

# wwPDB X-ray Structure Validation Summary Report (i)

#### Feb 14, 2024 – 11:10 PM EST

PDB ID	:	3N4P
Title	:	Human cytomegalovirus terminase nuclease domain
Authors	:	Nadal, M.; Mas, P.J.; Blanco, A.G.; Arnan, C.; Sola, M.; Hart, D.J.; Coll, M.
Deposited on	:	2010-05-22
Resolution	:	2.15  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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\;DIFFRACTION$ 

The reported resolution of this entry is 2.15 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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 c	of chain		
1	А	279	4% 51%	23%		23%
1	В	279	4% 53%	20%	8%	19%
1	С	279	2% 53%	19%	5%	22%
1	D	279	3% 49%	20%	6% •	24%



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7146 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.

Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
1	Λ	216	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0
	A	210	1736	1113	292	325	6	0		
1	В	227	Total	С	Ν	Ο	S	0	1	0
	D		1838	1176	315	341	6	0	1	0
1	C	218	Total	С	Ν	0	S	0	0	0
		218	1747	1120	292	329	6			
1	1 D	010	Total	С	Ν	Ο	S	0	1	0
	212	1720	1103	290	321	6	0	L	U	

• Molecule 1 is a protein called Terminase subunit UL89 protein.

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	396	MET	-	expression tag	UNP P16732
А	397	GLY	-	expression tag	UNP P16732
А	398	HIS	-	expression tag	UNP P16732
А	399	HIS	-	expression tag	UNP P16732
А	400	HIS	-	expression tag	UNP P16732
А	401	HIS	-	expression tag	UNP P16732
А	402	HIS	-	expression tag	UNP P16732
А	403	HIS	-	expression tag	UNP P16732
А	404	ASP	-	expression tag	UNP P16732
А	405	TYR	-	expression tag	UNP P16732
А	406	ASP	-	expression tag	UNP P16732
А	407	ILE	-	expression tag	UNP P16732
А	408	PRO	-	expression tag	UNP P16732
А	409	THR	-	expression tag	UNP P16732
А	410	THR	-	expression tag	UNP P16732
А	411	GLU	-	expression tag	UNP P16732
А	412	ASN	-	expression tag	UNP P16732
А	413	LEU	-	expression tag	UNP P16732
А	414	TYR	-	expression tag	UNP P16732
А	415	PHE	-	expression tag	UNP P16732
А	416	GLN	-	expression tag	UNP P16732





Chain	Residue	Modelled	Actual	Comment	Reference
А	417	GLY	-	expression tag	UNP P16732
В	396	MET	-	expression tag	UNP P16732
В	397	GLY	-	expression tag	UNP P16732
В	398	HIS	-	expression tag	UNP P16732
В	399	HIS	-	expression tag	UNP P16732
В	400	HIS	-	expression tag	UNP P16732
В	401	HIS	-	expression tag	UNP P16732
В	402	HIS	-	expression tag	UNP P16732
В	403	HIS	-	expression tag	UNP P16732
В	404	ASP	-	expression tag	UNP P16732
В	405	TYR	-	expression tag	UNP P16732
В	406	ASP	-	expression tag	UNP P16732
В	407	ILE	-	expression tag	UNP P16732
В	408	PRO	-	expression tag	UNP P16732
В	409	THR	-	expression tag	UNP P16732
В	410	THR	-	expression tag	UNP P16732
В	411	GLU	-	expression tag	UNP P16732
В	412	ASN	-	expression tag	UNP P16732
В	413	LEU	-	expression tag	UNP P16732
В	414	TYR	-	expression tag	UNP P16732
В	415	PHE	-	expression tag	UNP P16732
В	416	GLN	-	expression tag	UNP P16732
В	417	GLY	-	expression tag	UNP P16732
С	396	MET	-	expression tag	UNP P16732
С	397	GLY	-	expression tag	UNP P16732
С	398	HIS	-	expression tag	UNP P16732
С	399	HIS	-	expression tag	UNP P16732
С	400	HIS	-	expression tag	UNP P16732
С	401	HIS	-	expression tag	UNP P16732
С	402	HIS	-	expression tag	UNP P16732
C	403	HIS	-	expression tag	UNP P16732
С	404	ASP	-	expression tag	UNP P16732
С	405	TYR	-	expression tag	UNP P16732
С	406	ASP	-	expression tag	UNP P16732
С	407	ILE	-	expression tag	UNP P16732
С	408	PRO	-	expression tag	UNP P16732
С	409	THR	-	expression tag	UNP P16732
C	410	THR	-	expression tag	UNP P16732
C	411	GLU	-	expression tag	UNP P16732
C	412	ASN	-	expression tag	UNP P16732
C	413	LEU	-	expression tag	UNP P16732
C	414	TYR	-	expression tag	UNP P16732

Continued from previous page...

