



## Full wwPDB EM Validation Report ⓘ

May 4, 2024 – 10:57 am BST

PDB ID : 6HU7  
EMDB ID : EMD-0273  
Title : phosphorylated F97L Hepatitis B core protein capsid  
Authors : Bottcher, B.; Nassal, M.  
Deposited on : 2018-10-05  
Resolution : 2.80 Å(reported)  
Based on initial model : 6HU4

This is a Full wwPDB EM Validation 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

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

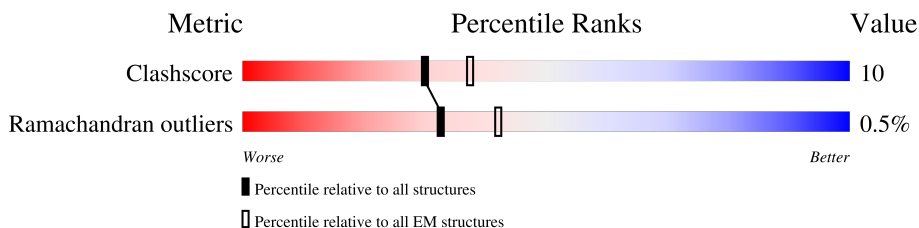
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.80 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	158937	4297
Ramachandran outliers	154571	4023

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	183	
1	B	183	
1	C	183	
1	D	183	
1	F	183	
1	G	183	
1	H	183	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4890 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 Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	152	Total	C	N	O	S	0	0
			1218	787	205	220	6		
1	A	147	Total	C	N	O	S	2	0
			1190	770	198	216	6		
1	C	151	Total	C	N	O	S	1	0
			1218	787	205	220	6		
1	D	151	Total	C	N	O	S	0	0
			1207	781	201	219	6		
1	F	2	Total	C	N	O	S	0	0
			15	8	3	3	1		
1	G	3	Total	C	N	O	S	0	0
			21	11	4	5	1		
1	H	3	Total	C	N	O	S	0	0
			21	11	4	5	1		

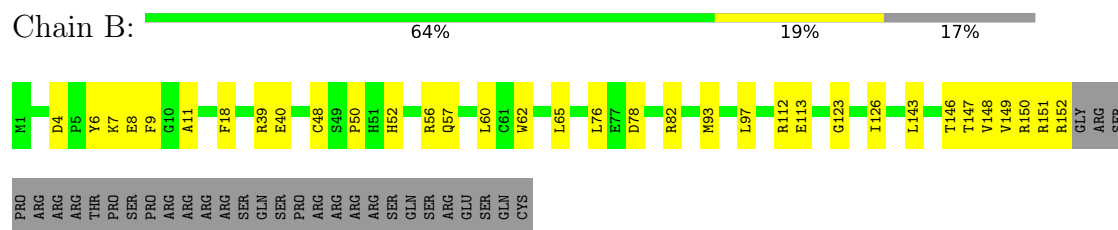
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	97	LEU	PHE	engineered mutation	UNP D0EYZ6
A	97	LEU	PHE	engineered mutation	UNP D0EYZ6
C	97	LEU	PHE	engineered mutation	UNP D0EYZ6
D	97	LEU	PHE	engineered mutation	UNP D0EYZ6
F	97	LEU	PHE	engineered mutation	UNP D0EYZ6
G	97	LEU	PHE	engineered mutation	UNP D0EYZ6
H	97	LEU	PHE	engineered mutation	UNP D0EYZ6

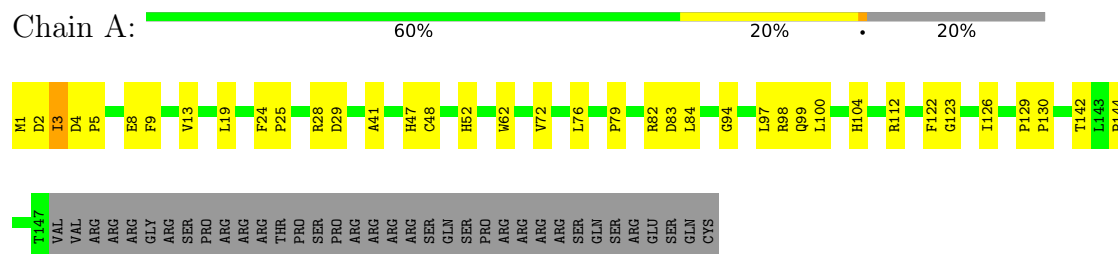
### 3 Residue-property plots [i](#)

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. 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. 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.

