



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 11:25 AM GMT

PDB ID : 1V7M  
Title : Human Thrombopoietin Functional Domain Complexed To Neutralizing Antibody TN1 Fab  
Authors : Feese, M.D.; Tamada, T.; Kato, Y.; Maeda, Y.; Hirose, M.; Matsukura, Y.; Shigematsu, H.; Kato, T.; Miyazaki, H.; Kuroki, R.  
Deposited on : 2003-12-18  
Resolution : 2.51 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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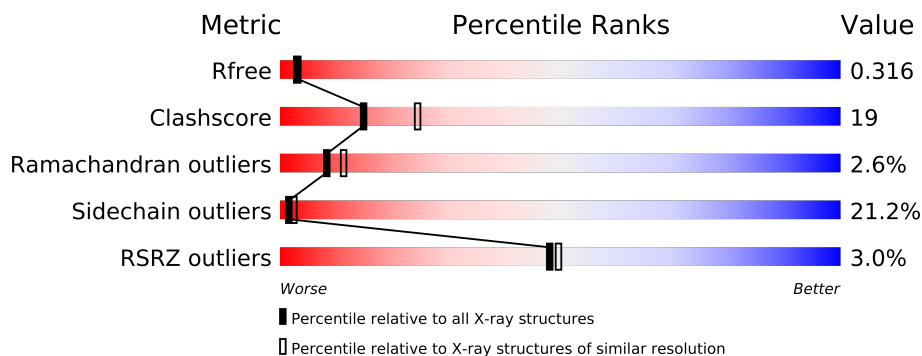
The following versions of software and data (see [references](#)) were used in the production of this report:

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

# 1 Overall quality at a glance

The reported resolution of this entry is 2.51 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))
$R_{free}$	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	L	213	
1	M	213	
2	H	217	
2	I	217	
3	V	163	
3	X	163	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8902 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 Monoclonal TN1 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	212	Total	C	N	O	S	0	0	0
			1632	1015	277	332	8			
1	M	212	Total	C	N	O	S	0	0	0
			1632	1015	277	332	8			

- Molecule 2 is a protein called Monoclonal TN1 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	217	Total	C	N	O	S	0	0	0
			1643	1038	273	324	8			
2	I	217	Total	C	N	O	S	0	0	0
			1643	1038	273	324	8			

- Molecule 3 is a protein called Thrombopoietin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	V	145	Total	C	N	O	S	0	0	0
			1098	699	196	196	7			
3	X	145	Total	C	N	O	S	0	0	0
			1098	699	196	196	7			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	35	Total	O	0	0
			35	35		
4	I	33	Total	O	0	0
			33	33		
4	L	27	Total	O	0	0
			27	27		
4	M	36	Total	O	0	0
			36	36		

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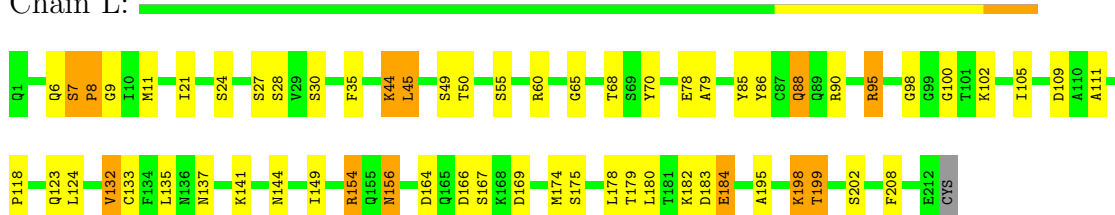
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	V	12	Total 12	O 12	0	0
4	X	13	Total 13	O 13	0	0

