



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2018 – 10:56 AM EST

PDB ID : 5NSK  
Title : apo Structure of Leucyl aminopeptidase from Trypanosoma brucei  
Authors : Timm, J.; Wilson, K.S.  
Deposited on : 2017-04-26  
Resolution : 2.60 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) : 1.9-1692  
EDS : rb-20030736  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20030736

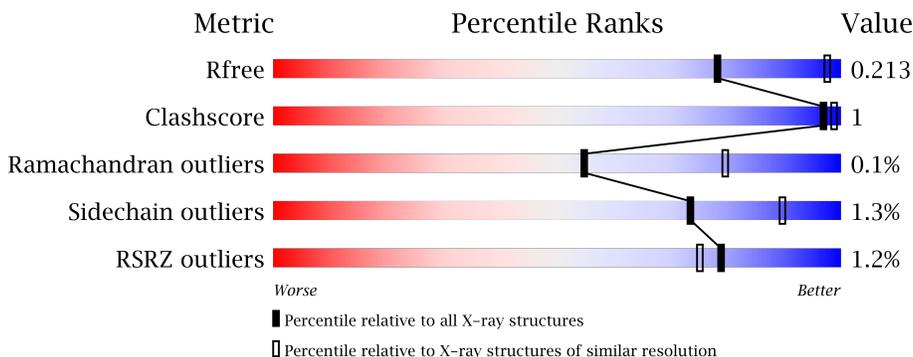
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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.



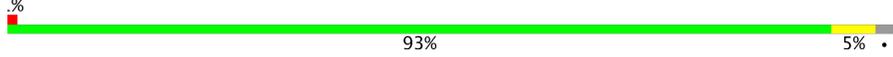
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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	521	 .% 93% . .
1	B	521	 .% 91% 5% . .
1	C	521	 .% 93% . .
1	D	521	 .% 94% . .
1	E	521	 .% 93% . .

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Mol	Chain	Length	Quality of chain
1	F	521	 <p>.% 93% 5% .</p>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22652 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 Aminopeptidase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	507	3683	2329	627	707	20	0	0	0
1	B	506	3683	2327	628	709	19	0	0	0
1	C	506	3700	2335	632	714	19	0	0	0
1	D	506	3675	2320	627	709	19	0	0	0
1	E	506	3704	2342	633	709	20	0	0	0
1	F	508	3707	2342	632	713	20	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	ALA	THR	conflict	UNP Q385B0
A	140	THR	ALA	conflict	UNP Q385B0
B	33	ALA	THR	conflict	UNP Q385B0
B	140	THR	ALA	conflict	UNP Q385B0
C	33	ALA	THR	conflict	UNP Q385B0
C	140	THR	ALA	conflict	UNP Q385B0
D	33	ALA	THR	conflict	UNP Q385B0
D	140	THR	ALA	conflict	UNP Q385B0
E	33	ALA	THR	conflict	UNP Q385B0
E	140	THR	ALA	conflict	UNP Q385B0
F	33	ALA	THR	conflict	UNP Q385B0
F	140	THR	ALA	conflict	UNP Q385B0

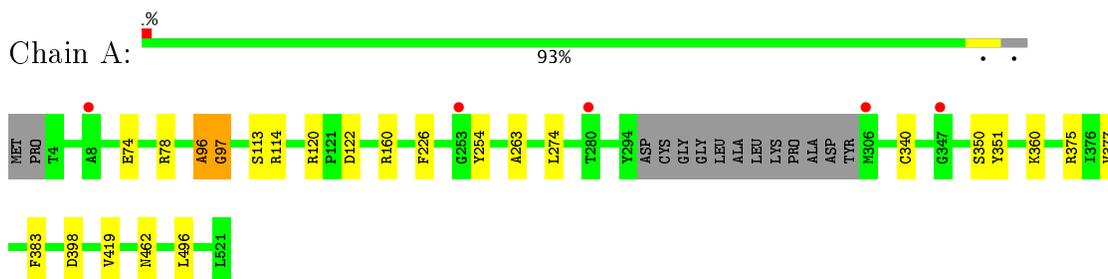
- Molecule 2 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	A	83	Total 83	O 83	0	0
2	B	62	Total 62	O 62	0	0
2	C	119	Total 119	O 119	0	0
2	D	71	Total 71	O 71	0	0
2	E	87	Total 87	O 87	0	0
2	F	78	Total 78	O 78	0	0

