

Full wwPDB X-ray Structure Validation Report (i)

Oct 2, 2023 – 10:16 AM EDT

PDB ID	:	6MO0
Title	:	Structure of dengue virus protease with an allosteric Inhibitor that blocks
		replication
Authors	:	Lin, YL.; Nie, S.; Hua, Y.; Wu, J.; Wu, F.; Huo, T.; Yao, Y.; Song, Y.
Deposited on		
Resolution	:	2.70 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 (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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
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)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



6MO0

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2578 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	Atoms					ZeroOcc	AltConf	Trace
1	Δ	164	Total	С	Ν	0	S	0	0	0
1	A	104	1256	796	217	240	3	0	0	0
1	D	164	Total	С	Ν	0	S	0	0	0
	D	104	1256	796	217	240	3	0	0	0

• Molecule 1 is a protein called FLAVIVIRUS_NS2B/Peptidase S7.

Chain	Residue	Modelled	Actual	Comment	Reference
А	43	GLY	-	expression tag	UNP A0A0B4L2Y4
А	44	SER	- expression tag		UNP A0A0B4L2Y4
А	45	HIS	-	expression tag	UNP A0A0B4L2Y4
А	46	MET	-	expression tag	UNP A0A0B4L2Y4
А	47	LEU	-	expression tag	UNP A0A0B4L2Y4
А	48	MET	-	expression tag	UNP A0A0B4L2Y4
А	992	GLY	-	linker	UNP A0A0B4L2Y4
А	993	GLY	-	linker	UNP A0A0B4L2Y4
А	994	GLY	-	linker	UNP A0A0B4L2Y4
А	995	GLY	-	linker	UNP A0A0B4L2Y4
A	996	SER	-	linker	UNP A0A0B4L2Y4
A	997	GLY	-	linker	UNP A0A0B4L2Y4
А	998	GLY	-	linker	UNP A0A0B4L2Y4
А	999	GLY	-	linker	UNP A0A0B4L2Y4
А	1000	GLY	-	linker	UNP A0A0B4L2Y4
А	1167	ASN	GLN	conflict	UNP Q91H74
В	43	GLY	-	expression tag	UNP A0A0B4L2Y4
В	44	SER	-	expression tag	UNP A0A0B4L2Y4
В	45	HIS	-	expression tag	UNP A0A0B4L2Y4
В	46	MET	-	expression tag	UNP A0A0B4L2Y4
В	47	LEU	-	expression tag	UNP A0A0B4L2Y4
В	48	MET	-	expression tag	UNP A0A0B4L2Y4
В	992	GLY	-	linker	UNP A0A0B4L2Y4
В	993	GLY	-	linker	UNP A0A0B4L2Y4
В	994	GLY	-	linker	UNP A0A0B4L2Y4

There are 32 discrepancies between the modelled and reference sequences:

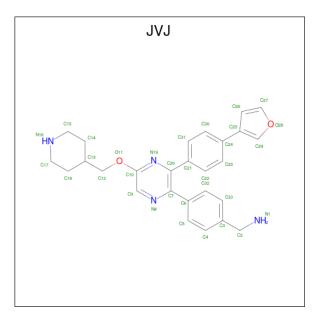
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Chain	Residue	Modelled	Actual	Comment	Reference				
В	995	GLY	-	linker	UNP A0A0B4L2Y4				
В	996	SER	-	linker	UNP A0A0B4L2Y4				
В	997	GLY	-	linker	UNP A0A0B4L2Y4				
В	998	GLY	-	linker	UNP A0A0B4L2Y4				
В	999	GLY	-	linker	UNP A0A0B4L2Y4				
В	1000	GLY	-	linker	UNP A0A0B4L2Y4				
В	1167	ASN	GLN	conflict	UNP Q91H74				

