



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:42 PM BST

PDB ID : 3IYJ  
EMDB ID: : EMD-5155  
Title : Bovine papillomavirus type 1 outer capsid  
Authors : Wolf, M.; Garcea, R.L.; Grigorieff, N.; Harrison, S.C.  
Deposited on : 2009-12-15  
Resolution : 4.20 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
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/EMValidationReportHelp>

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MolProbity : 4.02b-467  
Mogul : unknown  
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) : trunk27241

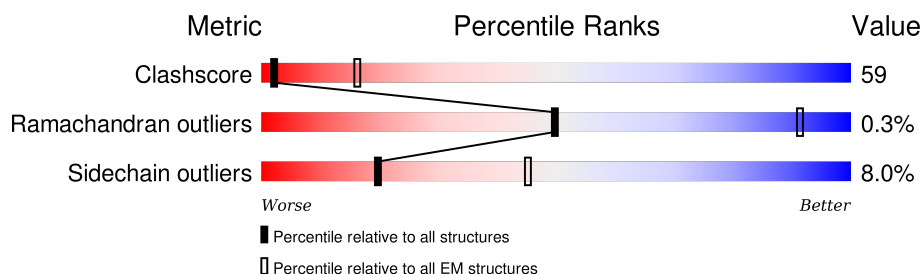
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.20 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	495	36% 57% 5% .
1	B	495	34% 55% 5% 5%
1	C	495	35% 57% 5% .
1	D	495	37% 55% 5% .
1	E	495	38% 54% 5% .
1	F	495	37% 54% . 5%

## 2 Entry composition

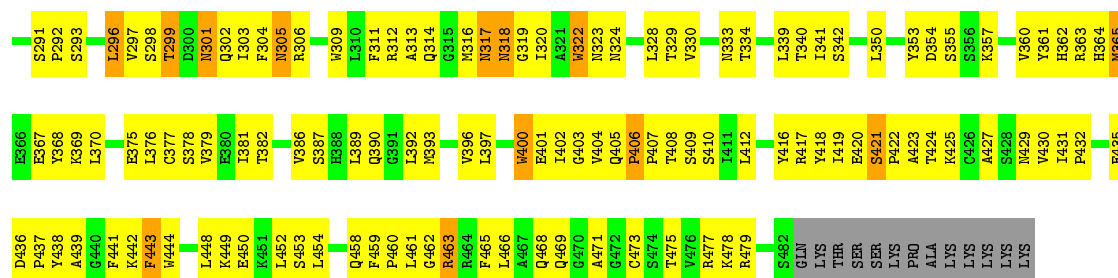
There is only 1 type of molecule in this entry. The entry contains 22614 atoms, of which 0 are hydrogens and 0 are deuteriums.

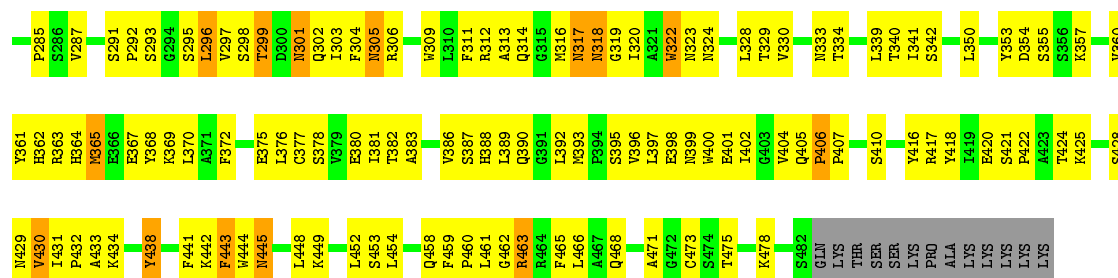
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Major capsid protein L1.

