



# wwPDB X-ray Structure Validation Summary Report i

Mar 1, 2014 – 03:29 AM GMT

PDB ID : 2ANT  
Title : THE 2.6 Å STRUCTURE OF ANTITHROMBIN INDICATES A CONFORMATIONAL CHANGE AT THE HEPARIN BINDING SITE  
Authors : Skinner, R.; Abrahams, J.-P.; Whisstock, J.C.; Lesk, A.M.; Carrell, R.W.; Wardell, M.R.  
Deposited on : 1997-01-28  
Resolution : 2.60 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683



## 2 Entry composition (i)

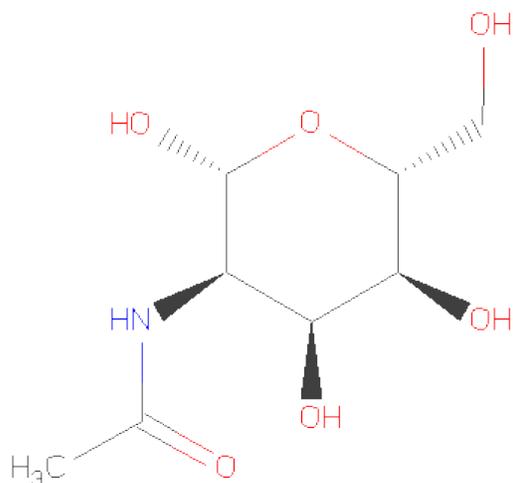
There are 3 unique types of molecules in this entry. The entry contains 6636 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ANTITHROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	398	Total 3181	C 2029	N 534	O 600	S 18	0	0	0
1	I	419	Total 3348	C 2133	N 568	O 629	S 18	0	0	0

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAA) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	L	1	Total 14	C 8	N 1	O 5	1	0
2	I	1	Total 14	C 8	N 1	O 5	1	0

- Molecule 3 is water.

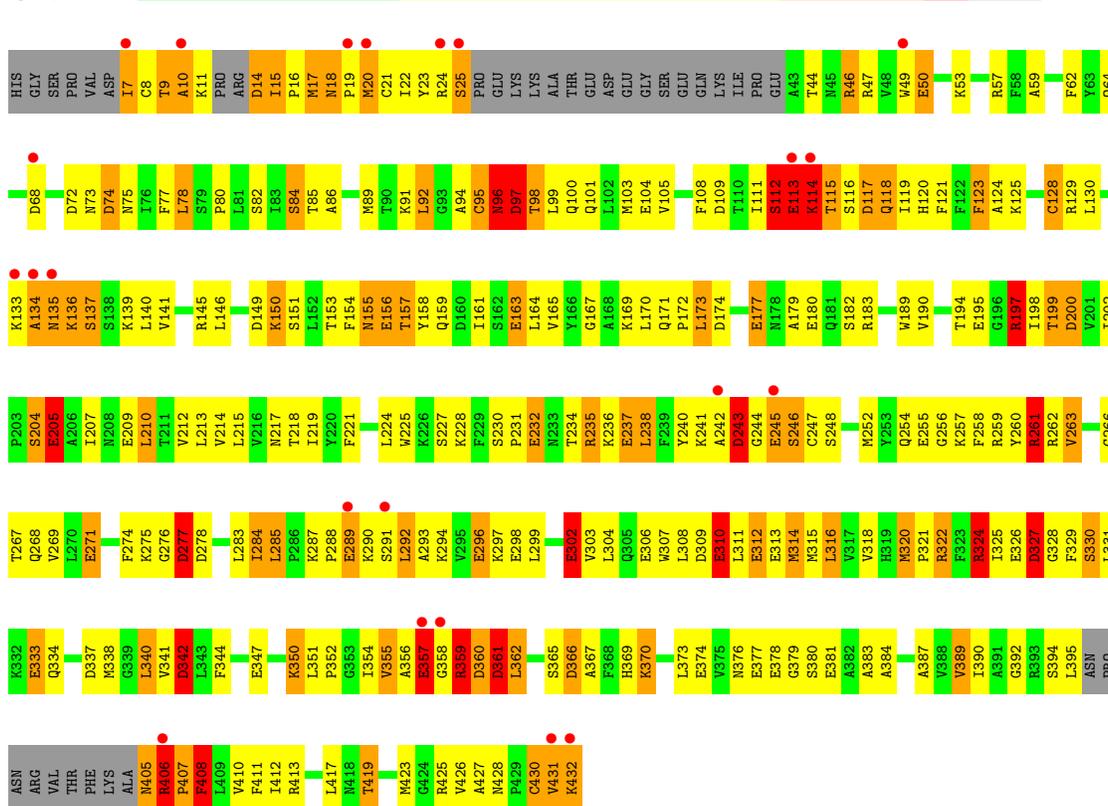
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	I	42	Total O 42 42	0	0
3	L	37	Total O 37 37	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

