



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2023 – 12:54 PM EDT

PDB ID : 1LL6
Title : STRUCTURE OF THE D169N MUTANT OF C. IMMITIS CHITINASE 1
Authors : Bortone, K.; Monzingo, A.F.; Ernst, S.; Robertus, J.D.
Deposited on : 2002-04-26
Resolution : 2.80 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

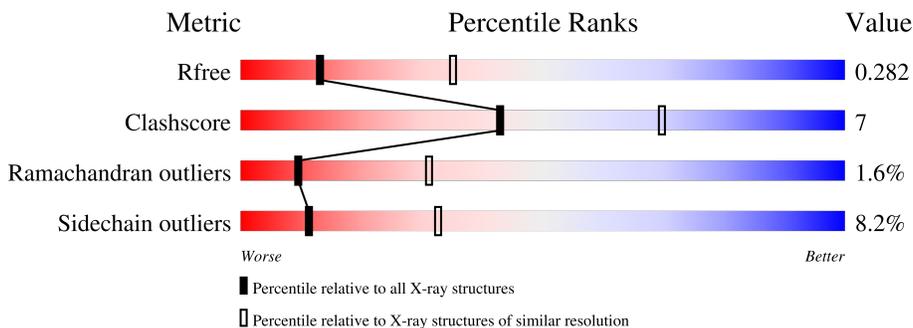
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	392	72% (green), 24% (yellow), 4% (orange), 0% (red), 0% (grey)
1	B	392	72% (green), 23% (yellow), 5% (orange), 0% (red), 0% (grey)
1	C	392	71% (green), 25% (yellow), 3% (orange), 1% (red), 0% (grey)
1	D	392	71% (green), 23% (yellow), 5% (orange), 0% (red), 0% (grey)

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12375 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 CHITINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	392	3083	1963	511	597	12	0	0	0
1	B	392	3083	1963	511	597	12	0	0	0
1	C	392	3083	1963	511	597	12	0	0	0
1	D	392	3083	1963	511	597	12	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	ASN	ASP	engineered mutation	UNP P54196
B	169	ASN	ASP	engineered mutation	UNP P54196
C	169	ASN	ASP	engineered mutation	UNP P54196
D	169	ASN	ASP	engineered mutation	UNP P54196

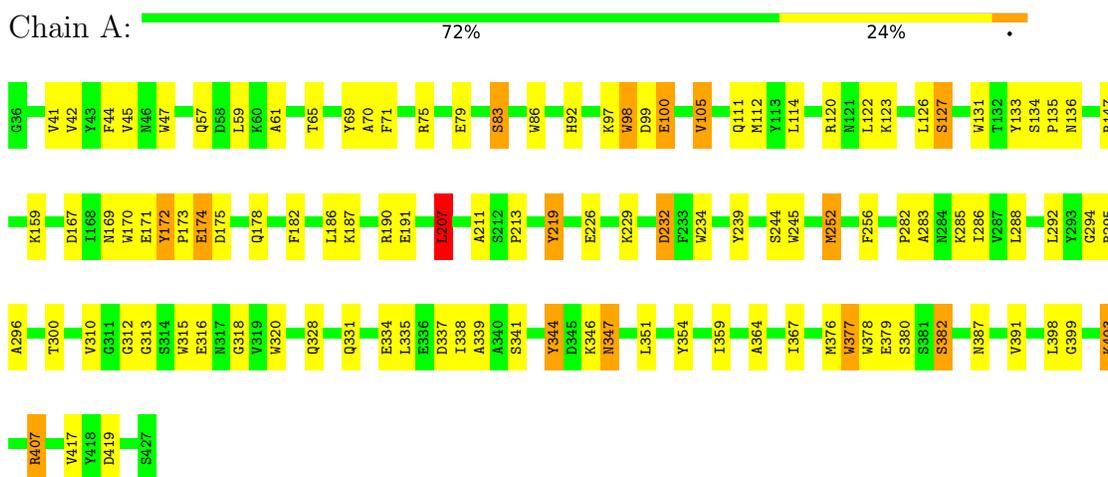
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	12	Total	O	0	0
			12	12		
2	B	12	Total	O	0	0
			12	12		
2	C	7	Total	O	0	0
			7	7		
2	D	12	Total	O	0	0
			12	12		