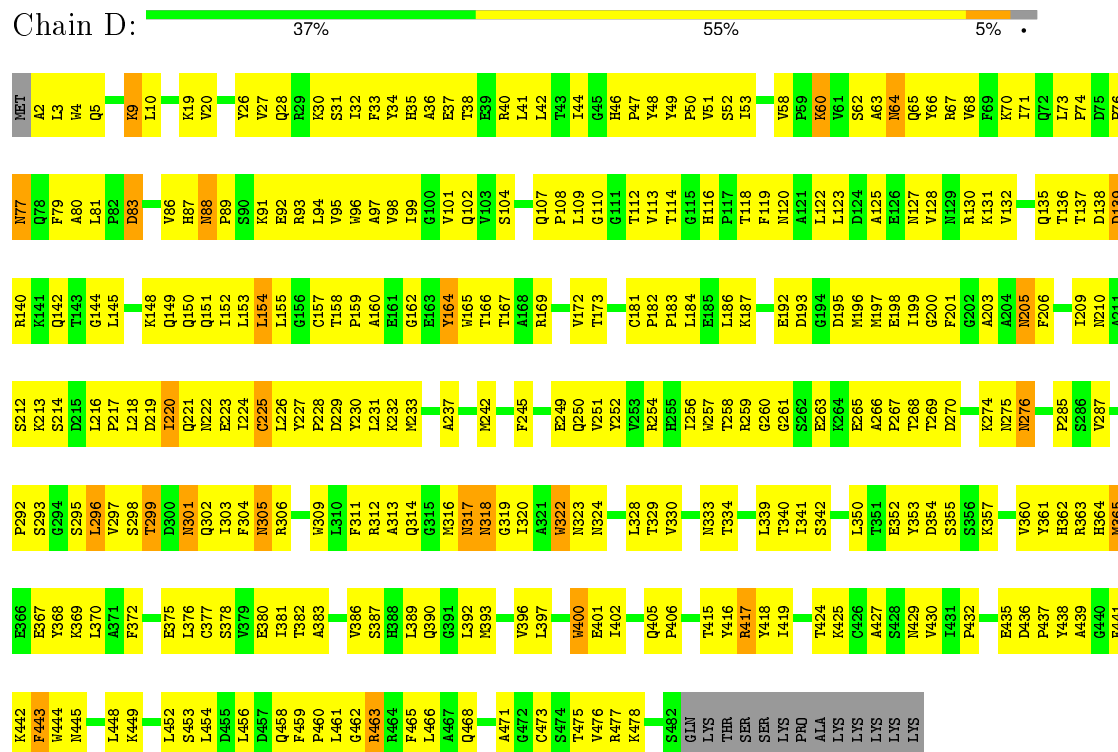
Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	469	Total	C	N	O	S	0	0
			3701	2345	639	702	15		
1	A	481	Total	C	N	O	S	0	0
			3803	2414	656	718	15		
1	B	469	Total	C	N	O	S	0	0
			3701	2345	639	702	15		
1	C	481	Total	C	N	O	S	0	0
			3803	2414	656	718	15		
1	D	481	Total	C	N	O	S	0	0
			3803	2414	656	718	15		
1	E	481	Total	C	N	O	S	0	0
			3803	2414	656	718	15		



