

Full wwPDB X-ray Structure Validation Report (i)

Oct 2, 2023 – 02:39 AM EDT

PDB ID : 6MCS

Title : X-ray crystal structure of wild type HIV-1 protease in complex with GRL-003 Authors : Bulut, H.; Hayashi, H.; Hattori, S.I.; Aoki, M.; Das, D.; Ghosh, A.K.; Mitsuya,

Η.

Deposited on : 2018-09-02

Resolution : 1.52 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-RAY DIFFRACTION

The reported resolution of this entry is 1.52 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.



2 Entry composition (i)

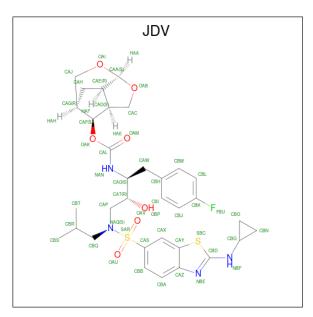
There are 3 unique types of molecules in this entry. The entry contains 1762 atoms, of which 882 are hydrogens and 0 are deuteriums.

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 Protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	99	Total 1628	C 511	H 841	N 134	O 138	S 4	0	6	0

• Molecule 2 is (3S,3aR,5R,7aS,8S)-hexahydro-4H-3,5-methanofuro[2,3-b]pyran-8-yl [(2S,3R)-4-[{[2-(cyclopropylamino)-1,3-benzothiazol-6-yl]sulfonyl}(2-methylpropyl)amino]-1-(4-fluorophenyl)-3-hydroxybutan-2-yl]carbamate (three-letter code: JDV) (formula: $C_{33}H_{41}FN_4O_7S_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf			
9	Λ	1	Total	С	F	Н	N	О	S	0	0
2	A	1	88	33	1	41	4	7	2	0	U

• Molecule 3 is water.

\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	46	Total O 46 46	0	0



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



3 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants	62.51Å 62.51Å 82.95Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.92 - 1.52	Depositor
% Data completeness	99.0 (32.92-1.52)	Depositor
(in resolution range)	,	-
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.15 (at 1.52Å)	Xtriage
Refinement program	PHENIX (1.13rc2_2981: ???)	Depositor
R, R_{free}	0.206 , 0.242	Depositor
Wilson B-factor (\mathring{A}^2)	21.7	Xtriage
Anisotropy	0.044	Xtriage
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1762	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.95% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



 $^{^1 {\}rm Intensities}$ 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)

1 ligand 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	Dec	Link	В	ond leng	${ m ths}$	Bond angles		
MIOI	туре		rtes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	JDV	A	101	-	49,53,53	3.00	19 (38%)	64,79,79	1.96	20 (31%)

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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	JDV	A	101	-	-	6/38/72/72	0/8/7/7

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(\AA)$	Ideal(Å)
2	A	101	JDV	OAV-SAR	-7.56	1.35	1.43
2	A	101	JDV	CBA-CAZ	-7.33	1.29	1.41
2	A	101	JDV	CAS-SAR	-7.03	1.66	1.76
2	A	101	JDV	OAU-SAR	6.98	1.51	1.43
2	A	101	JDV	CAW-CBH	-6.86	1.34	1.51
2	A	101	JDV	FBU-CBK	5.14	1.48	1.36
2	A	101	JDV	CAG-CAF	-4.79	1.46	1.53
2	A	101	JDV	SAR-NAQ	3.83	1.68	1.63
2	A	101	JDV	CAH-CAE	-3.66	1.43	1.53
2	A	101	JDV	CAX-CAY	-3.31	1.30	1.38
2	A	101	JDV	OAB-CAA	3.31	1.48	1.41
2	A	101	JDV	CBQ-NAQ	-3.21	1.42	1.47
2	A	101	JDV	OAK-CAF	-3.13	1.40	1.44
2	A	101	JDV	CBN-CBG	2.70	1.54	1.48
2	A	101	JDV	OBP-CAT	-2.64	1.37	1.43
2	A	101	JDV	CAP-CAT	2.32	1.55	1.52
2	A	101	JDV	CAP-NAQ	-2.17	1.44	1.47
2	A	101	JDV	OAM-CAL	-2.13	1.17	1.21
2	A	101	JDV	CAZ-NBE	-2.12	1.32	1.38