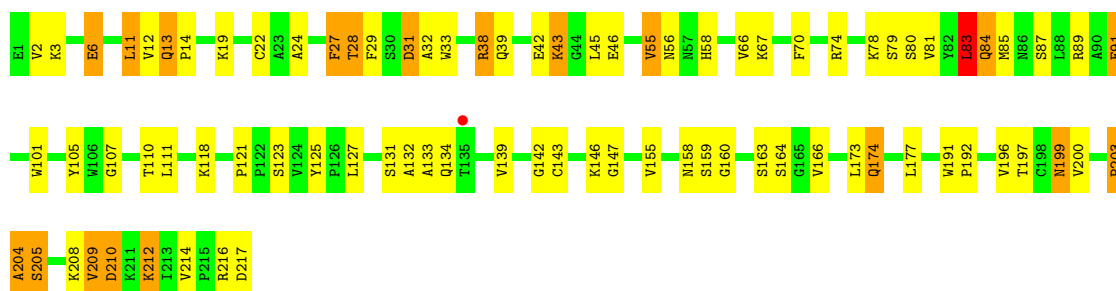
### 3 Residue-property plots

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: Monoclonal TN1 Fab Light Chain

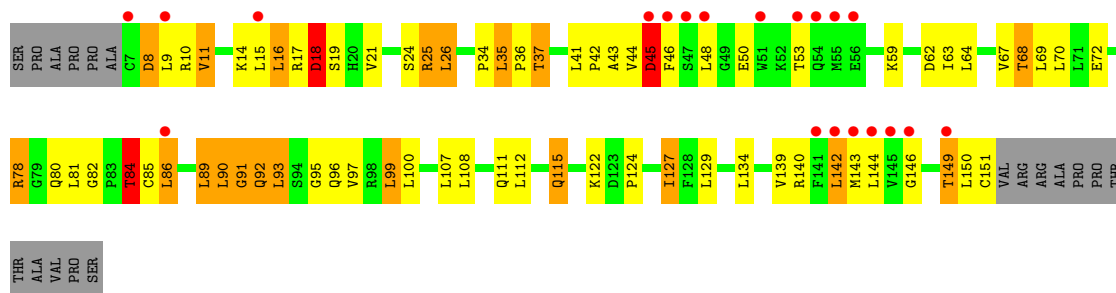
Chain L:





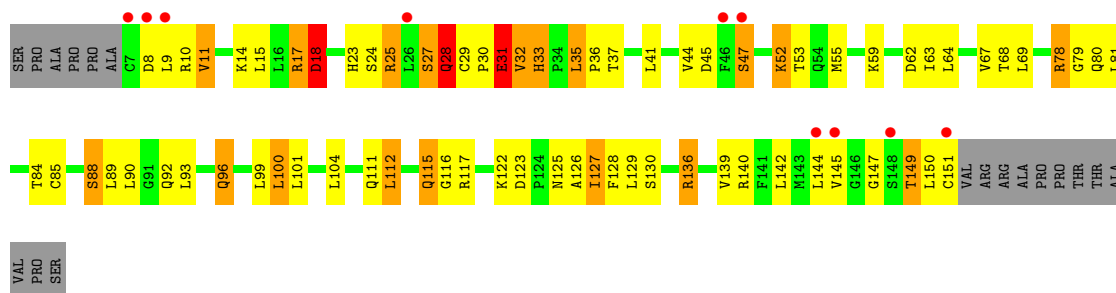
### • Molecule 3: Thrombopoietin

Chain V:



### • Molecule 3: Thrombopoietin

Chain X:



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.10Å 46.77Å 185.15Å 90.00° 90.48° 90.00°	Depositor
Resolution (Å)	45.28 – 2.51 45.28 – 2.51	Depositor EDS
% Data completeness (in resolution range)	92.9 (45.28-2.51) 92.9 (45.28-2.51)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.48 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.228 , 0.316 0.238 , 0.316	Depositor DCC
$R_{free}$ test set	1852 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 27.1	EDS
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	3 of 36765 reflections (0.008%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8902	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.04 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.2117e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality i

### 5.1 Standard geometry i

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	L	0.91	1/1670 (0.1%)	1.07	9/2266 (0.4%)
1	M	0.98	1/1670 (0.1%)	1.11	10/2266 (0.4%)
2	H	0.98	1/1687 (0.1%)	1.13	14/2302 (0.6%)
2	I	0.96	2/1687 (0.1%)	1.05	4/2302 (0.2%)
3	V	0.79	0/1117	1.05	4/1515 (0.3%)
3	X	0.81	0/1117	1.01	3/1515 (0.2%)
All	All	0.92	5/8948 (0.1%)	1.08	44/12166 (0.4%)