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• Molecule 2 is 1-(4-{3-[4-(furan-3-yl)phenyl]-5-[(piperidin-4-yl)methoxy]pyrazin-2-yl}phenyl) methanamine (three-letter code: JVJ) (formula: $C_{27}H_{28}N_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccccc} \text{Total} & \text{C} & \text{N} & \text{O} \\ 33 & 27 & 4 & 2 \end{array}$	0	0
2	В	1	Total C N O 33 27 4 2	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants	109.11Å 109.11 Å 75.85 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.13 - 2.70	Depositor
% Data completeness	99.7 (40.13-2.70)	Depositor
(in resolution range)		-
R_{merge}	0.40	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.89 (at 2.69 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.256 , 0.311	Depositor
Wilson B-factor ($Å^2$)	56.9	Xtriage
Anisotropy	0.027	Xtriage
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.037 for -h,-k,l	Xtriage
Total number of atoms	2578	wwPDB-VP
Average B, all atoms $(Å^2)$	56.0	wwPDB-VP

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.70% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

2 ligands are 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



			Bond lengths Bond angles							Pag	Tiple	Bond lengths			gles
Mol	Type	Chain	Res	5 Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2					
2	JVJ	А	1201	-	34,37,37	2.41	14 (41%)	43,50,50	2.35	14 (32%)					
2	JVJ	В	1201	-	34,37,37	2.64	13 (38%)	43,50,50	1.78	7 (16%)					

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).

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	JVJ	А	1201	-	-	6/19/27/27	0/5/5/5
2	JVJ	В	1201	-	-	1/19/27/27	0/5/5/5

Mol Chain Res Type Atoms \mathbf{Z} Observed(Å) Ideal(Å) 2В 1201 JVJ C29-C258.75 1.471.37 $\mathbf{2}$ В 1201 JVJ C21-C206.231.561.49 $\overline{2}$ А 1201 JVJ C20-N19 5.571.431.34 2А 1201 JVJ C29-C255.191.431.372А 1201 JVJ C30-C244.811.491.39 $\overline{2}$ А JVJ C30-C31 1201 3.901.451.38 2 В 1201 JVJ C20-N19 3.73 1.40 1.34 $\overline{2}$ В 1201 JVJ C30-C31 3.561.451.382JVJ А 1201 O11-C10 1.431.363.52JVJ C22-C21 2А 1201 3.43 1.461.392А 1201 JVJ C21-C20 1.523.281.492А JVJ 1201 C6-C7 -3.221.451.49 $\overline{2}$ В JVJ 1201 C32-C33 3.17 1.44 1.38 2В JVJ 1201 C6-C71.451.49-3.08 $\mathbf{2}$ В 1201 JVJ C10-N19 3.011.381.332 В JVJ C30-C24 1201 2.971.451.392 А 1201 JVJ C4-C52.961.441.382В 1201 JVJ C22-C232.891.441.382В 1201 JVJ C22-C21 2.771.391.452 А 1201 JVJ C10-N19 2.491.371.33 2В 1201 JVJ C23-C242.431.44 1.39 $\overline{2}$ В 1201 JVJ C33-C3 1.44 2.431.382А 1201 JVJ C32-C6 2.33 1.44 1.39

All (27) bond length outliers are listed below:

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Mol	Chain		• •	Atoms	\mathbf{Z}	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	В	1201	JVJ	C25-C24	2.31	1.54	1.49
2	А	1201	JVJ	C31-C21	2.29	1.44	1.39
2	А	1201	JVJ	C9-C10	2.29	1.43	1.39
2	А	1201	JVJ	C4-C3	2.26	1.43	1.38