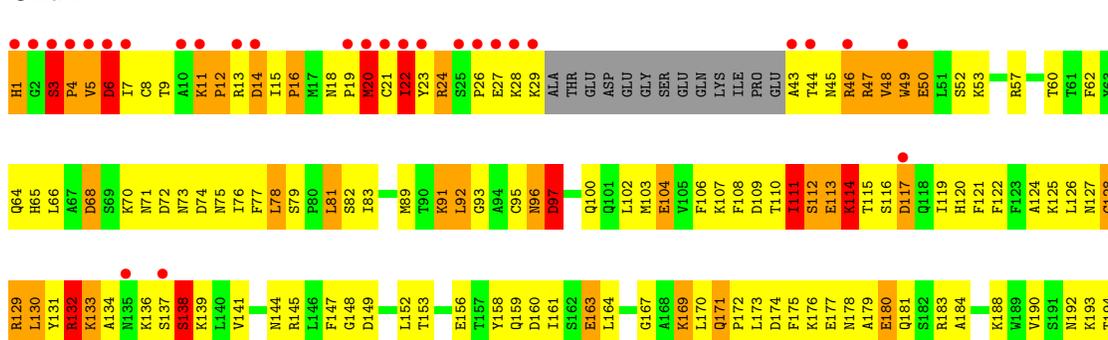
- Molecule 1: ANTITHROMBIN

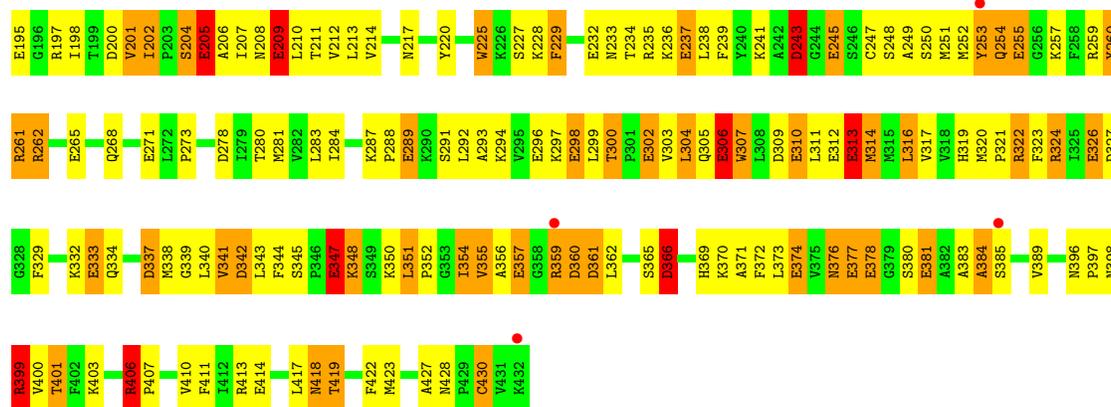
## Chain L:



- Molecule 1: ANTITHROMBIN

## Chain I:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.41Å 98.31Å 90.41Å 90.00° 103.32° 90.00°	Depositor
Resolution (Å)	26.90 – 2.60 19.92 – 2.62	Depositor EDS
% Data completeness (in resolution range)	74.0 (26.90-2.60) 78.2 (19.92-2.62)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.94 (at 2.63Å)	Xtrriage
Refinement program	TNT V. 5-D	Depositor
R, $R_{free}$	0.217 , 0.290 0.229 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	36.6	Xtrriage
Anisotropy	0.336	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 90.9	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Outliers	0 of 25487 reflections	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	6636	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.34% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: NAA

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	I	0.91	27/3415 (0.8%)	1.34	42/4608 (0.9%)
1	L	0.92	30/3240 (0.9%)	1.43	56/4367 (1.3%)
All	All	0.91	57/6655 (0.9%)	1.38	98/8975 (1.1%)

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	1	0

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	377	GLU	CD-OE2	6.52	1.32	1.25
1	L	104	GLU	CD-OE2	6.48	1.32	1.25
1	L	232	GLU	CD-OE2	6.23	1.32	1.25
1	I	312	GLU	CD-OE1	6.22	1.32	1.25
1	L	195	GLU	CD-OE2	6.19	1.32	1.25

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	406	ARG	C-N-CD	-27.57	59.94	120.60
1	I	406	ARG	NE-CZ-NH1	11.58	126.09	120.30
1	L	18	ASN	C-N-CD	-10.48	97.55	120.60
1	I	3	SER	C-N-CD	-10.25	98.05	120.60
1	L	135	ASN	N-CA-C	9.99	137.97	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	L	112	SER	CA

There are no planarity outliers.