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
2	H	0	1
3	X	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	184	GLU	CD-OE2	6.08	1.32	1.25
1	M	147	TRP	CB-CG	-5.46	1.40	1.50
2	H	208	LYS	CD-CE	5.18	1.64	1.51
2	I	55	VAL	CB-CG2	5.14	1.63	1.52
2	I	43	LYS	CD-CE	5.12	1.64	1.51

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	V	62	ASP	CB-CG-OD2	8.94	126.34	118.30
3	X	62	ASP	CB-CG-OD2	8.79	126.21	118.30
2	H	31	ASP	CB-CG-OD2	8.54	125.98	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	109	ASP	CB-CG-OD2	8.18	125.67	118.30
1	M	60	ARG	NE-CZ-NH2	-7.89	116.36	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	203	PRO	Peptide
3	X	33	HIS	Peptide

## 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	L	1632	0	1568	44	0
1	M	1632	0	1568	52	0
2	H	1643	0	1594	61	0
2	I	1643	0	1594	93	0
3	V	1098	0	1152	45	0
3	X	1098	0	1152	54	0
4	H	35	0	0	10	0
4	I	33	0	0	22	0
4	L	27	0	0	8	0
4	M	36	0	0	12	0
4	V	12	0	0	7	0
4	X	13	0	0	7	0
All	All	8902	0	8628	332	0

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 19.

The worst 5 of 332 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:I:11:LEU:HG	4:I:227:HOH:O	1.20	1.32
3:X:85:CYS:HA	4:X:173:HOH:O	1.17	1.30

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:I:209:VAL:HG12	4:I:231:HOH:O	1.19	1.27
1:M:8:PRO:HD2	4:M:241:HOH:O	1.17	1.27
2:H:209:VAL:HG23	4:H:228:HOH:O	1.18	1.26

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	L	210/213 (99%)	201 (96%)	7 (3%)	2 (1%)	22	38
1	M	210/213 (99%)	197 (94%)	9 (4%)	4 (2%)	12	19
2	H	215/217 (99%)	197 (92%)	13 (6%)	5 (2%)	10	14
2	I	215/217 (99%)	202 (94%)	9 (4%)	4 (2%)	12	19
3	V	143/163 (88%)	116 (81%)	20 (14%)	7 (5%)	3	3
3	X	143/163 (88%)	113 (79%)	22 (15%)	8 (6%)	3	2
All	All	1136/1186 (96%)	1026 (90%)	80 (7%)	30 (3%)	8	11

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	7	SER
2	H	65	SER
2	H	134	GLN
2	H	137	SER
2	H	204	ALA

### 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	L	185/186 (100%)	156 (84%)	29 (16%)	4	6
1	M	185/186 (100%)	153 (83%)	32 (17%)	3	5
2	H	185/185 (100%)	148 (80%)	37 (20%)	2	3
2	I	185/185 (100%)	146 (79%)	39 (21%)	1	2
3	V	124/138 (90%)	86 (69%)	38 (31%)	0	0
3	X	124/138 (90%)	90 (73%)	34 (27%)	0	1
All	All	988/1018 (97%)	779 (79%)	209 (21%)	1	2

5 of 209 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	V	115	GLN
1	M	106	LYS
3	X	69	LEU
3	V	140	ARG
1	M	20	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
3	V	132	GLN
1	M	37	GLN
3	X	111	GLN
1	M	6	GLN
1	M	88	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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	L	212/213 (99%)	-0.51	0 100 100	26, 39, 57, 75	0
1	M	212/213 (99%)	-0.46	0 100 100	26, 39, 60, 77	0
2	H	217/217 (100%)	-0.40	3 (1%) 72 74	26, 41, 62, 86	0
2	I	217/217 (100%)	-0.38	1 (0%) 88 90	29, 42, 62, 79	0
3	V	145/163 (88%)	0.66	20 (13%) 4 3	30, 75, 112, 118	0
3	X	145/163 (88%)	0.35	10 (6%) 17 16	33, 66, 101, 116	0
All	All	1148/1186 (96%)	-0.20	34 (2%) 48 50	26, 44, 93, 118	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	V	144	LEU	12.7
3	X	7	CYS	8.9
3	V	7	CYS	8.1
3	V	141	PHE	6.4
3	V	46	PHE	5.3

### 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 ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.