



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 26, 2017 – 08:35 PM EDT

PDB ID : 4AN7
Title : Kunitz type trypsin inhibitor complex with porcine trypsin
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Deposited on : 2012-03-15
Resolution : 2.23 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029077

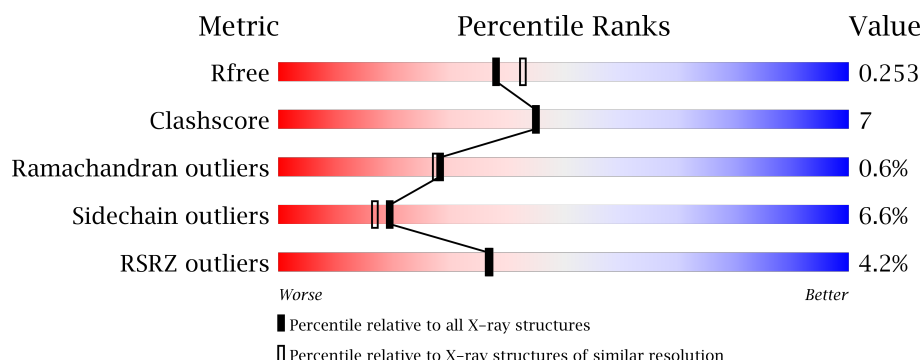
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.23 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}	100719	1804 (2.26-2.22)
Clashscore	112137	1957 (2.26-2.22)
Ramachandran outliers	110173	1916 (2.26-2.22)
Sidechain outliers	110143	1917 (2.26-2.22)
RSRZ outliers	101464	1809 (2.26-2.22)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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	231	
2	B	185	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3020 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1642	1020	287	321	14			

- Molecule 2 is a protein called TRYPSIN INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	156	Total	C	N	O	S	0	0	0
			1222	782	210	226	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	53	ILE	LEU	conflict	UNP F4ZZG4
B	153	ASN	ASP	conflict	UNP F4ZZG4

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

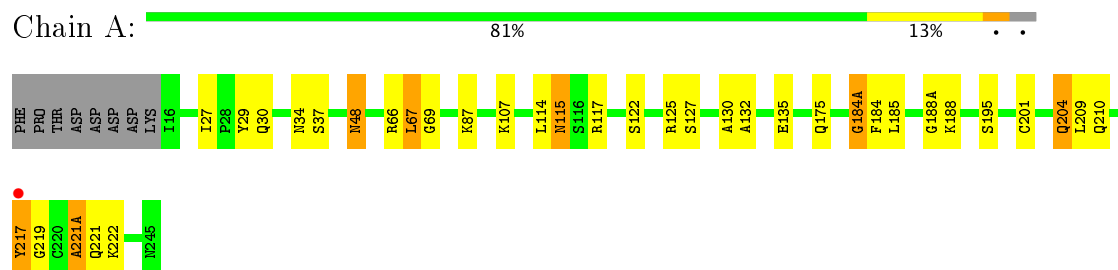
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	121	Total	O	0	0
			121	121		
4	B	34	Total	O	0	0
			34	34		

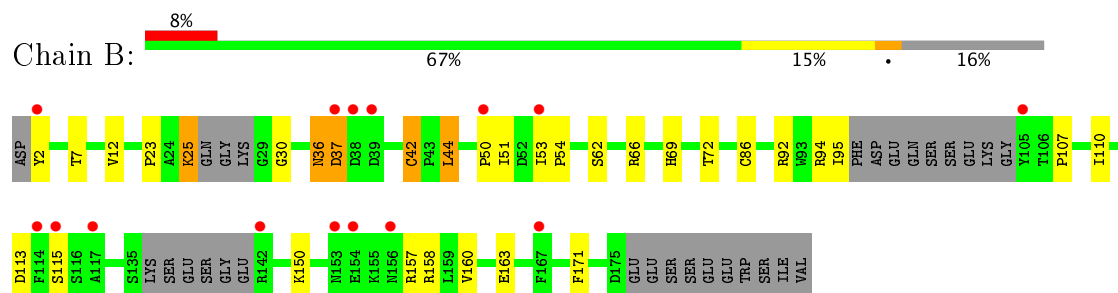
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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