## 5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	3348	0	3357	348	10
1	L	3181	0	3183	316	10
2	I	14	0	12	1	0
2	L	14	0	12	2	0
3	I	42	0	0	10	0
3	L	37	0	0	8	0
All	All	6636	0	6564	662	10

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 50.

The worst 5 of 662 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:50:GLU:HB3	1:L:111:ILE:HG22	1.22	1.19
1:L:355:VAL:HG13	1:L:359:ARG:HD2	1.31	1.08
1:L:355:VAL:H	1:L:359:ARG:HD3	1.20	1.06
1:I:75:ASN:ND2	1:I:427:ALA:H	1.56	1.04
1:I:152:LEU:HA	1:I:356:ALA:HB1	1.40	1.03

The worst 5 of 10 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	Distance(Å)	Clash(Å)
1:L:261:ARG:NH2	1:I:13:ARG:CB[1_554]	1.31	0.89
1:L:310:GLU:OE2	1:I:47:ARG:NH2[1_554]	1.54	0.66
1:L:261:ARG:NH1	1:I:13:ARG:CB[1_554]	1.59	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:261:ARG:CZ	1:I:13:ARG:CB[1_554]	1.60	0.60
1:L:261:ARG:NH2	1:I:13:ARG:CG[1_554]	1.83	0.37

## 5.3 Torsion angles

### 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	I	415/432 (96%)	353 (85%)	38 (9%)	24 (6%)	3	2
1	L	390/432 (90%)	342 (88%)	25 (6%)	23 (6%)	2	2
All	All	805/864 (93%)	695 (86%)	63 (8%)	47 (6%)	3	2

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	9	THR
1	L	19	PRO
1	L	97	ASP
1	L	113	GLU
1	L	133	LYS

### 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	I	372/383 (97%)	303 (82%)	69 (18%)	2	4
1	L	353/383 (92%)	288 (82%)	65 (18%)	2	4
All	All	725/766 (95%)	591 (82%)	134 (18%)	2	4

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	408	PHE
1	I	81	LEU
1	I	374	GLU
1	L	419	THR
1	I	22	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	100	GLN
1	I	159	GLN
1	I	396	ASN
1	I	118	GLN
1	I	127	ASN

### 5.3.3 RNA [i](#)

There are no RNA chains 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](#)

2 ligands are 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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAA	I	500	1	12,14,15	1.05	1 (8%)	15,19,21	4.09	11 (73%)
2	NAA	L	500	1	12,14,15	0.95	1 (8%)	15,19,21	6.59	10 (66%)

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
2	NAA	I	500	1	-	0/6/23/26	0/1/1/1
2	NAA	L	500	1	2/2/5/7	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	500	NAA	C7-N2	2.72	1.45	1.34
2	I	500	NAA	C7-N2	2.64	1.45	1.34

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	500	NAA	C3-C2-N2	-18.21	84.03	111.76
2	L	500	NAA	O5-C5-C6	11.24	118.77	106.98
2	I	500	NAA	O5-C5-C6	8.97	116.39	106.98
2	L	500	NAA	O5-C5-C4	8.43	121.35	110.65
2	I	500	NAA	O5-C5-C4	7.64	120.35	110.65

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	L	500	NAA	C4
2	L	500	NAA	C1

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	I	419/432 (96%)	-0.08	32 (7%) 14 11	26, 47, 121, 162	0
1	L	398/432 (92%)	-0.09	22 (5%) 24 20	27, 54, 121, 136	0
All	All	817/864 (94%)	-0.08	54 (6%) 18 15	26, 49, 121, 162	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	20	MET	9.5
1	I	6	ASP	8.3
1	I	26	PRO	7.6
1	I	4	PRO	7.6
1	I	3	SER	7.1

### 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

There are no carbohydrates in this entry.

### 6.4 Ligands

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAA	I	500	14/15	0.18	0.66	2,69,398,468	1
2	NAA	L	500	14/15	0.20	-0.40	2,99,518,652	1

## 6.5 Other polymers

There are no such residues in this entry.