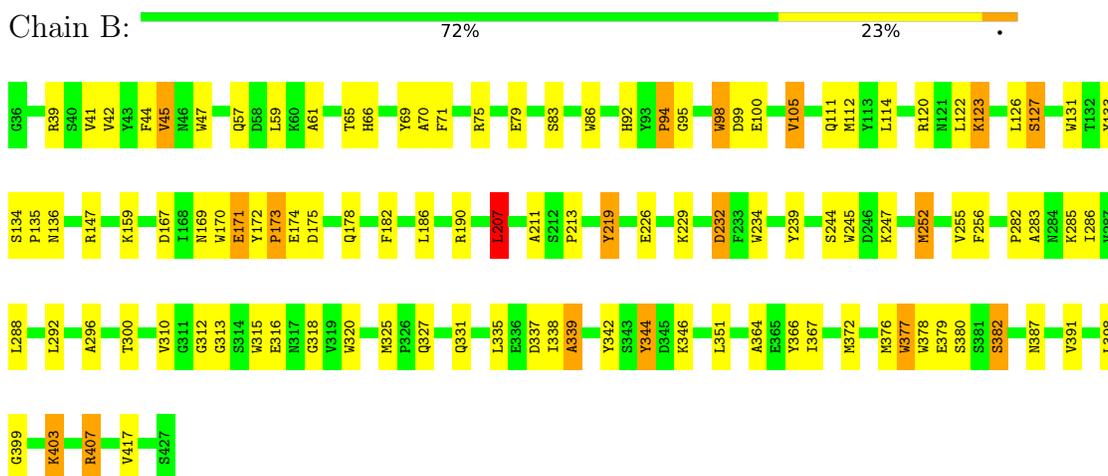
3 Residue-property plots [i](#)

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.