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
2	A	101	JDV	OAV-SAR-OAU	-4.70	111.91	119.52
2	A	101	JDV	CAF-OAK-CAL	4.12	123.16	117.11

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	101	JDV	CAO-NAN-CAL	4.05	129.96	122.37
2	A	101	JDV	CBQ-NAQ-SAR	-3.97	108.80	117.52
2	A	101	JDV	OAK-CAL-NAN	3.88	115.35	110.32
2	A	101	JDV	CBR-CBQ-NAQ	-3.80	108.01	112.41
2	A	101	JDV	CBH-CAW-CAO	-3.78	106.78	113.33
2	A	101	JDV	CBL-CBK-CBJ	-3.52	118.14	122.83
2	A	101	JDV	OAV-SAR-CAS	3.48	112.44	108.05
2	A	101	JDV	OAK-CAL-OAM	-3.05	119.94	124.53
2	A	101	JDV	CBI-CBJ-CBK	2.71	121.17	118.36
2	A	101	JDV	CAW-CAO-NAN	-2.53	106.39	110.07
2	A	101	JDV	CAC-OAB-CAA	2.49	110.19	106.86
2	A	101	JDV	CBO-CBG-NBF	-2.49	114.29	118.52
2	A	101	JDV	CAY-CAZ-NBE	2.47	113.78	108.04
2	A	101	JDV	CAZ-CAY-SBC	-2.39	108.68	111.85
2	A	101	JDV	CBS-CBR-CBQ	-2.14	102.18	111.02
2	A	101	JDV	CAX-CAY-SBC	2.09	129.28	125.10
2	A	101	JDV	CBN-CBO-CBG	2.02	61.53	59.84
2	A	101	JDV	FBU-CBK-CBL	2.01	121.96	118.54

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	${f Atoms}$
2	A	101	JDV	NAN-CAO-CAT-CAP
2	A	101	JDV	CBQ-NAQ-SAR-OAV
2	A	101	JDV	NAN-CAL-OAK-CAF
2	A	101	JDV	OAM-CAL-OAK-CAF
2	A	101	JDV	CBQ-NAQ-SAR-CAS
2	A	101	JDV	CAW-CAO-CAT-CAP

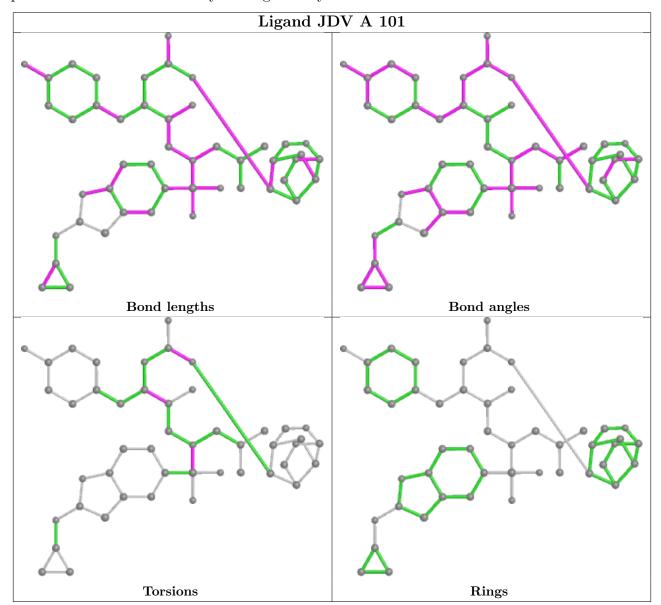
There are no ring outliers.

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.

