

Full wwPDB X-ray Structure Validation Report (i)

Oct 3, 2023 – 04:39 AM EDT

PDB ID	:	6OXX
Title	:	HIV-1 Protease NL4-3 WT in Complex with LR2-18
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Deposited on		
Resolution	:	1.96 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 1.96 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.



60XX

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3214 atoms, of which 1562 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.

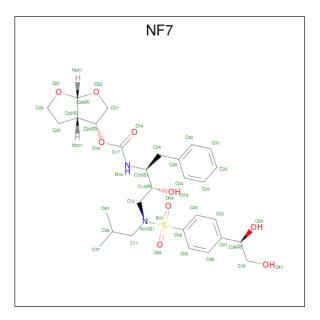
• Molecule 1 is a protein called Protease NL4-3.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	В	99	Total 1533	-			-		0	1	0
1	А	99	Total 1466	-	Н 736		-	${S \atop 4}$	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	7	LYS	GLN	engineered mutation	UNP Q8ULI9
А	7	LYS	GLN	engineered mutation	UNP Q8ULI9

• Molecule 2 is (3R,3aS,6aR)-hexahydrofuro[2,3-b]furan-3-yl $\{(2S,3R)-4-[(\{4-[(1R)-1,2-dihy droxyethyl]phenyl\}$ sulfonyl)(2-methylpropyl)amino]-3-hydroxy-1-phenylbutan-2-ylcarba mate (three-letter code: NF7) (formula: $C_{29}H_{40}N_2O_9S$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
2	А	1	Total 81	C 29	Н 40	N 2	0 9	S 1	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	66	Total O 66 66	0	0
3	А	68	Total O 68 68	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 21 21 21	Depositor	
Cell constants	50.99Å 57.91 Å 62.31 Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	27.43 - 1.96	Depositor	
% Data completeness	96.7 (27.43-1.96)	Depositor	
(in resolution range)		Depositor	
R _{merge}	(Not available)	Depositor	
R _{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$4.67 (at 1.96 \text{\AA})$	Xtriage	
Refinement program	PHENIX 1.12-2829	Depositor	
R, R_{free}	0.192 , 0.233	Depositor	
Wilson B-factor $(Å^2)$	20.6	Xtriage	
Anisotropy	0.236	Xtriage	
L-test for twinning ²	$ < L >=0.51, < L^2>=0.34$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	3214	wwPDB-VP	
Average B, all atoms $(Å^2)$	24.0	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 13.63% 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)

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	Res	Link	В	ond leng	gths	Bond angles			
	Chain			Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
2	NF7	А	101	-	43,44,44	<mark>5.34</mark>	28 (65%)	53,62,62	2.27	12 (22%)

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	NF7	А	101	-	-	3/42/61/61	0/4/4/4

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	101	NF7	C23-C20	-10.90	1.33	1.53
2	А	101	NF7	C05-C04	9.16	1.53	1.38
2	А	101	NF7	C02-C01	8.50	1.52	1.39
2	А	101	NF7	C03-C02	8.16	1.53	1.38
2	А	101	NF7	C34-C29	8.12	1.56	1.38
2	А	101	NF7	C06-C01	7.96	1.51	1.39
2	А	101	NF7	O27-C24	-7.43	1.26	1.41
2	А	101	NF7	C03-C04	7.34	1.50	1.38
2	А	101	NF7	C25-C26	-7.25	1.31	1.51
2	А	101	NF7	S07-N10	7.13	1.73	1.63
2	А	101	NF7	C06-C05	7.12	1.51	1.38
2	А	101	NF7	O27-C26	7.04	1.64	1.42
2	А	101	NF7	C30-C29	6.71	1.53	1.38
2	А	101	NF7	O22-C24	6.61	1.55	1.41
2	А	101	NF7	C17-N16	6.50	1.50	1.34
2	А	101	NF7	C31-C30	6.33	1.52	1.38
2	А	101	NF7	C32-C31	6.30	1.54	1.38
2	А	101	NF7	C33-C32	6.20	1.54	1.38
2	А	101	NF7	C21-C20	6.18	1.64	1.52
2	А	101	NF7	C33-C34	5.89	1.51	1.38
2	А	101	NF7	C04-S07	4.93	1.83	1.76
2	А	101	NF7	O22-C21	-4.44	1.34	1.43
2	А	101	NF7	C24-C23	3.90	1.58	1.52
2	А	101	NF7	O19-C17	3.48	1.41	1.35
2	А	101	NF7	O09-S07	3.17	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	101	NF7	O08-S07	3.11	1.47	1.43
2	А	101	NF7	C11-C36	2.38	1.59	1.52
2	А	101	NF7	O14-C13	-2.13	1.38	1.43

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All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	101	NF7	O09-S07-O08	-7.38	107.56	119.52
2	А	101	NF7	O08-S07-N10	7.25	113.30	106.69
2	А	101	NF7	O09-S07-N10	5.72	111.91	106.69
2	А	101	NF7	C04-S07-N10	-4.17	102.33	107.30
2	А	101	NF7	C06-C01-C02	4.09	123.39	118.29
2	А	101	NF7	O08-S07-C04	3.04	111.90	108.05
2	А	101	NF7	C03-C02-C01	-3.03	118.15	121.20
2	А	101	NF7	C05-C04-S07	-2.91	116.70	119.76
2	А	101	NF7	C05-C06-C01	-2.87	118.31	121.20
2	А	101	NF7	C26-C25-C23	2.51	106.84	103.32
2	А	101	NF7	C05-C04-C03	2.47	123.90	120.44
2	А	101	NF7	C29-C28-C15	-2.43	109.11	113.33

There are no chirality outliers.

All (3) torsion outliers are listed below:

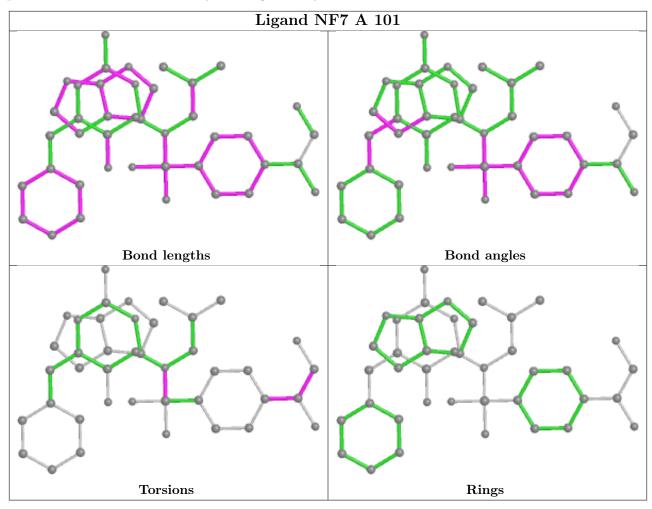
Mol	Chain	Res	Type	Atoms
2	А	101	NF7	C11-N10-S07-O09
2	А	101	NF7	O41-C35-C38-C01
2	А	101	NF7	C02-C01-C38-O39

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.