Continued on next page...



Chain	Residue	Modelled	Actual	Comment	Reference
С	415	PHE	-	expression tag	UNP P16732
С	416	GLN	-	expression tag	UNP P16732
С	417	GLY	-	expression tag	UNP P16732
D	396	MET	-	expression tag	UNP P16732
D	397	GLY	-	expression tag	UNP P16732
D	398	HIS	-	expression tag	UNP P16732
D	399	HIS	-	expression tag	UNP P16732
D	400	HIS	-	expression tag	UNP P16732
D	401	HIS	-	expression tag	UNP P16732
D	402	HIS	-	expression tag	UNP P16732
D	403	HIS	-	expression tag	UNP P16732
D	404	ASP	-	expression tag	UNP P16732
D	405	TYR	-	expression tag	UNP P16732
D	406	ASP	-	expression tag	UNP P16732
D	407	ILE	-	expression tag	UNP P16732
D	408	PRO	-	expression tag	UNP P16732
D	409	THR	-	expression tag	UNP P16732
D	410	THR	-	expression tag	UNP P16732
D	411	GLU	-	expression tag	UNP P16732
D	412	ASN	-	expression tag	UNP P16732
D	413	LEU	-	expression tag	UNP P16732
D	414	TYR	-	expression tag	UNP P16732
D	415	PHE	-	expression tag	UNP P16732
D	416	GLN	-	expression tag	UNP P16732
D	417	GLY	-	expression tag	UNP P16732

Continued from previous page...

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Mg 1 1	0	0
2	В	2	Total Mg 2 2	0	0
2	С	2	Total Mg 2 2	0	0
2	D	2	Total Mg 2 2	0	0

• Molecule 3 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	35	$\begin{array}{cc} \text{Total} & \text{O} \\ 35 & 35 \end{array}$	0	0
3	В	25	Total O 25 25	0	0
3	С	27	Total O 27 27	0	0
3	D	11	Total         O           11         11	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Terminase subunit UL89 protein

# I600 F594 M472 K872 Y598 M472 V601 H694 M472 V601 H694 H444 V601 H694 H444 V601 H614 V606 H614 V606 H444 V603 H614 V606 H614 V606 H444 H614 V606 H446 H617 H618 H654 H624 H625 H426 H625 H434 H656 H626 H249 H656 H627 H233 H656 H628 H249 H656

• Molecule 1: Terminase subunit UL89 protein





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	82.86Å 87.96Å 188.38Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Bosolution(A)	19.99 - 2.15	Depositor
Resolution (A)	19.99 - 2.15	EDS
% Data completeness	98.7 (19.99-2.15)	Depositor
(in resolution range)	98.7 (19.99-2.15)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.53 (at 2.15 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
P. P.	0.219 , $0.272$	Depositor
$n, n_{free}$	0.230 , $0.275$	DCC
$R_{free}$ test set	3760 reflections $(5.04%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	43.7	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.30 , 29.8	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.46, < L^2>=0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7146	wwPDB-VP
Average B, all atoms $(Å^2)$	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: MG

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).

Mal	Chain	Bo	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	1.20	5/1770~(0.3%)	1.16	12/2399~(0.5%)	
1	В	1.03	5/1875~(0.3%)	1.00	4/2542~(0.2%)	
1	С	1.14	5/1781~(0.3%)	1.05	2/2416~(0.1%)	
1	D	0.97	1/1754~(0.1%)	1.00	7/2378~(0.3%)	
All	All	1.09	16/7180~(0.2%)	1.05	25/9735~(0.3%)	