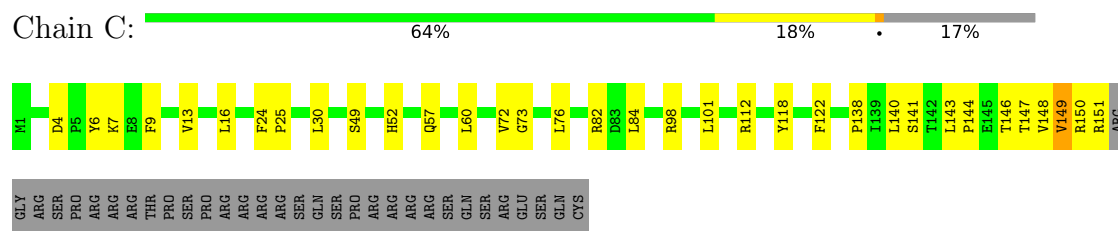
#### • Molecule 1: Capsid protein



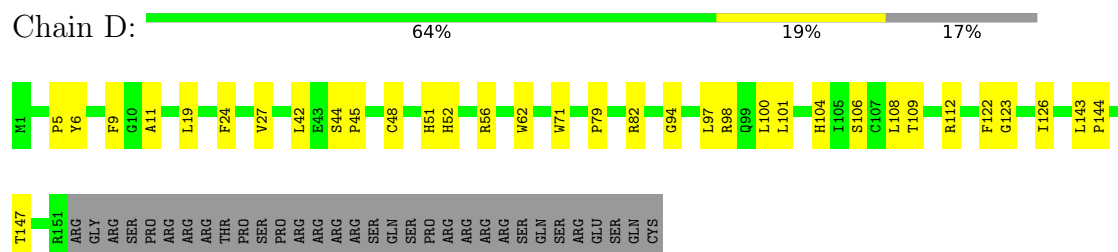
#### • Molecule 1: Capsid protein



#### • Molecule 1: Capsid protein



#### • Molecule 1: Capsid protein



[illegible]

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	31635	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	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  >5	RMSZ	# Z  >5
1	A	0.40	0/1228	0.51	0/1681
1	B	0.41	0/1253	0.50	0/1715
1	C	0.41	0/1253	0.49	0/1715
1	D	0.41	0/1242	0.49	0/1701
1	F	0.19	0/14	0.32	0/17
1	G	0.22	0/20	0.37	0/25
1	H	0.26	0/20	0.29	0/25
All	All	0.41	0/5030	0.50	0/6879

There are no bond length outliers.

There are no bond angle outliers.

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	1190	0	1181	29	0
1	B	1218	0	1213	31	0
1	C	1218	0	1212	30	0
1	D	1207	0	1200	25	0
1	F	15	0	12	1	0
1	G	21	0	17	0	0
1	H	21	0	17	2	0
All	All	4890	0	4852	97	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 10.

