

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

#### Sep 11, 2023 – 02:32 AM EDT

PDB ID : 4J2Y

Title: Crystal structure of a plant trypsin inhibitor EcTI in complex with bovine

trypsin.

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Deposited on : 2013-02-05

Resolution : 2.00 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:

Mol Probity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

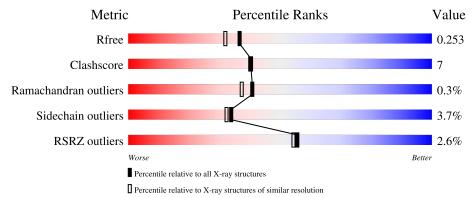
Validation Pipeline (wwPDB-VP) : 2.35.1

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	A	176	73% 18	% • 6%
2	В	223	83%	17%



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3095 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 Trypsin inhibitor.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	165	Total 1313	C 837	N 228	O 244	S 4	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

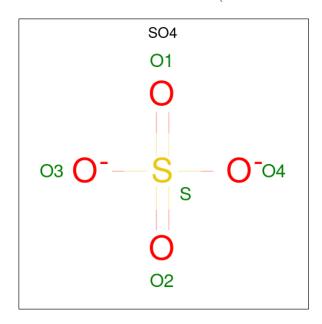
Chain	Residue	Modelled	Actual	Comment	Reference
A	49	SER	GLY	conflict	UNP P86451
A	81	ARG	LYS	conflict	UNP P86451
A	88	GLU	ARG	conflict	UNP P86451
A	95	TRP	ARG	conflict	UNP P86451
A	96	LYS	GLU	conflict	UNP P86451
A	97	VAL	GLU	conflict	UNP P86451
A	99	GLY	GLN	conflict	UNP P86451
A	100	GLU	HIS	conflict	UNP P86451
A	102	GLN	-	insertion	UNP P86451
A	106	ILE	LEU	conflict	UNP P86451
A	112	GLU	ALA	conflict	UNP P86451
A	113	GLN	ALA	conflict	UNP P86451
A	114	HIS	ALA	conflict	UNP P86451
A	115	LEU	-	insertion	UNP P86451
A	118	SER	UNK	conflict	UNP P86451
A	119	PHE	GLU	conflict	UNP P86451
A	121	ILE	LEU	conflict	UNP P86451
A	130	LEU	ILE	conflict	UNP P86451
A	136	ASN	GLY	conflict	UNP P86451
A	156	LEU	ARG	conflict	UNP P86451

• Molecule 2 is a protein called Cationic trypsin.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	223	Total	С	N	0	S	0	1	0
	_		1630	1012	279	324	15	Ü	_	)



 $\bullet$  Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	A	1	Total 5	O 4	S 1	0	0

• Molecule 4 is water.

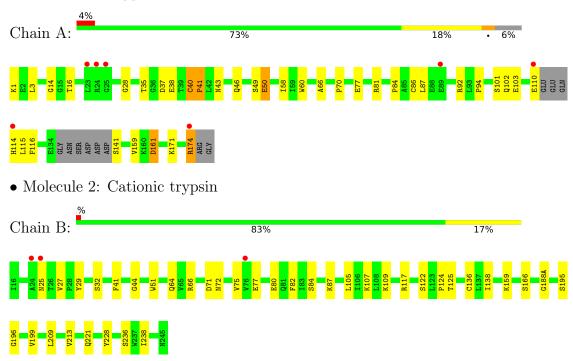
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	65	Total O 65 65	0	0
4	В	82	Total O 82 82	0	0



# 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: Trypsin inhibitor





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	73.26Å 38.58Å 122.82Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 104.19° 90.00°	Depositor
Resolution (Å)	19.84 - 2.00	Depositor
Resolution (A)	19.84 - 2.00	EDS
% Data completeness	92.2 (19.84-2.00)	Depositor
(in resolution range)	92.2 (19.84-2.00)	EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.72 (at 2.01Å)	Xtriage
Refinement program	PHENIX 1.7.3_928	Depositor
D D	0.196 , 0.258	Depositor
$R, R_{free}$	0.193 , $0.253$	DCC
$R_{free}$ test set	844 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.5	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 56.4	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3095	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.41% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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: SO4

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
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.49	0/1339	0.62	0/1808
2	В	0.40	0/1666	0.56	0/2258
All	All	0.44	0/3005	0.59	0/4066

There are no bond length outliers.

There are no bond angle outliers.

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	A	1313	0	1326	22	1
2	В	1630	0	1588	22	0
3	A	5	0	0	0	0
4	A	65	0	0	3	0
4	В	82	0	0	1	0
All	All	3095	0	2914	42	1

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.

