



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2014 – 12:57 AM GMT

PDB ID : 1D0E  
Title : CRYSTAL STRUCTURES OF THE N-TERMINAL FRAGMENT FROM  
MOLONEY MURINE LEUKEMIA VIRUS REVERSE TRANSCRIPTASE  
COMPLEXED WITH NUCLEIC ACID: FUNCTIONAL IMPLICATIONS  
FOR TEMPLATE-PRIMER BINDING TO THE FINGERS DOMAIN  
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Deposited on : 1999-09-09  
Resolution : 3.00 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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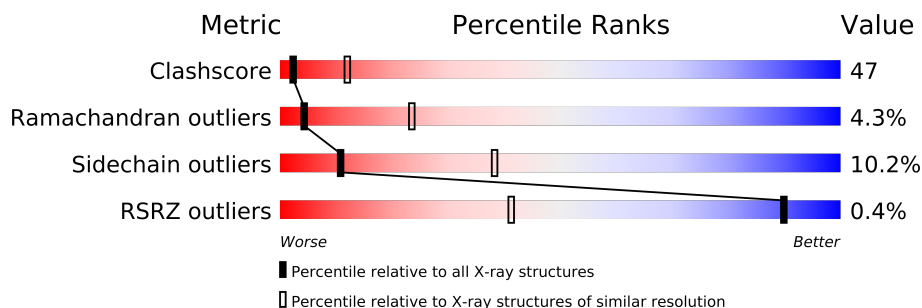
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.00 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	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	E	11	
1	F	11	
2	A	259	
2	B	259	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4570 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called 5'-D(\*TP\*TP\*TP\*CP\*AP\*TP\*GP\*CP\*AP\*TP\*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	11	Total	C	N	O	P	0	0	0
			221	108	36	67	10			
1	F	11	Total	C	N	O	P	0	0	0
			221	108	36	67	10			

- Molecule 2 is a protein called REVERSE TRANSCRIPTASE.

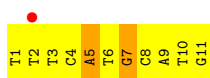
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	259	Total	C	N	O	S	0	0	0
			2069	1327	362	372	8			
2	B	257	Total	C	N	O	S	0	0	0
			2059	1322	360	369	8			

### 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.

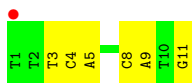
- Molecule 1: 5'-D(\*TP\*TP\*TP\*CP\*AP\*TP\*GP\*CP\*AP\*TP\*G)-3'

Chain E: 



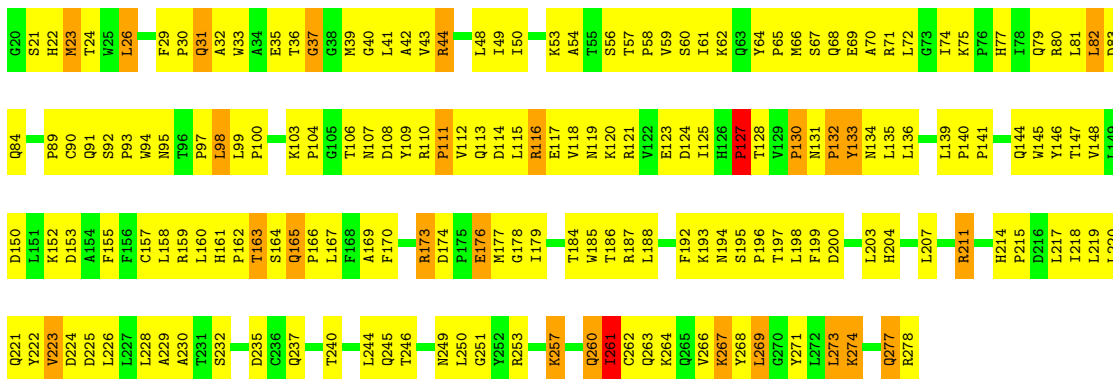
- Molecule 1: 5'-D(\*TP\*TP\*TP\*CP\*AP\*TP\*GP\*CP\*AP\*TP\*G)-3'

Chain F: 



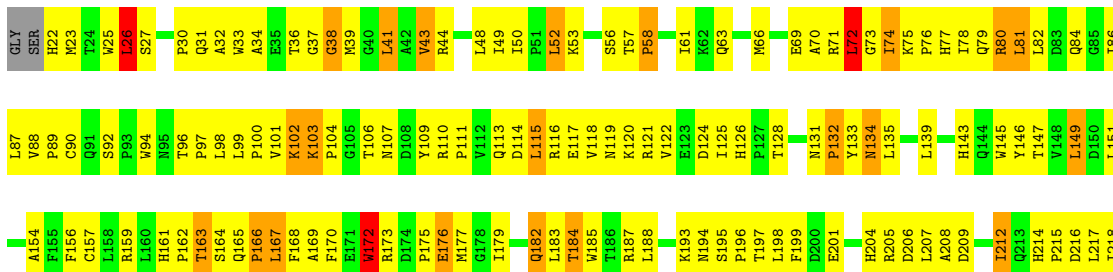
- Molecule 2: REVERSE TRANSCRIPTASE

Chain A: 



