

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

#### Nov 7, 2023 – 06:21 AM EST

PDB ID	:	1C1V
Title	:	RECRUITING ZINC TO MEDIATE POTENT, SPECIFIC INHIBITION OF
		SERINE PROTEASES
Authors	:	Katz, B.A.; Luong, C.
Deposited on		
Resolution	:	1.98 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:

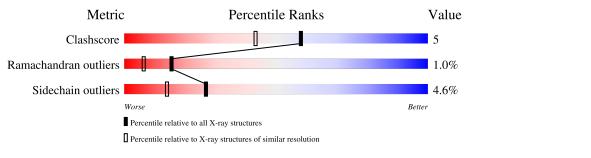
MolProbity : 4.02b-467	
Mogul : $1.8.5$ (274361), CSD as541be (2020)	
Xtriage (Phenix) : 1.13	
EDS : 2.36	
buster-report : $1.1.7$ (2018)	
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2	019)
Refmac : 5.8.0158	,
CCP4 : 7.0.044 (Gargrove)	
Ideal geometry (proteins) : Engh & Huber (2001)	
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)	
Validation Pipeline (wwPDB-VP) : 2.36	

# 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 1.98 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	Similar resolution
Metric	$(\# {\rm Entries})$	$(\# { m Entries},  { m resolution}  { m range}({ m \AA}))$
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)

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%

Mol	Chain	Length	Quality of chair	1	
1	L	36	61%	31%	6% •
2	Н	259	75%		19% ••••
3	Ι	11	64%	18%	18%



#### $1\mathrm{C1V}$

# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5639 atoms, of which 2918 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		A	Atoms	s			ZeroOcc	AltConf	Trace
1	т	36	Total	С	Η	Ν	Ο	$\mathbf{S}$	0	0	0
1	L	- 50	565	177	278	48	61	1	0	0	

• Molecule 2 is a protein called Thrombin heavy chain.

Mol	Chain	Residues			Atom	S			ZeroOcc	AltConf	Trace
2	Н	252	Total 4052	C 1299	Н 2013	N 360	O 366	S 14	0	0	0

• Molecule 3 is a protein called Hirudin-2.

Mol	Chain	Residues		I	Aton	ns			ZeroOcc	AltConf	Trace
3	Ι	11	Total 188	C 64	Н 84	N 12	O 27	S 1	0	0	0

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

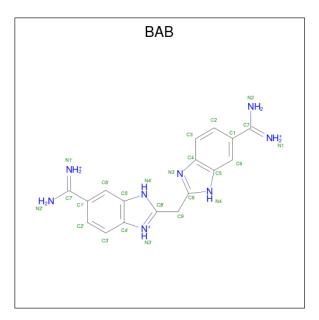
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Н	2	Total Zn 2 2	0	0

• Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Н	1	Total Na 1 1	0	0

• Molecule 6 is BIS (5-AMIDINO-BENZIMIDAZOLYL)METHANE (three-letter code: BAB) (formula:  $\rm C_{17}H_{19}N_8).$ 





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	Н	1	Total	C	H	N	0	0
			42	17	17	8		

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	35	Total H O 105 70 35	0	1
7	Н	216	Total H O 648 432 216	0	3
7	Ι	12	Total H O 36 24 12	0	1



# 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.

- Chain L:
   61%
   31%
   6%

   Molecule 2:
   Thrombin heavy chain

   Chain H:
   75%
   19%

   Molecule 2:
   Thrombin heavy chain

   Molecule 2:
   Thrombin heavy chain

   Molecule 3:
   Molecule 3:

