

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

#### Aug 26, 2023 - 07:23 PM EDT

PDB ID	:	3GIC
Title	:	Structure of thrombin mutant delta(146-149e) in the free form
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Deposited on		
Resolution	:	1.55  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:

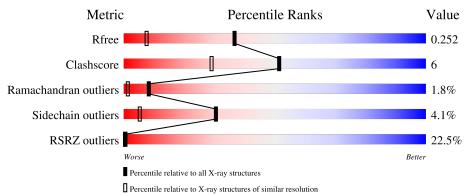
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.55 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain	
1	А	36	78%	22%
2	В	250	80%	16% ••



### 3GIC

## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2577 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 Thrombin light chain.

Mol	Chain	Residues		Atc	$\mathbf{ms}$			ZeroOcc	AltConf	Trace
1	А	28	Total 236	C 148	N 37	O 50	S 1	0	1	0

• Molecule 2 is a protein called Thrombin heavy chain.

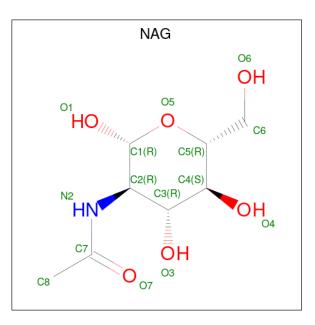
Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	248	Total 2070	C 1326	N 362	0 364	S 18	0	12	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	?	-	LYS	deletion	UNP P00734
В	?	-	GLU	deletion	UNP P00734
В	?	-	THR	deletion	UNP P00734
В	?	-	TRP	deletion	UNP P00734
В	?	-	THR	deletion	UNP P00734
В	?	-	ALA	deletion	UNP P00734
В	?	-	ASN	deletion	UNP P00734
В	?	-	VAL	deletion	UNP P00734
В	?	-	GLY	deletion	UNP P00734

• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	В	1	Total 14	C 8	N 1	O 5	0	0

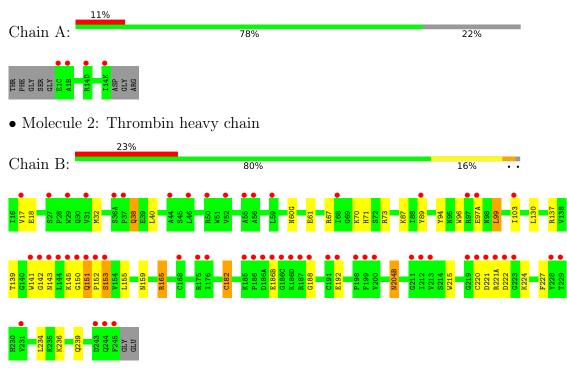
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	257	Total         O           257         257	0	0



# 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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: Thrombin light chain



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants	58.23Å $58.23$ Å $119.56$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	24.19 - 1.55	Depositor
Resolution (A)	24.19 - 1.55	EDS
% Data completeness	$94.3\ (24.19-1.55)$	Depositor
(in resolution range)	$94.3\ (24.19-1.55)$	EDS
R <sub>merge</sub>	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.22 (at 1.55 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
$R, R_{free}$	0.187 , $0.220$	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.229 , $0.252$	DCC
$R_{free}$ test set	2747 reflections $(5.07%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	19.7	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.41 , $54.7$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.055 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2577	wwPDB-VP
Average B, all atoms $(Å^2)$	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.01% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

## 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.63	0/242	0.68	0/322	
2	В	0.53	0/2151	0.70	1/2909~(0.0%)	
All	All	0.54	0/2393	0.70	1/3231~(0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^{o})$	$Ideal(^{o})$
2	В	165	ARG	NE-CZ-NH2	-5.75	117.42	120.30

There are no chirality outliers.

There are no planarity outliers.

## 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	236	0	233	0	0
2	В	2070	0	2058	26	0
3	В	14	0	13	1	0
4	В	257	0	0	1	0
All	All	2577	0	2304	26	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 6.



Atom-1	Atom-2	Interatomic	Clash
9.D.109[D].CVC.CC	2:B:227:PHE:CE2	$\frac{\text{distance (Å)}}{2.80}$	$\frac{\text{overlap (Å)}}{0.75}$
2:B:182[B]:CYS:SG 2:B:143:ASN:ND2			
	2:B:192[A]:GLU:O	2.25	0.69
2:B:137:ARG:HE	2:B:159:ASN:HD21	1.42	0.67
2:B:60(G):ASN:HD21	3:B:303:NAG:H2	1.62	0.64
2:B:151:GLN:HB3	2:B:152:PRO:CD	2.28	0.63
2:B:38:GLN:HE22	2:B:67:ARG:HH12	1.46	0.61
2:B:103:ILE:HG21	2:B:234[B]:LEU:HD23	1.87	0.54
2:B:151:GLN:HB3	2:B:152:PRO:HD3	1.88	0.53
2:B:139[B]:THR:OG1	2:B:155:LEU:HG	2.09	0.51
2:B:61:GLU:HG2	2:B:87:LYS:HA	1.92	0.51
2:B:32[B]:MET:HG2	2:B:141[B]:TRP:CZ3	2.46	0.50
2:B:99:LEU:HD23	2:B:215:TRP:HB2	1.94	0.49
2:B:87:LYS:HG2	2:B:89:TYR:CZ	2.49	0.48
2:B:18:GLU:HB2	2:B:188:GLY:HA2	1.96	0.47
2:B:71:HIS:HD2	4:B:307:HOH:O	1.99	0.46
2:B:32[B]:MET:HE2	2:B:40:LEU:HD13	1.97	0.46
2:B:17:VAL:HG13	2:B:220[A]:CYS:SG	2.57	0.45
2:B:221(A):ARG:HB3	2:B:224:LYS:HB2	1.99	0.45
2:B:32[A]:MET:HG3	2:B:141[A]:TRP:CZ3	2.54	0.43
2:B:96:TRP:HA	2:B:99:LEU:HD12	2.00	0.43
2:B:38:GLN:HE22	2:B:67:ARG:NH1	2.15	0.42
2:B:236:LYS:HD2	2:B:239:GLN:HE21	1.84	0.42
2:B:204(B):ASN:C	2:B:204(B):ASN:HD22	2.23	0.42
2:B:94:TYR:CZ	2:B:96:TRP:HB3	2.55	0.41
2:B:145:LYS:HG2	2:B:150:GLY:H	1.85	0.41
2:B:73:ARG:HB2	2:B:141[B]:TRP:CD1	2.56	0.41