- Molecule 2: REVERSE TRANSCRIPTASE

Chain B: 



L219	L220	Q221	Y222	V223	D224	D225	D226	L227	L228	A229	A230	T231	S232	E233	L234	D235	L244	G248	N249	L250	G251	Y252	R253	A254	S255	A256	K257	K258	L261	Q265	V266	K267	Y268	L269	G270	Y271	L272	L273	K274	Q277	R278
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.16Å 63.54Å 73.50Å 90.00° 103.85° 90.00°	Depositor
Resolution (Å)	500.00 – 3.00 28.48 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.7 (500.00-3.00) 95.9 (28.48-3.00)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.78 (at 3.00Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.215 , 0.298 0.216 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	29.1	Xtriage
Anisotropy	0.706	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 21.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 11540 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	4570	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.80% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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	E	0.51	0/246	0.68	0/378
1	F	0.44	0/246	0.76	0/378
2	A	0.63	5/2126 (0.2%)	0.89	7/2896 (0.2%)
2	B	0.56	1/2116 (0.0%)	0.95	5/2883 (0.2%)
All	All	0.59	6/4734 (0.1%)	0.90	12/6535 (0.2%)

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	E	0	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	273	LEU	CA-C	9.15	1.76	1.52
2	A	274	LYS	N-CA	7.89	1.62	1.46
2	A	127	PRO	N-CA	7.48	1.59	1.47
2	A	261	ILE	C-N	-6.50	1.19	1.34
2	B	107	ASN	N-CA	5.96	1.58	1.46

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	27	SER	N-CA-CB	-21.60	78.10	110.50
2	A	127	PRO	CA-N-CD	-11.83	94.94	111.50
2	B	26	LEU	CB-CA-C	11.12	131.33	110.20
2	A	273	LEU	CA-C-N	7.62	133.96	117.20
2	A	127	PRO	N-CA-C	7.21	130.84	112.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	5	DA	Sidechain
1	E	7	DG	Sidechain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	221	0	128	20	0
1	F	221	0	128	11	0
2	A	2069	0	2079	204	0
2	B	2059	0	2072	194	0
All	All	4570	0	4407	416	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 47.

The worst 5 of 416 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:273:LEU:CA	2:A:273:LEU:C	1.76	1.52
2:A:264:LYS:O	2:A:274:LYS:HB2	1.39	1.20
2:A:68:GLN:HE21	2:A:69:GLU:HG3	1.18	1.08
2:B:74:ILE:HG13	2:B:111:PRO:HG3	1.40	1.01
2:A:266:VAL:HG22	2:A:273:LEU:HD21	1.44	0.97

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	
2	A	257/259 (99%)	215 (84%)	32 (12%)	10 (4%)	5	26
2	B	255/259 (98%)	201 (79%)	42 (16%)	12 (5%)	4	21
All	All	512/518 (99%)	416 (81%)	74 (14%)	22 (4%)	4	23

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	132	PRO
2	A	133	TYR
2	A	163	THR
2	B	72	LEU
2	B	207	LEU

### 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	
2	A	227/227 (100%)	207 (91%)	20 (9%)	14	48
2	B	226/227 (100%)	200 (88%)	26 (12%)	8	32
All	All	453/454 (100%)	407 (90%)	46 (10%)	11	38

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	26	LEU
2	B	74	ILE
2	B	225	ASP
2	B	41	LEU
2	B	52	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	263	GLN
2	B	22	HIS
2	B	221	GLN

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Mol	Chain	Res	Type
2	A	245	GLN
2	A	249	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

### 5.7 Other polymers ⓘ

There are no such residues in this entry.

### 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	E	11/11 (100%)	0.17	1 (9%) 9 2	15, 40, 98, 98	0
1	F	11/11 (100%)	0.21	1 (9%) 9 2	15, 26, 99, 100	0
2	A	259/259 (100%)	-0.45	0 100 100	3, 16, 44, 74	0
2	B	257/259 (99%)	-0.36	0 100 100	5, 25, 64, 91	0
All	All	538/540 (99%)	-0.38	2 (0%) 90 41	3, 20, 55, 100	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	1	DT	4.5
1	E	2	DT	3.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.