All (97) 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:44:SER:HG	1:H:181:SER:N	1.73	0.87
1:B:150:ARG:NH1	1:C:143:LEU:O	2.13	0.80
1:A:2:ASP:OD1	1:A:3:ILE:N	2.16	0.77
1:C:7:LYS:HE2	1:D:45:PRO:HG3	1.68	0.74
1:D:62:TRP:HB2	1:D:97:LEU:HD21	1.69	0.73
1:B:60:LEU:HD13	1:A:5:PRO:HG3	1.71	0.72
1:D:24:PHE:O	1:D:98:ARG:NH1	2.28	0.66
1:B:149:VAL:HG21	1:C:118:TYR:HD1	1.62	0.64
1:C:148:VAL:HG12	1:C:149:VAL:HG23	1.81	0.63
1:B:48:CYS:HB2	1:B:52:HIS:CD2	2.34	0.63
1:A:83:ASP:OD1	1:A:84:LEU:N	2.31	0.62
1:C:60:LEU:HD13	1:D:5:PRO:HG3	1.81	0.62
1:A:62:TRP:HB2	1:A:97:LEU:HD21	1.82	0.62
1:D:79:PRO:HA	1:D:82:ARG:HG2	1.84	0.60
1:D:44:SER:OG	1:H:181:SER:N	2.37	0.57
1:C:73:GLY:HA2	1:C:82[B]:ARG:HE	1.69	0.56
1:C:73:GLY:HA2	1:C:82[A]:ARG:HE	1.69	0.56
1:C:57:GLN:HE22	1:D:100:LEU:HD21	1.70	0.56
1:B:76:LEU:HD23	1:B:78:ASP:H	1.71	0.55
1:A:79:PRO:HA	1:A:82:ARG:HG2	1.89	0.55
1:C:76:LEU:O	1:C:82[B]:ARG:NH1	2.40	0.55
1:C:76:LEU:O	1:C:82[A]:ARG:NH1	2.40	0.54
1:A:1:MET:HG3	1:A:3:ILE:HG13	1.89	0.54
1:A:9:PHE:O	1:A:112:ARG:HD2	2.08	0.54
1:A:72:VAL:HG13	1:A:76:LEU:HD22	1.89	0.54
1:A:62:TRP:HB2	1:A:97:LEU:CD2	2.38	0.54
1:C:6:TYR:CZ	1:C:16:LEU:HD22	2.44	0.53
1:B:56:ARG:NH1	1:A:8:GLU:OE1	2.42	0.53
1:A:48:CYS:HB2	1:A:52:HIS:CD2	2.44	0.53
1:A:4:ASP:OD1	1:A:13:VAL:HG23	2.10	0.52
1:A:76:LEU:O	1:A:82:ARG:NH1	2.43	0.51
1:C:72:VAL:HG12	1:C:82[B]:ARG:HG3	1.93	0.51
1:C:146:THR:HG22	1:C:150:ARG:HE	1.74	0.51
1:C:72:VAL:HG12	1:C:82[A]:ARG:HG3	1.93	0.51
1:B:65:LEU:HD21	1:B:93:MET:HE1	1.92	0.51
1:B:6:TYR:HB3	1:B:11:ALA:HB3	1.93	0.51
1:B:9:PHE:O	1:B:112:ARG:HD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:PHE:O	1:D:112:ARG:HD2	2.11	0.51
1:B:112:ARG:NH2	1:B:113:GLU:OE2	2.44	0.50
1:B:8:GLU:HG2	1:A:47:HIS:CD2	2.46	0.50
1:D:6:TYR:HB3	1:D:11:ALA:HB3	1.94	0.50
1:C:4:ASP:HB3	1:C:7:LYS:HB2	1.93	0.49
1:D:51:HIS:HB2	1:D:108:LEU:HD21	1.95	0.49
1:C:143:LEU:HD12	1:C:144:PRO:HD2	1.94	0.49
1:B:8:GLU:CG	1:A:47:HIS:HD2	2.26	0.49
1:B:123:GLY:HA2	1:B:126:ILE:HG22	1.94	0.48
1:B:147:THR:HB	1:C:138:PRO:HA	1.95	0.48
1:A:142:THR:O	1:A:144:PRO:HD3	2.13	0.48
1:B:57:GLN:HE22	1:A:100:LEU:HD21	1.78	0.48
1:A:19:LEU:HD23	1:A:122:PHE:CD2	2.49	0.48
1:C:9:PHE:O	1:C:112:ARG:HD2	2.14	0.48
1:D:48:CYS:HB2	1:D:52:HIS:CD2	2.49	0.48
1:A:25:PRO:O	1:A:98:ARG:HD2	2.15	0.47
1:A:123:GLY:HA2	1:A:126:ILE:HG22	1.97	0.47
1:A:41:ALA:HA	1:F:182:GLN:HG3	1.96	0.47
1:C:30:LEU:HD23	1:C:101:LEU:HB3	1.97	0.46
1:C:84:LEU:HB3	1:D:71:TRP:HH2	1.80	0.46
1:C:25:PRO:HB2	1:C:30:LEU:CD1	2.45	0.46
1:B:146:THR:O	1:B:147:THR:OG1	2.27	0.46
1:B:50:PRO:HG2	1:A:47:HIS:CE1	2.50	0.46
1:B:8:GLU:HG2	1:A:47:HIS:HD2	1.79	0.46