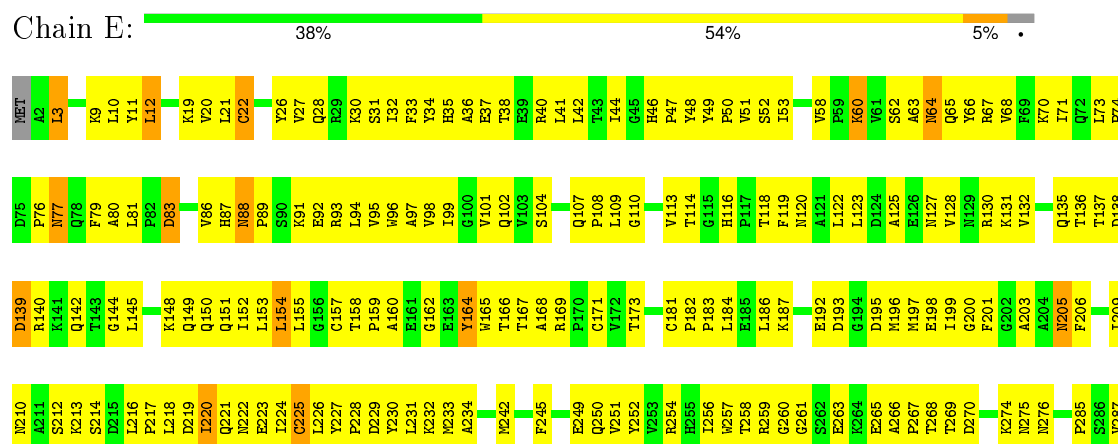




• Molecule 1: Major capsid protein L1



• Molecule 1: Major capsid protein L1






## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTFILT3 WITH INDIVIDUAL PARTICLE ADJUSTMENT	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25.00	Depositor
Minimum defocus (nm)	1800.00	Depositor
Maximum defocus (nm)	2900.00	Depositor
Magnification	59000	Depositor
Image detector	KODAK SO163 FILM	Depositor



## 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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	0.51	0/3896	0.77	4/5296 (0.1%)
1	B	0.50	0/3790	0.74	1/5150 (0.0%)
1	C	0.50	0/3896	0.76	1/5296 (0.0%)
1	D	0.49	0/3896	0.75	1/5296 (0.0%)
1	E	0.50	0/3896	0.76	1/5296 (0.0%)
1	F	0.50	0/3790	0.74	1/5150 (0.0%)
All	All	0.50	0/23164	0.75	9/31484 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	GLY	N-CA-C	5.75	127.49	113.10
1	E	205	ASN	N-CA-C	-5.55	96.01	111.00
1	A	205	ASN	N-CA-C	-5.49	96.17	111.00
1	B	205	ASN	N-CA-C	-5.46	96.27	111.00
1	C	205	ASN	N-CA-C	-5.45	96.29	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	A	3803	0	3748	536	0
1	B	3701	0	3644	464	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3803	0	3748	525	0
1	D	3803	0	3748	448	0
1	E	3803	0	3748	451	0
1	F	3701	0	3646	486	0
All	All	22614	0	22282	2640	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 59.

The worst 5 of 2640 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:153:LEU:CD1	1:E:330:VAL:HG22	1.43	1.47
1:B:153:LEU:CD1	1:B:330:VAL:HG22	1.43	1.46
1:D:87:HIS:CE1	1:D:94:LEU:HG	1.52	1.44
1:D:88:ASN:ND2	1:D:89:PRO:HD2	1.29	1.44
1:C:153:LEU:CD1	1:C:330:VAL:HG22	1.46	1.43

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 PDB entries followed by that with respect to all EM entries.

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	479/495 (97%)	436 (91%)	42 (9%)	1 (0%)	52	86
1	B	467/495 (94%)	430 (92%)	36 (8%)	1 (0%)	52	86
1	C	479/495 (97%)	435 (91%)	41 (9%)	3 (1%)	30	74
1	D	479/495 (97%)	444 (93%)	35 (7%)	0	100	100
1	E	479/495 (97%)	438 (91%)	39 (8%)	2 (0%)	39	80
1	F	467/495 (94%)	425 (91%)	41 (9%)	1 (0%)	52	86

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2850/2970 (96%)	2608 (92%)	234 (8%)	8 (0%)	50 83

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	406	PRO
1	A	406	PRO
1	C	406	PRO
1	C	430	VAL
1	E	432	PRO

### 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 PDB entries followed by that with respect to all EM entries.

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	417/430 (97%)	388 (93%)	29 (7%)	19 59
1	B	407/430 (95%)	372 (91%)	35 (9%)	13 50
1	C	417/430 (97%)	382 (92%)	35 (8%)	14 51
1	D	417/430 (97%)	382 (92%)	35 (8%)	14 51
1	E	417/430 (97%)	381 (91%)	36 (9%)	13 50
1	F	407/430 (95%)	379 (93%)	28 (7%)	19 59
All	All	2482/2580 (96%)	2284 (92%)	198 (8%)	20 53

5 of 198 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	443	PHE
1	C	296	LEU
1	E	301	ASN
1	C	6	GLN
1	C	88	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	318	ASN
1	C	142	GLN
1	E	250	GLN
1	B	338	ASN
1	C	64	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 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.