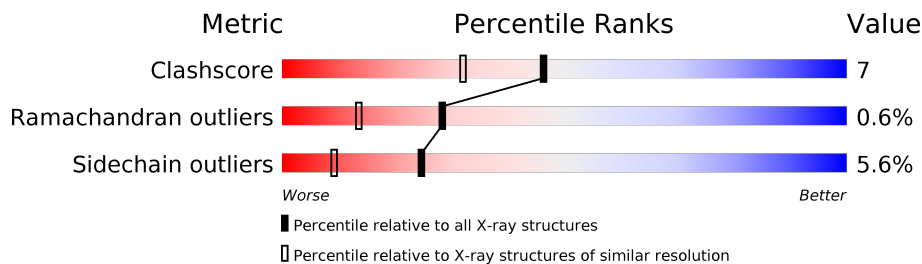
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.82 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	6856 (1.84-1.80)
Ramachandran outliers	110173	6780 (1.84-1.80)
Sidechain outliers	110143	6780 (1.84-1.80)

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	375	
1	B	375	
1	C	375	
1	D	375	
1	E	375	
1	F	375	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 17786 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 PROTEIN (AMINOPEPTIDASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2747	1719	499	516	13			
1	B	363	Total	C	N	O	S	0	0	0
			2747	1719	499	516	13			
1	C	363	Total	C	N	O	S	0	0	0
			2747	1719	499	516	13			
1	D	363	Total	C	N	O	S	0	0	0
			2747	1719	499	516	13			
1	E	363	Total	C	N	O	S	0	0	0
			2747	1719	499	516	13			
1	F	363	Total	C	N	O	S	0	0	0
			2747	1719	499	516	13			

- Molecule 2 is water.

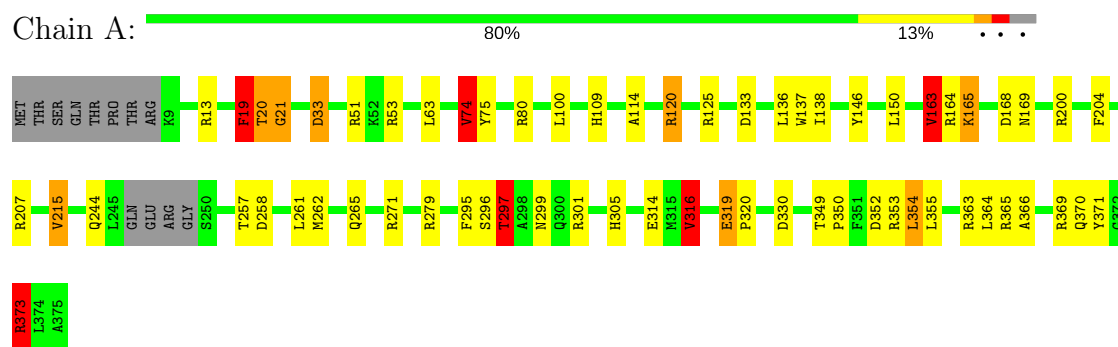
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	220	Total	O	0	0
			220	220		
2	B	220	Total	O	0	0
			220	220		
2	C	230	Total	O	0	0
			230	230		
2	D	216	Total	O	0	0
			216	216		
2	E	207	Total	O	0	0
			207	207		
2	F	211	Total	O	0	0
			211	211		