All (42) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:84:PRO:HG2	1:A:87:LEU:HD23	1.73	0.70
2:B:77:GLU:HB2	2:B:80:GLU:HG3	1.74	0.68
1:A:16:THR:HG22	1:A:58:ILE:HG12	1.76	0.68
1:A:101:SER:HB3	1:A:103:GLU:HG3	1.79	0.64
1:A:114:HIS:HD2	1:A:115:LEU:N	1.95	0.63
1:A:171:LYS:HD2	1:A:174:ARG:HD3	1.86	0.58
2:B:51:TRP:CE2	2:B:107:LYS:HD3	2.40	0.57
2:B:32:SER:HB3	2:B:66:ARG:HB2	1.86	0.57
1:A:102:GLN:HB3	1:A:159:VAL:HB	1.86	0.57
1:A:77:GLU:HB3	1:A:94:PRO:HA	1.88	0.55
1:A:114:HIS:CD2	1:A:115:LEU:N	2.75	0.55
1:A:114:HIS:CD2	1:A:116:PHE:H	2.26	0.54
2:B:27:VAL:HG13	2:B:29:TYR:CZ	2.44	0.53
2:B:51:TRP:CZ2	2:B:107:LYS:HD3	2.47	0.50
2:B:213:VAL:HA	2:B:228:TYR:CD2	2.47	0.50
2:B:87:LYS:HB2	2:B:107:LYS:HB3	1.94	0.49
2:B:51:TRP:CH2	2:B:107:LYS:HB2	2.48	0.49
2:B:188(A):GLY:O	4:B:370:HOH:O	2.20	0.48
1:A:141:SER:N	4:A:334:HOH:O	2.46	0.48
1:A:3:LEU:HG	1:A:70:PRO:HD3	1.96	0.48
1:A:92:ARG:NH1	2:B:221:GLN:OE1	2.48	0.47
2:B:136:CYS:O	2:B:159:LYS:HA	2.15	0.47
2:B:84:SER:HB2	2:B:109:LYS:HD3	1.96	0.47
2:B:77:GLU:O	2:B:80:GLU:HB2	2.16	0.46
2:B:71:ASP:HB2	2:B:117:ARG:HH21	1.79	0.46
1:A:86:CYS:HB2	1:A:87:LEU:HD22	1.97	0.46
2:B:64:GLN:HE22	2:B:82:PHE:HD2	1.65	0.45
1:A:14:GLY:HA2	1:A:60:TRP:HB3	1.98	0.45
1:A:37:ASP:OD1	4:A:322:HOH:O	2.20	0.45
1:A:66:ALA:HB3	2:B:41:PHE:HA	1.99	0.44
2:B:72:ASN:HB3	2:B:75:VAL:HB	2.00	0.44
2:B:138:ILE:HG12	2:B:199:VAL:HG13	2.00	0.43
1:A:35:THR:O	1:A:38:GLU:HG2	2.20	0.42
1:A:102:GLN:HB2	4:A:329:HOH:O	2.18	0.42
2:B:25:ASN:HB3	2:B:117:ARG:HD2	2.01	0.42
1:A:50:GLU:H	1:A:50:GLU:HG2	1.64	0.42
2:B:44:GLY:HA2	2:B:196:GLY:O	2.20	0.42
1:A:40:CYS:HA	1:A:41:PRO:HD3	1.87	0.41
2:B:105:LEU:HD11	2:B:238:ILE:HA	2.02	0.41
1:A:28:GLY:O	1:A:46:GLN:HG3	2.21	0.41
1:A:35:THR:OG1	1:A:43:ASN:OD1	2.29	0.40
2:B:124:PRO:HD3	2:B:209:LEU:O	2.21	0.40



All (1) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:81:ARG:NH2	1:A:161:ASP:OD2[1_565]	2.18	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	Perce	entiles
1	A	$159/176\ (90\%)$	149 (94%)	9 (6%)	1 (1%)	25	19
2	В	$222/223 \ (100\%)$	216 (97%)	6 (3%)	0	100	100
All	All	381/399~(96%)	365 (96%)	15 (4%)	1 (0%)	41	37

#### All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	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	A	142/151 (94%)	135 (95%)	7 (5%)	25 21		
2	В	185/184 (100%)	180 (97%)	5 (3%)	44 46		
All	All	327/335 (98%)	315 (96%)	12 (4%)	34 32		



All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	LYS
1	A	40	CYS
1	A	49	SER
1	A	50	GLU
1	A	110	GLU
1	A	161	ASP
1	A	174	ARG
2	В	122	SER
2	В	125	THR
2	В	166	SER
2	В	195	SER
2	В	236	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	HIS

#### 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	Res	Link	В	ond leng	${ m gths}$	В	ond ang	gles
MIOI	туре	Chain	n res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2	
	3	SO4	A	201	-	4,4,4	0.22	0	6,6,6	0.36	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	165/176~(93%)	-0.07	7 (4%) 36 35	19, 31, 72, 85	0
2	В	223/223 (100%)	-0.23	3 (1%) 77 76	18, 33, 55, 81	0
All	All	388/399 (97%)	-0.16	10 (2%) 56 54	18, 32, 62, 85	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	GLY	4.7
1	A	174	ARG	4.6
1	A	114	HIS	4.1
2	В	25	ASN	3.1
1	A	23	LEU	2.9
2	В	76	VAL	2.7
1	A	110	GLU	2.4
1	A	24	ARG	2.4
2	В	24	ALA	2.3
1	A	89	GLU	2.1

## 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	SO4	A	201	5/5	0.99	0.07	21,22,27,30	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

