



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 3, 2020 – 06:50 pm BST

PDB ID : 4QPG
Title : Crystal structure of empty hepatitis A virus
Authors : Wang, X.; Ren, J.; Gao, Q.; Hu, Z.; Sun, Y.; Li, X.; Rowlands, D.J.; Yin, W.;
Wang, J.; Stuart, D.I.; Rao, Z.; Fry, E.E.
Deposited on : 2014-06-23
Resolution : 3.50 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

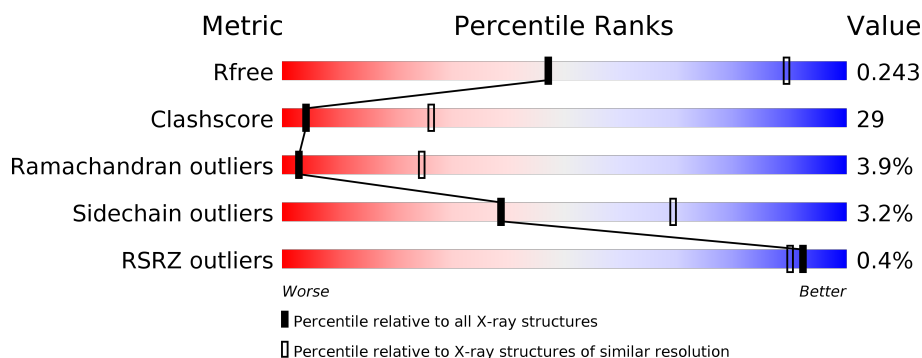
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 ≥ 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 $\leq 5\%$. 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	225	<div> <div style="width: 49%; background-color: green;"></div> <div style="width: 45%; background-color: yellow;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> </div> <div>49% 45% 5% .</div>
2	B	204	<div> <div style="width: 56%; background-color: green;"></div> <div style="width: 40%; background-color: yellow;"></div> <div style="width: 2%; background-color: orange;"></div> </div> <div>56% 40% .</div>
3	C	246	<div> <div style="width: 51%; background-color: green;"></div> <div style="width: 47%; background-color: yellow;"></div> <div style="width: 2%; background-color: orange;"></div> </div> <div>51% 47% .</div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CL	A	302	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5368 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1785	1151	290	338	6			

- Molecule 2 is a protein called Capsid protein VP0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	204	Total	C	N	O	S	0	0	0
			1615	1042	274	296	3			

- Molecule 3 is a protein called Capsid protein VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	246	Total	C	N	O	S	0	0	0
			1956	1248	331	363	14			

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

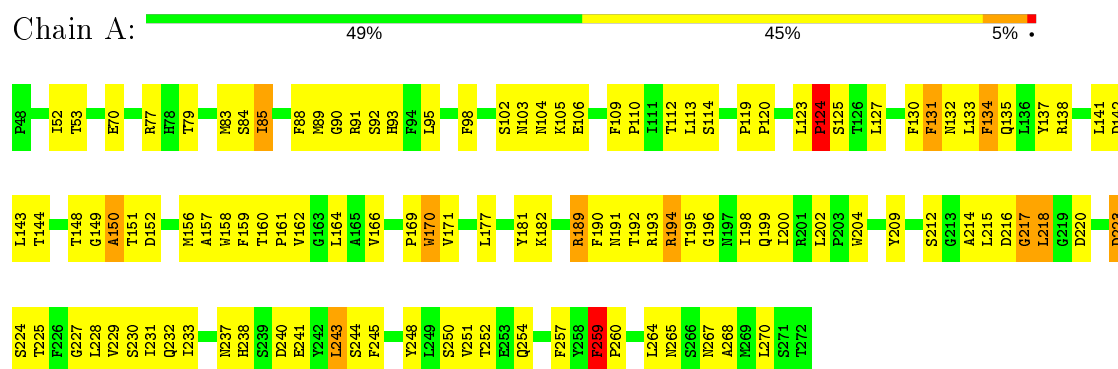


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		

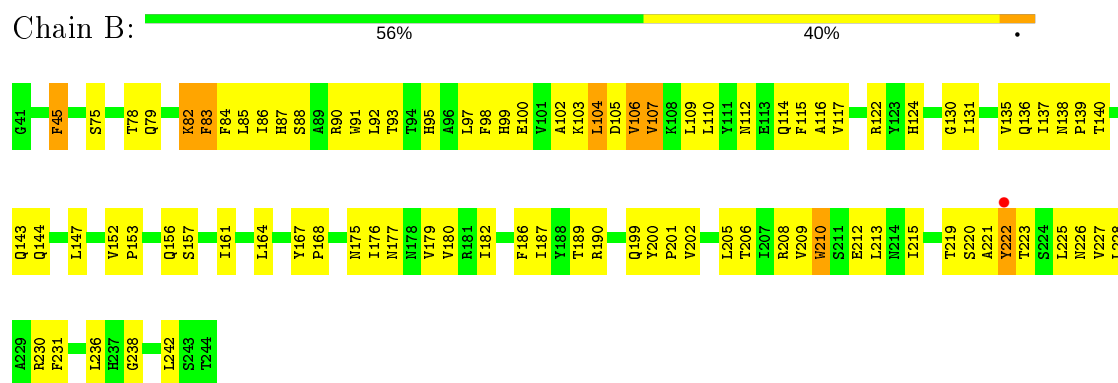
3 Residue-property plots [i](#)

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.

