Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 02:53 PM EDT

PDB ID	:	1HAV
Title	:	HEPATITIS A VIRUS 3C PROTEINASE
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Deposited on	:	1996-10-23
Resolution	:	2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

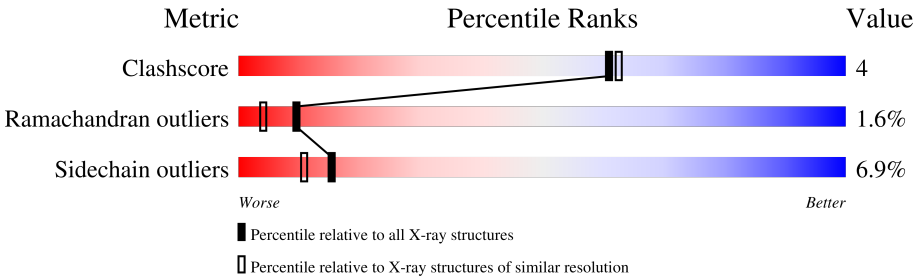
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	217	86% 12% .
2	B	217	82% 14% ..

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3430 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 HEPATITIS A VIRUS 3C PROTEINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1668	1064	286	309	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	SER	CYS	engineered mutation	UNP P08617

- Molecule 2 is a protein called HEPATITIS A VIRUS 3C PROTEINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1654	1052	283	310	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	24	SER	CYS	engineered mutation	UNP P08617
B	172	OCS	CYS	conflict	UNP P08617

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	61	Total	O	0	0
			61	61		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	46	Total	O	0	0
			46	46		

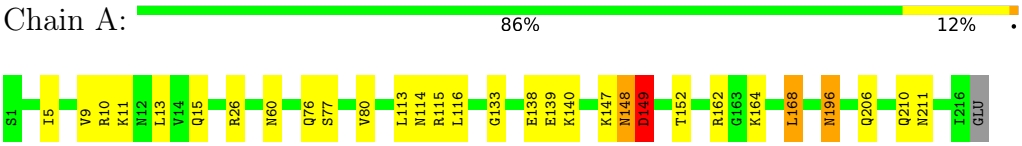
3 Residue-property plots (i)

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.

Note EDS was not executed.

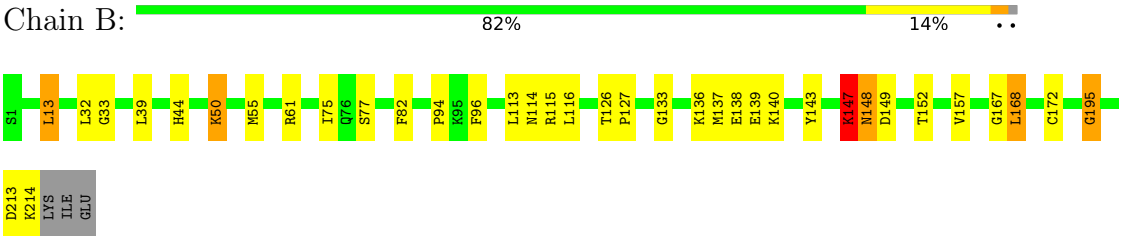
• Molecule 1: HEPATITIS A VIRUS 3C PROTEINASE

Chain A:



• Molecule 2: HEPATITIS A VIRUS 3C PROTEINASE

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	53.60Å 53.55Å 53.20Å 99.08° 129.00° 103.31°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	87.0 (20.00-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.211 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3430	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.52	0/1698	0.80	1/2294 (0.0%)
2	B	0.52	0/1674	0.84	0/2261
All	All	0.52	0/3372	0.82	1/4555 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	13	LEU	CA-CB-CG	6.59	130.45	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1668	0	1703	11	0
2	B	1654	0	1678	19	0
3	B	1	0	0	0	0
4	A	61	0	0	0	0
4	B	46	0	0	0	0
All	All	3430	0	3381	30	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 4.