All (26) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	Perce	ntiles
1	А	27/36~(75%)	26~(96%)	1 (4%)	0	100	100
2	В	258/250~(103%)	244~(95%)	9 (4%)	5 (2%)	8	1
All	All	285/286~(100%)	270~(95%)	10 (4%)	5 (2%)	8	1

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	222	ASP
2	В	153	SER
2	В	142	GLY
2	В	151	GLN
2	В	186(B)	GLU

#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	27/31~(87%)	27~(100%)	0	100 100		
2	В	228/218~(105%)	217~(95%)	11 (5%)	25 3		
All	All	255/249~(102%)	244 (96%)	11 (4%)	30 5		

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	38	GLN
2	В	70	LYS
2	В	97(A)	GLU
2	В	99	LEU
2	В	130	LEU
2	В	153	SER
2	В	165	ARG
2	В	182[A]	CYS
2	В	182[B]	CYS
2	В	204(B)	ASN
2	В	221	ASP



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	38	GLN
2	В	60(G)	ASN
2	В	62	ASN
2	В	71	HIS
2	В	156	GLN
2	В	159	ASN
2	В	204(B)	ASN
2	В	209	GLN
2	В	239	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)

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	Dog	Link	Bo	ond leng	ths	В	ond ang	les
WIOI	Type	Ullalli	nes		Counts   RMS2		# Z >2	Counts	RMSZ	# Z >2
3	NAG	В	303	-	$14,\!14,\!15$	0.53	0	17,19,21	0.76	0

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
3	NAG	В	303	-	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	303	NAG	O5-C5-C6-O6
3	В	303	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	303	NAG	1	0

## 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)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median,  $95^{th}$  percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	$\langle RSRZ \rangle$	#RSRZ>2		$OWAB(Å^2)$	Q < 0.9	
1	А	28/36~(77%)	0.59	4 (14%)	2	2	6, 12, 18, 22	0
2	В	248/250~(99%)	1.31	58 (23%)	0	0	3, 13, 22, 30	0
All	All	276/286~(96%)	1.24	62 (22%)	0	0	3, 13, 22, 30	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ	
2	В	144	144 LEU		
2	В	186(C) GLY		11.1	
2	В	152 PRO		10.6	
2	В	151 GLN		10.4	
2	В	150 GLY		9.2	
2	В	245	PHE	8.8	
2	В	143	ASN	8.8	
2	В	186	PRO	7.9	
2	В	145	LYS	7.8	
2	В	222	ASP	7.3	
2	В	187	ARG	7.0	
2	В	223	GLY	6.9	
2	В	186(A)	ASP	6.4	
2	В	186(D)	LYS	6.3	
1	А	1(B)	ALA	6.3	
2	В	219	GLY	5.8	
1	А	14(K)	ILE	5.8	
2	В	221	ASP	5.7	
2	В	221(A)	ARG	5.3	
2	В	186(B)	GLU	5.2	
2	В	244	GLN	5.1	
2	В	220[A]	20[A] CYS 4.		
2	В	191	CYS	4.5	
1	А	1(C)	GLU	4.4	

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Mol	Chain	Res	Type	RSRZ	
2	В	37 PRO		3.7	
2	В	175 ARG		3.7	
2	В	199 PHE		3.5	
2	В	153 SER		3.5	
2	В	212 ILE		3.4	
2	В	213 VAL		3.3	
2	В	185	LYS	3.2	
2	В	36(A)	SER	3.0	
2	В	168[A] CYS		2.8	
2	В	50 ARG		2.7	
2	В	200	VAL	2.7	
2	В	55	ALA	2.7	
2	В	56	ALA	2.7	
2	В	103	ILE	2.7	
2	В	68	ILE	2.6	
2	В	17	VAL	2.6	
2	В	59	59 LEU		
2	В	229	THR	2.6	
2	В	142	142 GLY		
2	В	29 TRP		2.5	
2	В	97(A) GLU		2.5	
2	В	228			
2	В	188	GLY	2.4	
2	В	243	ASP	2.4	
2	В	231	VAL	2.4	
2	В	44	ALA	2.3	
2	В	97	ARG	2.3	
2	В	176	ILE	2.3	
2	В	89	TYR	2.2	
2	В	52	VAL	2.2	
2	В	27[A]	SER	2.2	
2	В	46 LEU		2.2	
1	А	14(D)	ARG	2.2	
2	В	198	PRO	2.2	
2	В	31	VAL	2.1	
2	В	141[A]	TRP	2.1	
2	В	192[A]	GLU	2.1	
2	В	211	GLY	2.1	

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

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



## 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

## 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	В	303	14/15	0.39	0.35	$105,\!105,\!106,\!106$	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