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All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	1201	JVJ	C9-C10-N19	-8.69	116.72	122.99
2	В	1201	JVJ	C33-C32-C6	-5.98	112.52	121.13
2	А	1201	JVJ	C4-C5-C6	-4.25	115.02	121.13
2	А	1201	JVJ	C5-C6-C32	4.14	125.83	117.59
2	В	1201	JVJ	C5-C6-C32	3.93	125.42	117.59
2	В	1201	JVJ	C17-C18-C13	-3.75	106.33	112.14
2	А	1201	JVJ	C22-C23-C24	-3.67	115.84	121.13
2	А	1201	JVJ	C21-C20-N19	3.02	119.09	115.09
2	А	1201	JVJ	C29-C25-C24	-2.99	123.50	127.58
2	А	1201	JVJ	C23-C24-C30	2.94	123.44	117.59
2	А	1201	JVJ	C32-C6-C7	-2.90	116.01	120.61
2	А	1201	JVJ	C15-N16-C17	2.88	118.61	110.34
2	В	1201	JVJ	C6-C7-C20	-2.83	120.02	124.20
2	А	1201	JVJ	C30-C24-C25	-2.82	116.47	121.36
2	А	1201	JVJ	C30-C31-C21	-2.76	117.16	121.13
2	А	1201	JVJ	C4-C3-C33	2.73	122.45	118.17
2	В	1201	JVJ	C5-C4-C3	-2.70	117.31	121.03
2	В	1201	JVJ	C32-C6-C7	-2.45	116.72	120.61
2	В	1201	JVJ	C14-C13-C12	-2.42	105.22	111.28
2	А	1201	JVJ	C33-C32-C6	-2.21	117.95	121.13
2	А	1201	JVJ	C32-C33-C3	-2.01	118.26	121.03

There are no chirality outliers.

All (7) torsion outliers are listed below:

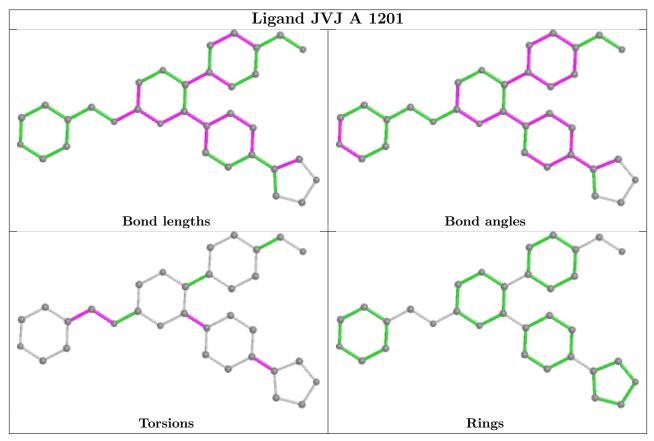
Mol	Chain	\mathbf{Res}	Type	Atoms
2	В	1201	JVJ	C13-C12-O11-C10
2	А	1201	JVJ	C13-C12-O11-C10
2	А	1201	JVJ	O11-C12-C13-C18
2	А	1201	JVJ	C30-C24-C25-C29
2	А	1201	JVJ	O11-C12-C13-C14
2	А	1201	JVJ	C7-C20-C21-C22
2	А	1201	JVJ	C7-C20-C21-C31



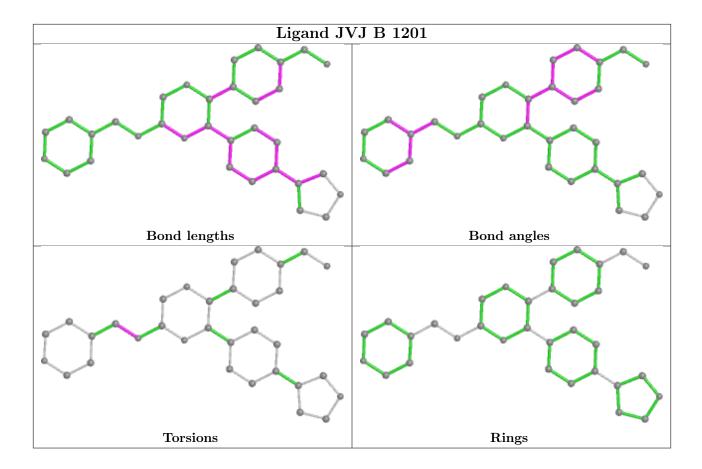
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