1:B:150:ARG:HA	1:C:141:SER:O	2.16	0.46
1:C:49:SER:H	1:C:52:HIS:HD2	1.64	0.46
1:A:24:PHE:CE2	1:A:99:GLN:HG2	2.51	0.46
1:B:18:PHE:HB3	1:B:126:ILE:HG21	1.98	0.45
1:B:151:ARG:HG2	1:B:152:ARG:H	1.82	0.45
1:D:42:LEU:O	1:D:56:ARG:HD3	2.17	0.44
1:B:4:ASP:HB3	1:B:7:LYS:HB2	1.98	0.44
1:B:149:VAL:HB	1:C:140:LEU:HD23	1.99	0.44
1:D:123:GLY:HA2	1:D:126:ILE:HG22	1.98	0.44
1:B:39:ARG:HG3	1:B:40:GLU:N	2.32	0.44
1:C:24:PHE:O	1:C:98:ARG:NH2	2.40	0.44
1:B:143:LEU:HD13	1:B:147:THR:HG22	2.00	0.43
1:B:60:LEU:HD11	1:A:3:ILE:HG22	2.00	0.43
1:D:9:PHE:CE2	1:D:104:HIS:HE1	2.37	0.43
1:D:144:PRO:HD2	1:D:147:THR:HG22	2.01	0.43
1:D:27:VAL:HG22	1:D:98:ARG:HB3	2.00	0.42
1:B:76:LEU:O	1:B:82:ARG:HD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:GLY:O	1:A:98:ARG:N	2.43	0.42
1:B:76:LEU:HD22	1:B:82:ARG:HG3	2.02	0.42
1:C:147:THR:HA	1:C:151:ARG:NH2	2.35	0.42
1:A:129:PRO:HA	1:A:130:PRO:HD3	1.96	0.42
1:D:44:SER:HA	1:D:45:PRO:HD3	1.86	0.42
1:A:9:PHE:CE2	1:A:104:HIS:HE1	2.38	0.42
1:B:62:TRP:HB2	1:B:97:LEU:HD22	2.01	0.41
1:D:106:SER:O	1:D:109:THR:O	2.38	0.41
1:A:28[B]:ARG:HG3	1:A:29:ASP:N	2.35	0.41
1:D:143:LEU:HB2	1:D:147:THR:HG21	2.01	0.41
1:C:4:ASP:OD1	1:C:13:VAL:HG23	2.20	0.41
1:C:30:LEU:HB3	1:C:101:LEU:HD23	2.02	0.41
1:C:122:PHE:CD1	1:C:138:PRO:HD2	2.55	0.41
1:B:78:ASP:O	1:B:82:ARG:HG3	2.21	0.41
1:D:19:LEU:HD23	1:D:122:PHE:CD2	2.56	0.40
1:B:143:LEU:CD1	1:C:138:PRO:HG3	2.52	0.40
1:D:62:TRP:HB2	1:D:97:LEU:CD2	2.45	0.40
1:D:97:LEU:HG	1:D:101:LEU:HD13	2.03	0.40
1:D:94:GLY:O	1:D:98:ARG:HG2	2.22	0.40

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 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	147/183 (80%)	142 (97%)	4 (3%)	1 (1%)	22	53
1	B	150/183 (82%)	144 (96%)	5 (3%)	1 (1%)	22	53
1	C	150/183 (82%)	144 (96%)	5 (3%)	1 (1%)	22	53
1	D	149/183 (81%)	147 (99%)	2 (1%)	0	100	100
1	G	1/183 (0%)	1 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	1/183 (0%)	1 (100%)	0	0	100	100
All	All	598/1098 (54%)	579 (97%)	16 (3%)	3 (0%)	32	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	149	VAL
1	B	148	VAL
1	A	3	ILE

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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](#)

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-0273. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 6.5 Orthogonal surface views

This section was not generated.

### 6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution ⓘ

This section was not generated.

### 7.2 Volume estimate versus contour level ⓘ

This section was not generated.

### 7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit ⓘ

This section was not generated.