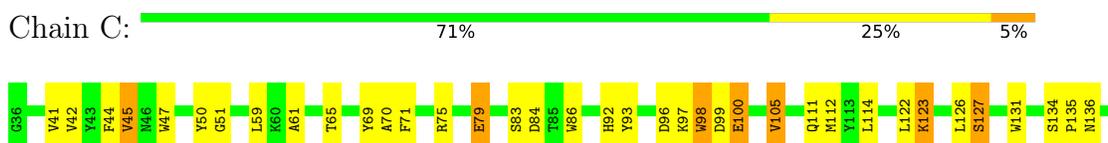
- Molecule 1: CHITINASE 1

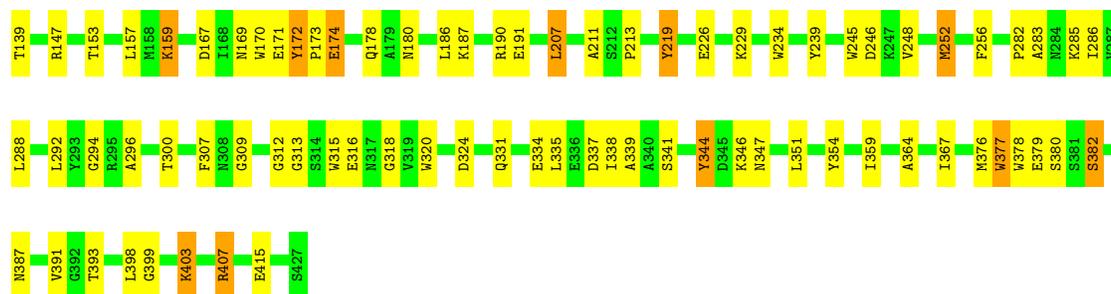


- Molecule 1: CHITINASE 1



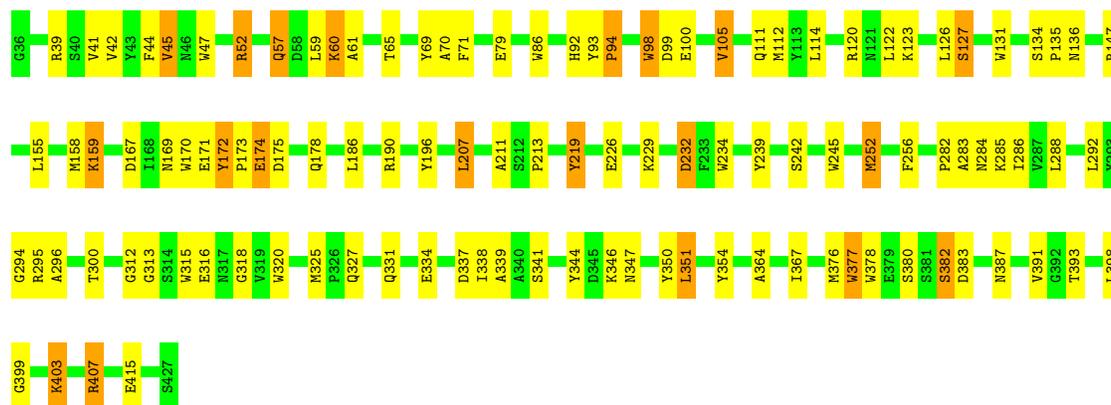
- Molecule 1: CHITINASE 1





- Molecule 1: CHITINASE 1

Chain D: 71% 23% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.89Å 78.18Å 88.43Å 80.51° 82.13° 66.99°	Depositor
Resolution (Å)	5.00 – 2.80 19.97 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (5.00-2.80) 89.5 (19.97-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.79Å)	Xtrriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.182 , 0.256 0.237 , 0.282	Depositor DCC
R_{free} test set	1609 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	15.6	Xtrriage
Anisotropy	0.072	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 55.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	12375	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.83	0/3165	1.53	52/4282 (1.2%)
1	B	0.84	0/3165	1.56	58/4282 (1.4%)
1	C	0.84	0/3165	1.56	61/4282 (1.4%)
1	D	0.85	1/3165 (0.0%)	1.53	54/4282 (1.3%)
All	All	0.84	1/12660 (0.0%)	1.55	225/17128 (1.3%)

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.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	378	TRP	CD1-NE1	-5.03	1.29	1.38

The worst 5 of 225 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	190	ARG	NE-CZ-NH1	11.28	125.94	120.30
1	B	407	ARG	NE-CZ-NH2	-10.96	114.82	120.30
1	A	407	ARG	NE-CZ-NH2	-10.87	114.87	120.30
1	C	407	ARG	NE-CZ-NH2	-10.56	115.02	120.30
1	B	252	MET	CG-SD-CE	-10.54	83.34	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	350	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	A	3083	0	2963	44	0
1	B	3083	0	2963	45	0
1	C	3083	0	2963	46	0
1	D	3083	0	2963	42	0
2	A	12	0	0	1	0
2	B	12	0	0	0	0
2	C	7	0	0	1	0
2	D	12	0	0	0	0
All	All	12375	0	11852	165	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 7.

The worst 5 of 165 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:B:95:GLY:H	1:C:51:GLY:HA2	1.33	0.92
1:A:347:ASN:HA	1:D:94:PRO:HG2	1.63	0.80
1:D:282:PRO:HG2	1:D:285:LYS:HD3	1.75	0.68
1:D:169:ASN:ND2	1:D:211:ALA:HB3	2.09	0.67
1:A:282:PRO:HG2	1:A:285:LYS:HD3	1.75	0.66

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	390/392 (100%)	367 (94%)	16 (4%)	7 (2%)	8	28
1	B	390/392 (100%)	369 (95%)	16 (4%)	5 (1%)	12	36
1	C	390/392 (100%)	368 (94%)	15 (4%)	7 (2%)	8	28
1	D	390/392 (100%)	367 (94%)	17 (4%)	6 (2%)	10	33
All	All	1560/1568 (100%)	1471 (94%)	64 (4%)	25 (2%)	9	31

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	ASP
1	B	99	ASP
1	C	99	ASP
1	D	99	ASP
1	A	83	SER

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	326/326 (100%)	299 (92%)	27 (8%)	11	32
1	B	326/326 (100%)	299 (92%)	27 (8%)	11	32
1	C	326/326 (100%)	300 (92%)	26 (8%)	12	34
1	D	326/326 (100%)	299 (92%)	27 (8%)	11	32
All	All	1304/1304 (100%)	1197 (92%)	107 (8%)	11	33

5 of 107 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	105	VAL
1	C	337	ASP
1	D	337	ASP

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Mol	Chain	Res	Type
1	C	126	LEU
1	C	207	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	327	GLN
1	D	169	ASN
1	D	347	ASN
1	D	327	GLN
1	B	111	GLN

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.