• Molecule 2: TRYPSIN INHIBITOR



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	61.08Å 67.12Å 91.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.22 – 2.23 45.18 – 2.23	Depositor EDS
% Data completeness (in resolution range)	93.8 (45.22-2.23) 93.8 (45.18-2.23)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.22Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.200 , 0.246 0.203 , 0.253	Depositor DCC
R_{free} test set	911 reflections (5.40%)	DCC
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3020	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% 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](#)

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

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	1.35	6/1671 (0.4%)	0.77	3/2264 (0.1%)
2	B	0.44	0/1247	0.69	0/1685
All	All	1.06	6/2918 (0.2%)	0.74	3/3949 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	217	TYR	C-N	27.32	1.82	1.33
1	A	204	GLN	C-N	21.98	1.84	1.34
1	A	184(A)	GLY	C-N	21.68	1.83	1.34
1	A	67	LEU	C-N	21.29	1.71	1.33
1	A	221(A)	ALA	C-N	16.78	1.72	1.34
1	A	34	ASN	C-N	11.51	1.60	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	GLN	O-C-N	-12.90	102.05	122.70
1	A	204	GLN	CA-C-N	-5.67	104.73	117.20
1	A	67	LEU	C-N-CA	-5.50	110.76	122.30

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	A	1642	0	1587	27	1
2	B	1222	0	1235	16	0
3	A	1	0	0	0	0
4	A	121	0	0	0	0
4	B	34	0	0	0	0
All	All	3020	0	2822	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.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:LEU:C	1:A:69:GLY:N	1.71	1.44
1:A:221(A):ALA:C	1:A:221:GLN:N	1.72	1.41
1:A:217:TYR:C	1:A:219:GLY:N	1.82	1.32
1:A:184(A):GLY:C	1:A:184:PHE:N	1.83	1.32
1:A:204:GLN:C	1:A:209:LEU:N	1.84	1.31
1:A:125:ARG:C	1:A:127:SER:N	2.01	1.13
1:A:130:ALA:C	1:A:132:ALA:N	2.04	1.10
1:A:188(A):GLY:C	1:A:188:LYS:N	2.21	0.93
1:A:188(A):GLY:O	1:A:188:LYS:N	2.12	0.83
1:A:125:ARG:H	1:A:204:GLN:HE21	1.39	0.70
1:A:67:LEU:C	1:A:69:GLY:CA	2.60	0.70
2:B:42:CYS:HB3	2:B:44:LEU:HD13	1.77	0.65
1:A:48:ASN:C	1:A:48:ASN:HD22	2.01	0.64
1:A:125:ARG:O	1:A:127:SER:N	2.34	0.60
2:B:107:PRO:HA	2:B:160:VAL:HG12	1.82	0.60
1:A:204:GLN:CA	1:A:209:LEU:N	2.67	0.55
2:B:150:LYS:HE3	2:B:160:VAL:HG11	1.87	0.55
2:B:25:LYS:HE2	2:B:25:LYS:N	2.22	0.54
1:A:217:TYR:C	1:A:219:GLY:CA	2.75	0.53
1:A:188(A):GLY:CA	1:A:188:LYS:N	2.72	0.52
1:A:87:LYS:HB2	1:A:107:LYS:HB3	1.93	0.51
1:A:130:ALA:C	1:A:132:ALA:CA	2.78	0.51
2:B:37:ASP:OD2	2:B:158:ARG:NH1	2.45	0.50
1:A:115:ASN:HD22	1:A:117:ARG:H	1.60	0.48
1:A:195:SER:OG	2:B:66:ARG:C	2.52	0.48
1:A:184(A):GLY:CA	1:A:184:PHE:N	2.72	0.48
2:B:53:ILE:HG23	2:B:54:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:PRO:CA	2:B:160:VAL:HG12	2.45	0.46
2:B:2:TYR:N	2:B:72:THR:HG1	2.14	0.45
1:A:67:LEU:CA	1:A:69:GLY:N	2.71	0.45
2:B:7:THR:HG23	2:B:171:PHE:O	2.17	0.45
1:A:204:GLN:O	1:A:209:LEU:N	2.42	0.45
2:B:92:ARG:O	2:B:110:ILE:HA	2.17	0.44
1:A:27:ILE:HG23	1:A:29:TYR:CZ	2.53	0.44
1:A:175:GLN:NE2	1:A:217:TYR:OH	2.49	0.44
1:A:184:PHE:CD1	1:A:188:LYS:HB2	2.52	0.44
2:B:95:ILE:C	2:B:95:ILE:HD12	2.38	0.43
2:B:36:ASN:HD22	2:B:36:ASN:C	2.24	0.41
2:B:12:VAL:O	2:B:69:HIS:HB2	2.21	0.41
1:A:115:ASN:ND2	1:A:117:ARG:H	2.18	0.41
2:B:23:PRO:HD3	2:B:30:GLY:O	2.22	0.40
2:B:50:PRO:HG2	2:B:51:ILE:HG23	2.03	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	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:GLU:CD	1:A:135:GLU:OE2[2_554]	2.07	0.13