All (30) 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)
2:B:33:GLY:HA2	2:B:39:LEU:HD23	1.64	0.79
2:B:143:TYR:OH	2:B:195:GLY:HA3	1.98	0.62
1:A:113:LEU:O	1:A:114:ASN:HB2	1.99	0.61
2:B:114:ASN:ND2	2:B:136:LYS:NZ	2.48	0.61
2:B:115:ARG:HH11	2:B:115:ARG:HG3	1.68	0.59
2:B:33:GLY:CA	2:B:39:LEU:HD23	2.30	0.59
2:B:13:LEU:HD13	2:B:32:LEU:HD13	1.85	0.58
2:B:50:LYS:O	2:B:50:LYS:HD2	2.05	0.56
1:A:138:GLU:HG3	1:A:162:ARG:HD3	1.92	0.52
2:B:113:LEU:O	2:B:115:ARG:NH1	2.43	0.52
2:B:137:MET:HG3	2:B:138:GLU:N	2.26	0.51
2:B:61:ARG:NH1	2:B:94:PRO:O	2.44	0.51
1:A:15:GLN:HB2	1:A:60:ASN:HB3	1.95	0.49
2:B:39:LEU:HD21	2:B:96:PHE:CZ	2.49	0.48
2:B:114:ASN:ND2	2:B:136:LYS:HZ1	2.11	0.47
1:A:76:GLN:NE2	1:A:211:ASN:HB2	2.30	0.46
2:B:77:SER:HB2	2:B:82:PHE:CE1	2.50	0.46
1:A:147:LYS:O	1:A:149:ASP:N	2.48	0.46
1:A:168:LEU:HD22	1:A:168:LEU:HA	1.86	0.45
1:A:139:GLU:O	1:A:140:LYS:HG3	2.17	0.45
1:A:5:ILE:O	1:A:9:VAL:HG23	2.17	0.45
2:B:126:THR:HA	2:B:127:PRO:HD3	1.78	0.45
2:B:167:GLY:O	2:B:168:LEU:HD13	2.17	0.45
2:B:39:LEU:HD21	2:B:96:PHE:CE2	2.52	0.44
1:A:147:LYS:O	1:A:148:ASN:C	2.55	0.44
2:B:44:HIS:HD2	2:B:147:LYS:HD2	1.83	0.44
1:A:11:LYS:HE2	1:A:11:LYS:HB2	1.84	0.41
2:B:140:LYS:HA	2:B:157:VAL:O	2.21	0.40
2:B:75:ILE:HG22	2:B:82:PHE:HE2	1.86	0.40
1:A:196:ASN:HD22	1:A:196:ASN:N	2.19	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 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	214/217 (99%)	195 (91%)	16 (8%)	3 (1%)	11 5
2	B	211/217 (97%)	192 (91%)	15 (7%)	4 (2%)	8 3
All	All	425/434 (98%)	387 (91%)	31 (7%)	7 (2%)	9 4

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	ASP
2	B	133	GLY
2	B	148	ASN
1	A	133	GLY
1	A	148	ASN
2	B	147	LYS
2	B	195	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	182/183 (100%)	169 (93%)	13 (7%)	14 10
2	B	179/182 (98%)	167 (93%)	12 (7%)	16 11
All	All	361/365 (99%)	336 (93%)	25 (7%)	15 11

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	26	ARG
1	A	77	SER
1	A	80	VAL
1	A	115	ARG
1	A	116	LEU
1	A	149	ASP
1	A	152	THR
1	A	164	LYS
1	A	168	LEU
1	A	196	ASN
1	A	206	GLN
1	A	210	GLN
2	B	13	LEU
2	B	50	LYS
2	B	55	MET
2	B	116	LEU
2	B	139	GLU
2	B	147	LYS
2	B	148	ASN
2	B	149	ASP
2	B	152	THR
2	B	168	LEU
2	B	213	ASP
2	B	214	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	83	GLN
1	A	181	GLN
1	A	196	ASN
2	B	76	GLN
2	B	114	ASN
2	B	148	ASN
2	B	159	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\#\|Z\| > 2$
2	OCS	B	172	2	7,8,9	0.92	0	6,11,13	5.31	4 (66%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OCS	B	172	2	-	0/4/7/9	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	172	OCS	OD1-SG-CB	-8.93	96.32	106.94
2	B	172	OCS	OD3-SG-CB	7.64	116.02	106.94
2	B	172	OCS	OD2-SG-OD3	-4.24	100.91	111.27
2	B	172	OCS	OD2-SG-OD1	3.04	118.70	111.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.