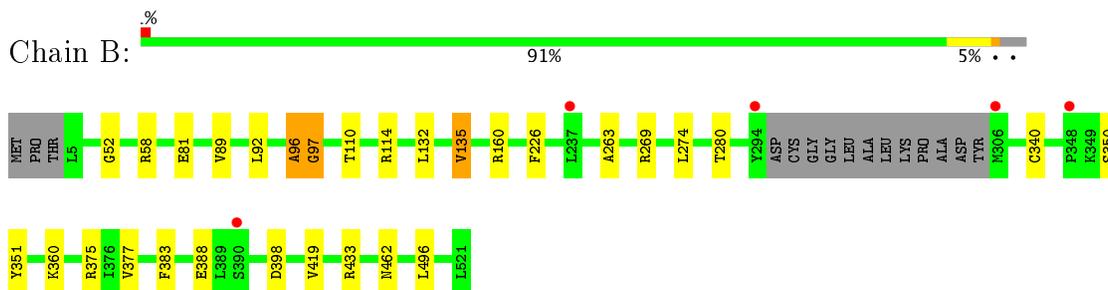
### 3 Residue-property plots [i](#)

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.

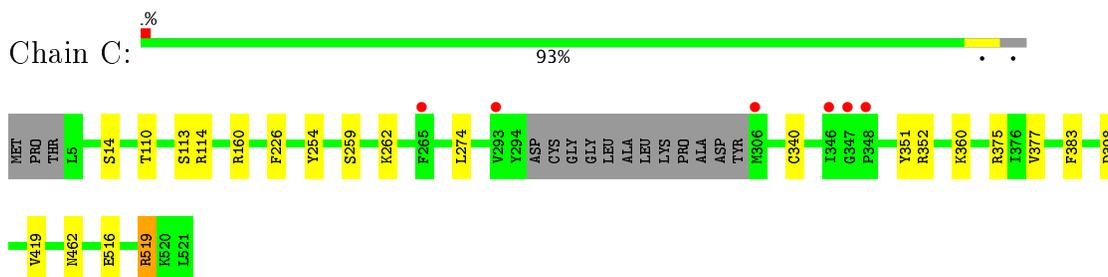
- Molecule 1: Aminopeptidase, putative



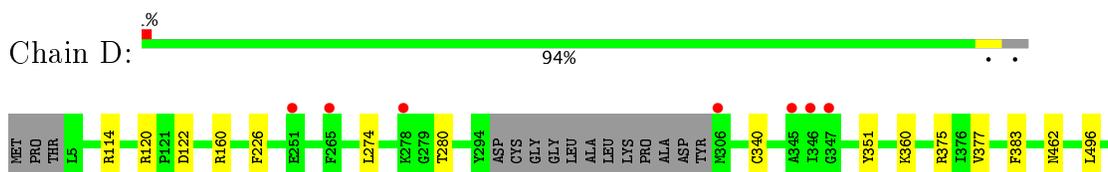
- Molecule 1: Aminopeptidase, putative



- Molecule 1: Aminopeptidase, putative

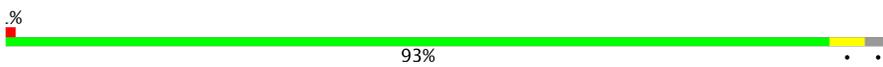


- Molecule 1: Aminopeptidase, putative



L521

- Molecule 1: Aminopeptidase, putative

Chain E:  93%



- Molecule 1: Aminopeptidase, putative

Chain F:  93% 5%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.33Å 162.45Å 176.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.61 – 2.60 72.61 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (72.61-2.60) 100.0 (72.61-2.60)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.191 , 0.211 0.196 , 0.213	Depositor DCC
$R_{free}$ test set	7257 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.1	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 26.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	22652	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.96% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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	0.81	1/3757 (0.0%)	0.79	1/5134 (0.0%)
1	B	0.84	2/3757 (0.1%)	0.83	7/5134 (0.1%)
1	C	0.84	2/3774 (0.1%)	0.81	5/5155 (0.1%)
1	D	0.79	0/3748	0.80	3/5122 (0.1%)
1	E	0.85	1/3778 (0.0%)	0.82	2/5159 (0.0%)
1	F	0.84	1/3782 (0.0%)	0.82	5/5169 (0.1%)
All	All	0.83	7/22596 (0.0%)	0.81	23/30873 (0.1%)