   Molecule 3:
   Hirudin-2

   Chain I:
   64%
- $\bullet$  Molecule 1: Thrombin light chain



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	72.47Å 72.09Å 73.11Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $101.51^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	7.50 - 1.98	Depositor
Resolution (A)	35.82 - 1.50	EDS
% Data completeness	62.0 (7.50-1.98)	Depositor
(in resolution range)	37.7 (35.82 - 1.50)	EDS
R <sub>merge</sub>	0.09	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.95 (at 1.50 \text{\AA})$	Xtriage
Refinement program	X-PLOR 3.1	Depositor
D D.	0.204 , $0.248$	Depositor
$R, R_{free}$	0.217 , (Not available)	DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor $(Å^2)$	0.5	Xtriage
Anisotropy	4.058	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.19, 86.4	EDS
L-test for twinning <sup>2</sup>	$ L  > = 0.45, < L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.81	EDS
Total number of atoms	5639	wwPDB-VP
Average B, all atoms $(Å^2)$	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.60% 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: NA, ZN, TYS, BAB

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	
IVIOI	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	L	1.50	0/290	1.39	0/384
2	Н	1.41	6/2091~(0.3%)	1.71	50/2823~(1.8%)
3	Ι	1.54	0/88	1.30	0/115
All	All	1.43	6/2469~(0.2%)	1.66	50/3322~(1.5%)

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	L	0	2
2	Н	0	10
All	All	0	12

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Н	223	GLU	CB-CG	5.84	1.63	1.52
2	Н	213	TRP	CG-CD2	-5.55	1.34	1.43
2	Н	29	TRP	CG-CD2	-5.42	1.34	1.43
2	Н	96	TRP	CG-CD2	-5.20	1.34	1.43
2	Н	60(D)	TRP	CG-CD2	-5.03	1.35	1.43

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	Н	243	TRP	CD1-NE1-CE2	10.50	118.45	109.00
2	Н	60(D)	TRP	CD1-NE1-CE2	9.94	117.94	109.00
2	Н	141	TRP	CD1-NE1-CE2	9.85	117.86	109.00

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	Chain	1	1 0	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	Н	221	TRP	CD1-NE1-CE2	9.51	117.56	109.00
2	Н	60(D)	TRP	NE1-CE2-CZ2	9.02	140.32	130.40

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There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Н	35	ARG	Sidechain
2	Н	50	ARG	Sidechain
2	Н	75	ARG	Sidechain
1	L	15	ARG	Sidechain
1	L	4	ARG	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	L	287	278	278	9	1
2	Н	2039	2013	2010	15	2
3	Ι	104	84	81	2	0
4	Н	2	0	0	0	0
5	Н	1	0	0	0	0
6	Н	25	17	19	0	0
7	Н	216	432	0	0	3
7	Ι	12	24	0	0	0
7	L	35	70	0	0	0
All	All	2721	2918	2388	23	3

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 5.

The worst 5 of 23 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:L:1(D):GLY:HA3	1:L:1:CYS:SG	2.26	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:168:VAL:HB	2:H:187:CYS:SG	2.35	0.66
1:L:1(H):THR:HG23	2:H:48:SER:HB3	1.86	0.56
3:I:58:GLU:H	3:I:58:GLU:CD	2.10	0.55
2:H:31:VAL:CG1	2:H:66:VAL:HG13	2.38	0.53

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All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:179:ILE:O	7:H:443:HOH:H2[4_546]	1.52	0.08
1:L:1(E):SER:OG	7:H:500:HOH:H2[4_556]	1.54	0.06
2:H:177:THR:O	7:H:550:HOH:H1[4_546]	1.58	0.02

### 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	Percent	tiles
1	L	34/36~(94%)	21~(62%)	12 (35%)	1 (3%)	4	)
2	Н	248/259~(96%)	226 (91%)	22 (9%)	0	100	100
3	Ι	8/11 (73%)	4 (50%)	2(25%)	2(25%)	0 (	)
All	All	290/306~(95%)	251 (87%)	36 (12%)	3 (1%)	15	6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	1(B)	ALA
3	Ι	61	GLU
3	Ι	60	PRO



#### 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	L	31/31~(100%)	26~(84%)	5~(16%)	2 0
2	Н	220/225~(98%)	213~(97%)	7 (3%)	39 28
3	Ι	10/10 (100%)	10 (100%)	0	100 100
All	All	261/266~(98%)	249~(95%)	12~(5%)	27 14