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	С	490	TYR	CD2-CE2	6.67	1.49	1.39
1	А	671	PHE	CE2-CZ	6.45	1.49	1.37
1	А	459	TYR	CD1-CE1	6.36	1.48	1.39
1	В	443	TYR	CD1-CE1	6.03	1.48	1.39
1	С	604	GLU	CB-CG	-5.78	1.41	1.52

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

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	D	612	LEU	CA-CB-CG	7.74	133.10	115.30
1	А	605	LEU	CA-CB-CG	7.35	132.20	115.30
1	В	662	LEU	CA-CB-CG	7.12	131.66	115.30
1	А	560	ARG	NE-CZ-NH2	-6.58	117.01	120.30
1	А	662	LEU	CB-CG-CD1	6.53	122.11	111.00

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	А	1736	0	1707	34	0
1	В	1838	0	1813	51	0
1	С	1747	0	1721	51	0
1	D	1720	0	1688	45	0
2	А	1	0	0	0	0
2	В	2	0	0	0	0
2	С	2	0	0	0	0
2	D	2	0	0	0	0
3	А	35	0	0	2	0
3	В	25	0	0	1	0
3	С	27	0	0	1	0
3	D	11	0	0	0	0
All	All	7146	0	6929	171	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 12.

The worst 5 of 171 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:D:550:ARG:HD3	1:D:674:SER:HB2	1.14	1.14
1:C:430:ILE:HD11	1:C:435:ARG:HG3	1.25	1.09
1:C:669:ILE:H	1:C:669:ILE:HD12	1.18	1.07
1:A:494:HIS:H	1:A:609:THR:HG21	1.24	1.03
1:C:430:ILE:HD11	1:C:435:ARG:CG	1.91	1.01

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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percer	ntiles
1	А	208/279~(75%)	196 (94%)	9~(4%)	3~(1%)	11	5
1	В	222/279~(80%)	206~(93%)	13~(6%)	3~(1%)	11	5
1	С	212/279~(76%)	204 (96%)	3~(1%)	5(2%)	6	1
1	D	205/279~(74%)	190~(93%)	13~(6%)	2(1%)	15	9
All	All	847/1116~(76%)	796~(94%)	38~(4%)	13~(2%)	10	5

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	569	GLN
1	А	612	LEU
1	В	467	THR
1	С	571	HIS
1	С	569	GLN

#### 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	А	188/242~(78%)	156~(83%)	32~(17%)	2 0
1	В	199/242~(82%)	165~(83%)	34~(17%)	2 0
1	С	189/242~(78%)	166 (88%)	23~(12%)	5 2
1	D	186/242~(77%)	147 (79%)	39~(21%)	1 0
All	All	762/968~(79%)	634 (83%)	128 (17%)	2 0

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	614	HIS
1	D	622	GLU
1	В	539	GLN

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	В	537	THR
1	D	627	LEU

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

Mol	Chain	Res	Type
1	С	625	GLN
1	D	538	ASN
1	D	625	GLN
1	D	554	GLN
1	В	536	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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.



## 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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2		$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	А	216/279~(77%)	0.54	11 (5%) 28	36	28, 53, 94, 132	2 (0%)
1	В	227/279~(81%)	0.64	12 (5%) 26	35	36, 62, 112, 137	2(0%)
1	С	218/279~(78%)	0.52	6 (2%) 53	62	31, 63, 101, 138	1 (0%)
1	D	212/279~(75%)	0.64	9 (4%) 36	45	39, 73, 108, 139	6 (2%)
All	All	873/1116 (78%)	0.59	38 (4%) 34	43	28, 62, 104, 139	11 (1%)

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	497	LEU	12.9
1	С	500	LEU	8.9
1	D	612	LEU	8.2
1	В	469	ASN	6.7
1	В	471	LYS	6.0

## 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 monosaccharides in this entry.

#### 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	MG	В	1	1/1	0.41	0.31	$151,\!151,\!151,\!151,\!151$	0
2	MG	С	2	1/1	0.45	0.35	130,130,130,130	0
2	MG	А	4	1/1	0.54	0.39	100,100,100,100	0
2	MG	С	7	1/1	0.55	0.23	102,102,102,102	0
2	MG	В	5	1/1	0.77	0.21	96,96,96,96	0
2	MG	D	6	1/1	0.81	0.40	130,130,130,130	0
2	MG	D	3	1/1	0.82	0.24	122,122,122,122	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