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	B	0	1
1	E	0	1
All	All	0	3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	113	SER	CB-OG	5.97	1.50	1.42
1	E	113	SER	CB-OG	5.71	1.49	1.42
1	B	388	GLU	CD-OE2	-5.57	1.19	1.25
1	A	113	SER	CB-OG	5.44	1.49	1.42
1	C	14	SER	CB-OG	-5.35	1.35	1.42

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	519	ARG	NE-CZ-NH2	8.25	124.43	120.30
1	C	519	ARG	NE-CZ-NH1	-7.25	116.68	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	160	ARG	NE-CZ-NH1	6.91	123.75	120.30
1	F	160	ARG	NE-CZ-NH1	6.44	123.52	120.30
1	B	269	ARG	CG-CD-NE	-6.33	98.50	111.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	96	ALA	Peptide
1	B	96	ALA	Peptide
1	E	97	GLY	Peptide

## 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	3683	0	3559	11	0
1	B	3683	0	3563	11	0
1	C	3700	0	3586	9	0
1	D	3675	0	3539	5	0
1	E	3704	0	3611	9	0
1	F	3707	0	3583	9	0
2	A	83	0	0	0	0
2	B	62	0	0	1	0
2	C	119	0	0	0	0
2	D	71	0	0	0	0
2	E	87	0	0	1	0
2	F	78	0	0	0	0
All	All	22652	0	21441	48	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 1.

The worst 5 of 48 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:F:516:GLU:OE1	1:F:519:ARG:NH1	2.26	0.68
1:B:114:ARG:NH2	1:C:419:VAL:O	2.28	0.66
1:A:340:CYS:HB3	1:A:377:VAL:HG13	1.80	0.64
1:B:419:VAL:O	1:C:114:ARG:NH2	2.30	0.64
1:C:352:ARG:HG2	1:F:295:ASP:HA	1.82	0.61

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	503/521 (96%)	492 (98%)	10 (2%)	1 (0%)	51	76
1	B	502/521 (96%)	488 (97%)	12 (2%)	2 (0%)	38	63
1	C	502/521 (96%)	491 (98%)	11 (2%)	0	100	100
1	D	502/521 (96%)	490 (98%)	12 (2%)	0	100	100
1	E	502/521 (96%)	491 (98%)	11 (2%)	0	100	100
1	F	504/521 (97%)	493 (98%)	11 (2%)	0	100	100
All	All	3015/3126 (96%)	2945 (98%)	67 (2%)	3 (0%)	55	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	97	GLY
1	A	97	GLY
1	B	280	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	374/411 (91%)	369 (99%)	5 (1%)	73	90
1	B	376/411 (92%)	369 (98%)	7 (2%)	62	84
1	C	380/411 (92%)	375 (99%)	5 (1%)	73	90
1	D	373/411 (91%)	369 (99%)	4 (1%)	78	92
1	E	381/411 (93%)	377 (99%)	4 (1%)	80	93
1	F	379/411 (92%)	374 (99%)	5 (1%)	73	90
All	All	2263/2466 (92%)	2233 (99%)	30 (1%)	73	90

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	226	PHE
1	C	398	ASP
1	F	351	TYR
1	C	351	TYR
1	D	226	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [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	507/521 (97%)	-0.16	5 (0%) 82 79	26, 35, 68, 115	0
1	B	506/521 (97%)	-0.05	5 (0%) 82 79	28, 40, 70, 130	0
1	C	506/521 (97%)	-0.32	6 (1%) 79 75	22, 30, 63, 121	0
1	D	506/521 (97%)	-0.20	7 (1%) 75 71	28, 37, 70, 116	0
1	E	506/521 (97%)	-0.20	7 (1%) 75 71	24, 34, 63, 133	0
1	F	508/521 (97%)	-0.17	5 (0%) 82 79	25, 36, 64, 116	0
All	All	3039/3126 (97%)	-0.18	35 (1%) 79 75	22, 36, 68, 133	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	346	ILE	6.2
1	A	347	GLY	6.0
1	B	306	MET	4.8
1	E	346	ILE	4.7
1	E	348	PRO	4.7

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.