 $5~{\rm of}~12$  residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
2	Н	94	TYR
2	Н	119	HIS
2	Н	247	VAL
2	Н	159	VAL
1	L	14(D)	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	Н	78	ASN
2	Н	131	GLN
2	Н	161	GLN
2	Н	210(B)	ASN
3	Ι	65	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)

1 non-standard protein/DNA/RNA residue 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	B	ond ang	les
IVIOI	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	TYS	Ι	63	3	15,16,17	1.37	2 (13%)	18,22,24	1.22	3 (16%)

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	TYS	Ι	63	3	-	0/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Ι	63	TYS	OH-S	3.91	1.64	1.58
3	Ι	63	TYS	OH-CZ	-2.59	1.38	1.42

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	Ι	63	TYS	CG-CB-CA	-2.66	108.71	114.10
3	Ι	63	TYS	O3-S-OH	2.24	111.23	105.83
3	Ι	63	TYS	OH-S-O1	2.06	113.70	107.71

All (3) bond angle outliers are listed below:

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



## 5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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	B	ond leng	gths	B	ond ang	les
IVI01	Type	Ullalli	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	BAB	Н	410	4	24,28,28	2.88	13 (54%)	22,41,41	1.86	6 (27%)

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
6	BAB	Н	410	4	-	1/12/12/12	0/4/4/4

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	Η	410	BAB	C9-C8	6.90	1.60	1.50
6	Н	410	BAB	C1-C7	-5.38	1.37	1.47
6	Н	410	BAB	C1'-C7'	-4.00	1.40	1.47
6	Н	410	BAB	C6-C5	-3.98	1.35	1.41
6	Н	410	BAB	C6'-C1'	3.62	1.43	1.37

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
6	Н	410	BAB	C2'-C3'-C4'	-3.91	115.92	120.84
6	Н	410	BAB	C2-C3-C4	-3.34	116.63	120.84
6	Н	410	BAB	C9-C8'-N4'	3.33	131.86	122.54
6	Н	410	BAB	N3-C8-N4	-2.26	108.99	115.89
6	Н	410	BAB	C6-C1-C7	-2.23	116.53	120.29

There are no chirality outliers.

All (1) torsion outliers are listed below:



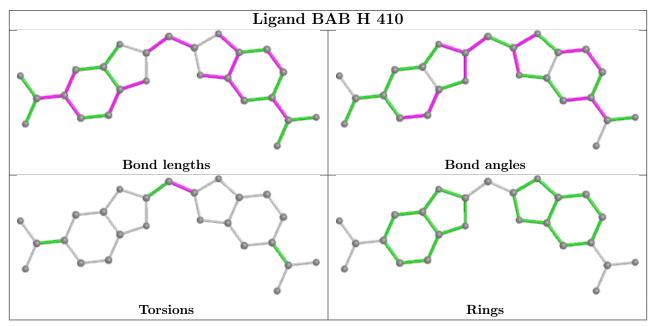
1	C1	V
т	U1	v

	Mol	Chain	Res	Type	Atoms
ſ	6	Н	410	BAB	N4-C8-C9-C8'

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.



#### 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)

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

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

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

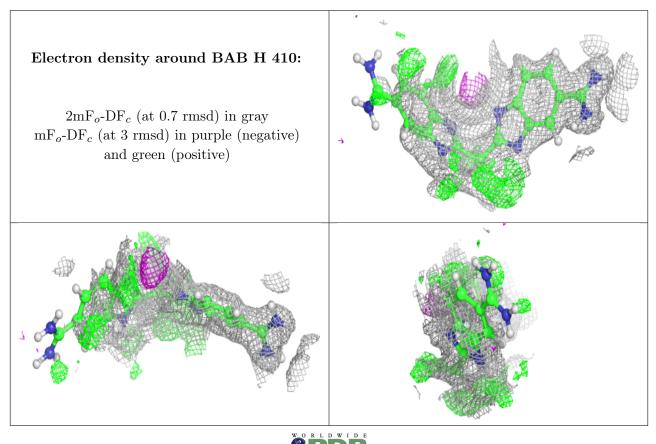
### 6.3 Carbohydrates (i)

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

## 6.4 Ligands (i)

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

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers (i)

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

