

# wwPDB X-ray Structure Validation Summary Report (i)

#### Aug 2, 2023 - 08:23 PM EDT

PDB ID	:	1I3P
Title	:	THE 3.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF A MU-
		TATED BACULOVIRUS P35 AFTER CASPASE CLEAVAGE
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Deposited on		
Resolution	:	3.10 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 (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:

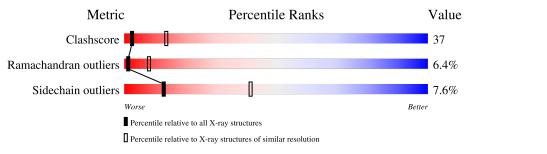
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
$\mathrm{EDS}$	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.10 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)

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	Qual	ity of chain	
1	А	298	45%	39%	7% • 8%



# 2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2077 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 EARLY 35 KDA PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	274	Total 2077	C 1339	N 335	0 394	S 9	0	0	0

There is a discrepancy between the modelled and reference sequences:

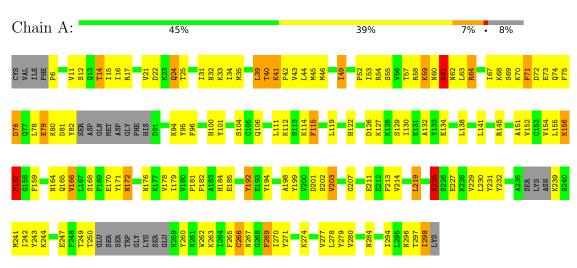
Chain	Residue	Modelled	Actual	Comment	Reference
А	71	PRO	VAL	engineered mutation	UNP P08160



# 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: EARLY 35 KDA PROTEIN



## 4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	75.81Å 75.81Å 120.69Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	14.95 - 3.10	Depositor
% Data completeness	99.0 (14.95-3.10)	Depositor
(in resolution range)	33.0 (14.35-3.10)	Depositor
$R_{merge}$	0.05	Depositor
R <sub>sym</sub>	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
$R, R_{free}$	0.239 , $0.291$	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2077	wwPDB-VP
Average B, all atoms $(Å^2)$	75.0	wwPDB-VP



# 5 Model quality (i)

## 5.1 Standard geometry (i)

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	Boi	nd lengths	Bond angles		
NIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.84	3/2117~(0.1%)	0.95	$4/2881 \ (0.1\%)$	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Ν	Лоl	Chain	#Chirality outliers	#Planarity outliers
	1	А	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	А	156	LYS	CE-NZ	6.55	1.65	1.49
1	А	266	CYS	CB-SG	-5.89	1.72	1.81
1	А	298	ILE	CG1-CD1	5.40	1.87	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	40	THR	N-CA-C	-8.81	87.22	111.00
1	А	39	LEU	N-CA-C	5.34	125.42	111.00
1	А	166	VAL	N-CA-C	-5.12	97.16	111.00
1	А	6	PRO	N-CA-CB	5.10	109.42	103.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	192	TYR	Sidechain
1	А	95	TYR	Sidechain



## 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	А	2077	0	1908	147	0
All	All	2077	0	1908	147	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 37.

The worst 5 of 147 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:298:ILE:CD1	1:A:298:ILE:CG1	1.87	1.52
1:A:31:ILE:HG12	1:A:166:VAL:HG22	1.37	1.05
1:A:74:GLN:HE22	1:A:239:LYS:NZ	1.55	1.04
1:A:57:THR:HG22	1:A:58:ARG:H	1.28	0.98
1:A:60:ASN:C	1:A:62:ASN:H	1.69	0.96

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	А	266/298~(89%)	212 (80%)	37 (14%)	17~(6%)	1 8

5 of 17 Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	А	41	LYS
1	А	61	ASN
1	А	33	LYS
1	А	59	LYS
1	А	225	ASN

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	211/280~(75%)	195~(92%)	16 (8%)	13 41

 $5~{\rm of}~16$  residues with a non-rotameric side chain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	244	LYS
1	А	225	ASN
1	А	157	PRO
1	А	219	LEU
1	А	155	LEU

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such side chains are listed below:

Mol	Chain	Res	Type
1	А	187	ASN
1	А	225	ASN
1	А	122	HIS
1	А	161	ASN
1	А	172	ASN

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

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

#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

There are no ligands in this entry.

#### 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 (i)

### 6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