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	215/231 (93%)	208 (97%)	7 (3%)	0	100	100
2	B	148/185 (80%)	139 (94%)	7 (5%)	2 (1%)	13	8
All	All	363/416 (87%)	347 (96%)	14 (4%)	2 (1%)	28	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	115	SER
2	B	113	ASP

5.3.2 Protein sidechains ⓘ

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	183/191 (96%)	172 (94%)	11 (6%)	22	20
2	B	136/162 (84%)	126 (93%)	10 (7%)	16	12
All	All	319/353 (90%)	298 (93%)	21 (7%)	19	17

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	37	SER
1	A	48	ASN
1	A	66	ARG
1	A	114	LEU
1	A	115	ASN
1	A	122	SER
1	A	185	LEU
1	A	201	CYS
1	A	210	GLN
1	A	222	LYS
2	B	25	LYS
2	B	36	ASN
2	B	37	ASP
2	B	42	CYS
2	B	44	LEU
2	B	62	SER
2	B	86	CYS
2	B	94	ARG
2	B	157	ARG
2	B	163	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	48	ASN
1	A	84	ASN
1	A	93	ASN
1	A	101	ASN
1	A	115	ASN
1	A	204	GLN
1	A	210	GLN
1	A	236	ASN
1	A	239	GLN
2	B	36	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	9

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	188(A):GLY	C	188:LYS	N	2.21
1	A	130:ALA	C	132:ALA	N	2.04
1	A	125:ARG	C	127:SER	N	2.01
1	A	204:GLN	C	209:LEU	N	1.84
1	A	184(A):GLY	C	184:PHE	N	1.83
1	A	217:TYR	C	219:GLY	N	1.82
1	A	221(A):ALA	C	221:GLN	N	1.72
1	A	67:LEU	C	69:GLY	N	1.71
1	A	34:ASN	C	37:SER	N	1.60

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	223/231 (96%)	-0.23	1 (0%) 92 93	26, 35, 47, 60	0
2	B	156/185 (84%)	0.35	15 (9%) 9 8	30, 55, 83, 104	0
All	All	379/416 (91%)	0.01	16 (4%) 37 37	26, 39, 77, 104	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	115	SER	4.3
2	B	114	PHE	4.3
2	B	154	GLU	3.7
2	B	38	ASP	3.4
2	B	117	ALA	3.2
2	B	105	TYR	3.1
2	B	2	TYR	3.0
2	B	39	ASP	3.0
2	B	37	ASP	2.9
2	B	153	ASN	2.7
2	B	142	ARG	2.6
1	A	217	TYR	2.6
2	B	50	PRO	2.5
2	B	167	PHE	2.3
2	B	156	ASN	2.1
2	B	53	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(\AA^2)	Q<0.9
3	CA	A	1246	1/1	0.99	0.12	-0.63	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.