### 3 Residue-property plots [i](#)

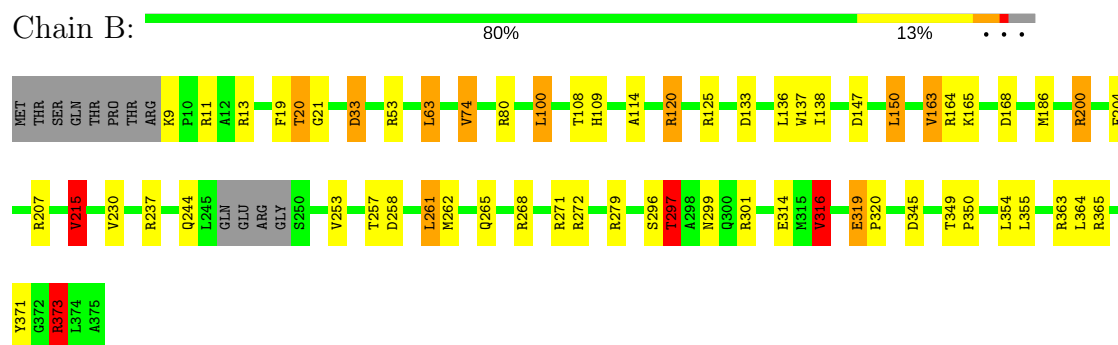
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

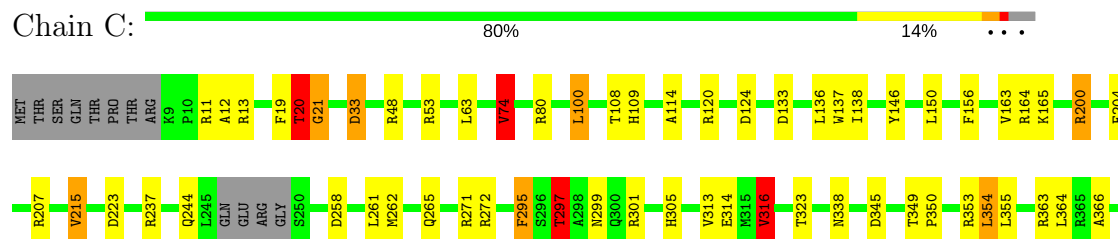
#### • Molecule 1: PROTEIN (AMINOPEPTIDASE)



#### • Molecule 1: PROTEIN (AMINOPEPTIDASE)



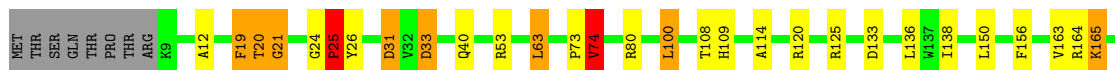
#### • Molecule 1: PROTEIN (AMINOPEPTIDASE)





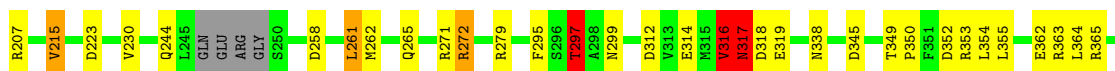
- Molecule 1: PROTEIN (AMINOPEPTIDASE)

Chain D: 78% 14% . . .



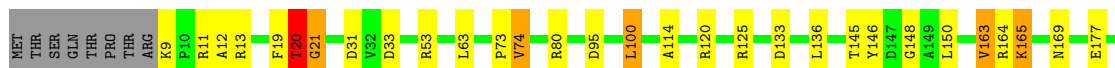
- Molecule 1: PROTEIN (AMINOPEPTIDASE)

Chain E: 80% 13% . . .



- Molecule 1: PROTEIN (AMINOPEPTIDASE)

Chain F: 79% 13% . . .



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	156.97Å 96.22Å 154.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.50 – 1.82	Depositor
% Data completeness (in resolution range)	95.8 (12.50-1.82)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.169 , 0.206	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	17786	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

## 5 Model quality i

### 5.1 Standard geometry i

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	0.64	0/2808	1.65	53/3820 (1.4%)
1	B	0.64	0/2808	1.73	59/3820 (1.5%)
1	C	0.63	0/2808	1.73	52/3820 (1.4%)
1	D	0.66	1/2808 (0.0%)	1.74	58/3820 (1.5%)
1	E	0.68	3/2808 (0.1%)	1.74	55/3820 (1.4%)
1	F	0.64	0/2808	1.68	48/3820 (1.3%)
All	All	0.65	4/16848 (0.0%)	1.71	325/22920 (1.4%)