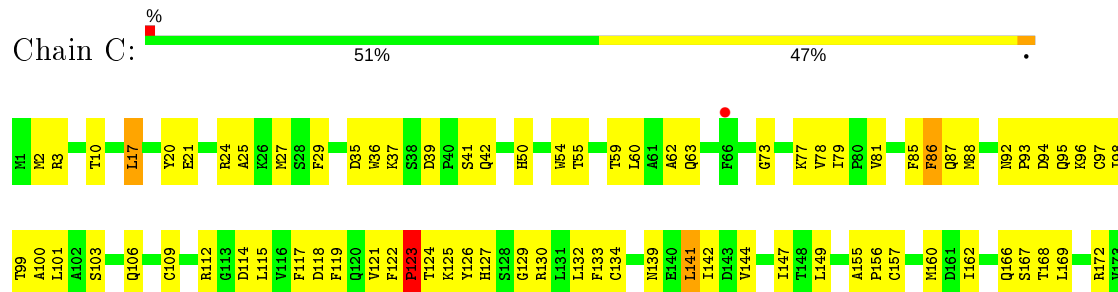
• Molecule 1: Capsid protein VP1



• Molecule 2: Capsid protein VP0



• Molecule 3: Capsid protein VP3



P174	W175	I176		Y181	R182	V183	N184	R185	Y186	T187	K188	E189	A190	H191	Q192	K193		Y196	T197		I203	V204	Y205	C206	Y207	N208	R209	L210	T211	S212	P213		V216	A217		V220	R221	Y222	N223	Y224	Y225	L226		L231	E232	C233	F234	A235	P236	L237	Y238	H239	A240	M241	D242	V243	T244	Q246
------	------	------	--	------	------	------	------	------	------	------	------	------	------	------	------	------	--	------	------	--	------	------	------	------	------	------	------	------	------	------	------	--	------	------	--	------	------	------	------	------	------	------	--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	366.11Å 442.91Å 289.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.67 – 3.50 49.67 – 3.48	Depositor EDS
% Data completeness (in resolution range)	67.8 (49.67-3.50) 66.9 (49.67-3.48)	Depositor EDS
R_{merge}	0.36	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 3.48Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.264 , 0.263 0.245 , 0.243	Depositor DCC
R_{free} test set	3996 reflections (1.01%)	wwPDB-VP
Wilson B-factor (Å ²)	175.5	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 129.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5368	wwPDB-VP
Average B, all atoms (Å ²)	180.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, CL

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	0.30	0/1838	0.55	0/2506
2	B	0.31	0/1659	0.56	0/2260
3	C	0.30	0/2007	0.53	0/2733
All	All	0.30	0/5504	0.55	0/7499

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	1785	0	1730	123	0
2	B	1615	0	1598	90	0
3	C	1956	0	1911	134	0
4	A	2	0	0	1	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
All	All	5368	0	5239	312	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 29.

The worst 5 of 312 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:A:193:ARG:NH2	4:A:301:CL:CL	2.32	0.98
2:B:92:LEU:H	2:B:95:HIS:HD2	1.14	0.92
2:B:92:LEU:H	2:B:95:HIS:CD2	1.89	0.91
1:A:265:ASN:HD21	1:A:267:ASN:HB2	1.38	0.89
2:B:102:ALA:HB1	2:B:104:LEU:HD11	1.57	0.84

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	223/225 (99%)	182 (82%)	31 (14%)	10 (4%)	2	21
2	B	202/204 (99%)	160 (79%)	36 (18%)	6 (3%)	4	30
3	C	244/246 (99%)	198 (81%)	36 (15%)	10 (4%)	3	23
All	All	669/675 (99%)	540 (81%)	103 (15%)	26 (4%)	3	25

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ALA
2	B	106	VAL
3	C	97	CYS
3	C	125	LYS
1	A	217	GLY

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	198/198 (100%)	188 (95%)	10 (5%)	24	57
2	B	177/177 (100%)	172 (97%)	5 (3%)	43	72
3	C	217/217 (100%)	213 (98%)	4 (2%)	59	81
All	All	592/592 (100%)	573 (97%)	19 (3%)	39	69

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	243	LEU
2	B	82	LYS
3	C	17	LEU
1	A	237	ASN
3	C	94	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	112	ASN
2	B	114	GLN
3	C	95	GLN
2	B	99	HIS
3	C	75	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SO4	B	301	-	4,4,4	0.22	0	6,6,6	0.04	0
5	SO4	A	303	-	4,4,4	0.20	0	6,6,6	0.06	0

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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	225/225 (100%)	-0.28	0 100 100	155, 181, 222, 268	0
2	B	204/204 (100%)	-0.31	1 (0%) 91 88	153, 174, 202, 269	0
3	C	246/246 (100%)	-0.38	2 (0%) 86 81	152, 176, 199, 261	0
All	All	675/675 (100%)	-0.32	3 (0%) 92 90	152, 177, 211, 269	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	222	TYR	2.3
3	C	207	TYR	2.3
3	C	66	PHE	2.3

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 ⓘ

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, 95th 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	B-factors(Å ²)	Q<0.9
4	CL	A	301	1/1	0.29	0.39	163,163,163,163	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	A	302	1/1	0.69	0.46	141,141,141,141	1
5	SO4	B	301	5/5	0.71	0.26	300,300,300,300	0
5	SO4	A	303	5/5	0.84	0.46	300,300,300,300	0

6.5 Other polymers [i](#)

There are no such residues in this entry.