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	A	0	1
1	D	0	2
1	E	0	3
All	All	0	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	317	ASN	CA-CB	9.04	1.76	1.53
1	E	92	TRP	CZ3-CH2	8.86	1.54	1.40
1	D	25	PRO	CA-CB	6.79	1.67	1.53
1	E	92	TRP	CZ2-CH2	6.29	1.49	1.37

The worst 5 of 325 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	373	ARG	NE-CZ-NH2	-29.83	105.39	120.30
1	E	373	ARG	NE-CZ-NH2	-28.43	106.08	120.30
1	D	373	ARG	NE-CZ-NH2	-28.11	106.25	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	373	ARG	NE-CZ-NH2	-26.91	106.84	120.30
1	C	373	ARG	NE-CZ-NH2	-26.02	107.29	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	19	PHE	Peptide
1	D	19	PHE	Peptide
1	D	206	GLY	Mainchain
1	E	19	PHE	Peptide
1	E	317	ASN	Mainchain

## 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	2747	0	2683	40	0
1	B	2747	0	2683	38	0
1	C	2747	0	2683	41	0
1	D	2747	0	2682	54	5
1	E	2747	0	2683	65	3
1	F	2747	0	2683	37	0
2	A	220	0	0	2	0
2	B	220	0	0	4	0
2	C	230	0	0	8	5
2	D	216	0	0	10	0
2	E	207	0	0	9	4
2	F	211	0	0	5	1
All	All	17786	0	16097	235	9

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 7.

The worst 5 of 235 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:E:317:ASN:CA	1:E:317:ASN:CB	1.76	1.55
1:E:317:ASN:C	1:E:317:ASN:CB	1.90	1.39
1:E:317:ASN:HB3	1:E:318:ASP:N	1.42	1.31
1:D:25:PRO:HB2	1:D:31:ASP:OD1	1.43	1.18
1:E:317:ASN:CB	1:E:318:ASP:N	2.01	1.17

The worst 5 of 9 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:317:ASN:CA	2:E:899:HOH:O[2_665]	1.71	0.49
1:D:25:PRO:CA	2:C:573:HOH:O[3_545]	1.88	0.32
1:E:317:ASN:CB	2:E:899:HOH:O[2_665]	1.94	0.26
1:D:33:ASP:OD1	2:C:589:HOH:O[3_545]	1.95	0.25
2:E:868:HOH:O	2:F:511:HOH:O[2_665]	1.95	0.25

## 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	359/375 (96%)	348 (97%)	9 (2%)	2 (1%)	28	13
1	B	359/375 (96%)	349 (97%)	9 (2%)	1 (0%)	44	28
1	C	359/375 (96%)	347 (97%)	10 (3%)	2 (1%)	28	13
1	D	359/375 (96%)	348 (97%)	8 (2%)	3 (1%)	22	8
1	E	359/375 (96%)	346 (96%)	11 (3%)	2 (1%)	28	13
1	F	359/375 (96%)	350 (98%)	7 (2%)	2 (1%)	28	13
All	All	2154/2250 (96%)	2088 (97%)	54 (2%)	12 (1%)	28	13

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	25	PRO
1	A	21	GLY
1	B	21	GLY
1	C	21	GLY
1	D	20	THR

### 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	286/297 (96%)	269 (94%)	17 (6%)	23	8
1	B	286/297 (96%)	269 (94%)	17 (6%)	23	8
1	C	286/297 (96%)	271 (95%)	15 (5%)	27	11
1	D	286/297 (96%)	272 (95%)	14 (5%)	29	12
1	E	286/297 (96%)	270 (94%)	16 (6%)	25	9
1	F	286/297 (96%)	269 (94%)	17 (6%)	23	8
All	All	1716/1782 (96%)	1620 (94%)	96 (6%)	25	9

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	297	THR
1	D	136	LEU
1	F	215	VAL
1	C	313	VAL
1	C	373	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	305	HIS
1	D	234	GLN
1	F	265	GLN
1	C	317	ASN

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Mol	Chain	Res	Type
1	D	109	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](#)

There are no ligands in this entry.

### 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.