

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

May 15, 2020 – 05:23 pm BST

PDB ID : 4TNF

Title : Crystal Structure of Human Transthyretin Lys15Trp Mutant

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Deposited on : 2014-06-03

Resolution : 1.60 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 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)

 $\begin{array}{ccc} \text{Xtriage (Phenix)} & : & 1.13 \\ \text{EDS} & : & 2.11 \end{array}$ 

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

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

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

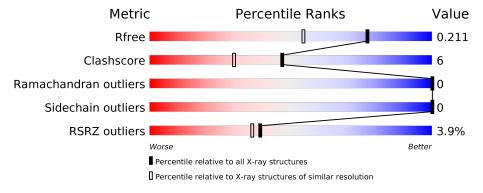
Validation Pipeline (wwPDB-VP) : 2.11

# 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 1.60 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar  resolution} \\ (\#{\rm Entries,  resolution  range(\AA)}) \end{array}$
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 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	125	6% 87%	5% • 7%
1	В	125	84%	7% • 8%



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1911 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 Transthyretin.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Λ	116	Total	С	N	О	S	0	0	0
1	Λ	110	906	579	148	177	2	U		
1	D	115	Total	С	N	О	S	0	1	0
1	Ъ	110	904	581	147	174	2	0	1	U

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	TRP	LYS	engineered mutation	UNP P02766
A	128	HIS	-	expression tag	UNP P02766
A	129	HIS	_	expression tag	UNP P02766
A	130	HIS	_	expression tag	UNP P02766
A	131	HIS	_	expression tag	UNP P02766
A	132	HIS	_	expression tag	UNP P02766
A	133	HIS	_	expression tag	UNP P02766
В	15	TRP	LYS	engineered mutation	UNP P02766
В	128	HIS	_	expression tag	UNP P02766
В	129	HIS	_	expression tag	UNP P02766
В	130	HIS	_	expression tag	UNP P02766
В	131	HIS	_	expression tag	UNP P02766
В	132	HIS	-	expression tag	UNP P02766
В	133	HIS	-	expression tag	UNP P02766

• Molecule 2 is water.

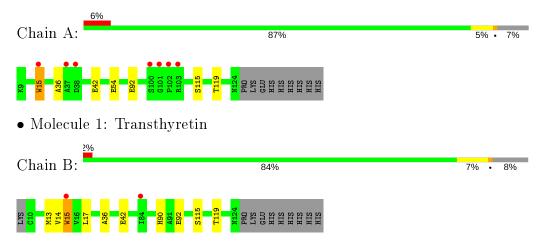
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	44	Total O 44 44	0	0
2	В	57	Total O 57 57	0	0



# 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: Transthyretin





# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 2	Depositor	
Cell constants	42.92Å 85.61Å 64.20Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	_	
Resolution (Å)	64.20 - 1.60	Depositor	
resolution (A)	51.36 - 1.60	EDS	
% Data completeness	99.8 (64.20-1.60)	Depositor	
(in resolution range)	99.8 (51.36-1.60)	EDS	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.94 (at 1.60Å)	Xtriage	
Refinement program	BUSTER 2.10.0	Depositor	
P. P.	0.200 , $0.213$	Depositor	
$R, R_{free}$	0.195 , $0.211$	DCC	
$R_{free}$ test set	1615 reflections $(5.06\%)$	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	20.5	Xtriage	
Anisotropy	0.323	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35, 42.4	EDS	
L-test for twinning <sup>2</sup>	$ < L >=0.48, < L^2>=0.32$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
$F_o$ , $F_c$ correlation	0.96	EDS	
Total number of atoms	1911	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	26.0	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 34.80 % 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 6.4460e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<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: OCS

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).

M	Mol	Chain	Boı	nd lengths	Bond angles		
WIOI CII		Chain	RMSZ	# Z  > 5	RMSZ	# Z >5	
1		A	0.64	$1/921 \; (0.1\%)$	0.64	0/1255	
1		В	0.62	2/925~(0.2%)	0.61	0/1265	
Al	1	All	0.63	$3/1846 \ (0.2\%)$	0.62	0/2520	

#### All (3) bond length outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$Ideal(\AA)$
1	A	15	TRP	CB-CG	-11.47	1.29	1.50
1	В	15[A]	TRP	CA-C	5.33	1.66	1.52
1	В	15[B]	TRP	CA-C	5.33	1.66	1.52

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	$\mathbf{H}(\mathbf{model})$	H(added)	Clashes	Symm-Clashes
1	Α	906	0	871	10	0
1	В	904	0	867	15	0
2	A	44	0	0	0	0
2	В	57	0	0	0	0
All	All	1911	0	1738	22	0



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 6.

All (22) 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:B:13:MET:HB2	1:B:15[B]:TRP:HZ3	1.18	1.06
1:B:13:MET:HB2	1:B:15[B]:TRP:CZ3	2.04	0.93
1:B:36:ALA:HB2	1:B:42:GLU:HG3	1.70	0.73
1:A:15:TRP:CE2	1:A:54:GLU:HG2	2.24	0.71
1:B:14:VAL:C	1:B:15[B]:TRP:HE3	1.96	0.69
1:A:36:ALA:HB2	1:A:42:GLU:HG3	1.73	0.69
1:A:15:TRP:CZ2	1:A:54:GLU:CG	2.79	0.66
1:B:15[A]:TRP:CZ2	1:B:17:LEU:HD21	2.34	0.63
1:B:13:MET:SD	1:B:15[B]:TRP:CH2	2.92	0.62
1:A:15:TRP:CZ2	1:A:54:GLU:HG2	2.35	0.61
1:B:90:HIS:HD2	1:B:92:GLU:HG2	1.66	0.60
1:A:15:TRP:CZ2	1:A:54:GLU:CD	2.76	0.59
1:A:119:THR:HG23	1:B:115:SER:HB2	1.85	0.58
1:B:13:MET:SD	1:B:15[B]:TRP:HH2	2.29	0.55
1:B:13:MET:CB	1:B:15[B]:TRP:CZ3	2.88	0.53
1:A:15:TRP:CH2	1:A:54:GLU:CG	2.92	0.52
1:B:90:HIS:CD2	1:B:92:GLU:HG2	2.44	0.50
1:A:115:SER:HB2	1:B:119:THR:HG23	1.96	0.47
1:A:15:TRP:CH2	1:A:54:GLU:HG3	2.51	0.45
1:A:92:GLU:HB2	1:B:92:GLU:HB2	2.00	0.44

There are no symmetry-related clashes.

### 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	113/125 (90%)	110 (97%)	3 (3%)	0	100 100	

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Mol	Chain	Analysed Favoured Allowed C		Outliers	Perce	$\mathbf{ntiles}$	
1	В	114/125 (91%)	113 (99%)	1 (1%)	0	100	100
All	All	227/250 (91%)	223 (98%)	4 (2%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	Percen	tiles
1	A	96/105~(91%)	96 (100%)	0	100	100
1	В	95/105 (90%)	95 (100%)	0	100	100
All	All	191/210 (91%)	191 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	В	90	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)

2 non-standard protein/DNA/RNA residues 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	Tuna	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Pog	Tink	В	Bond lengths			Bond angles		
	Type		Res	$\operatorname{Res} \mid \operatorname{Link} \mid$	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2													
1	OCS	A	10	1	7,8,9	1.35	1 (14%)	6,11,13	1.76	1 (16%)													
1	OCS	В	10	1	7,8,9	1.41	1 (14%)	6,11,13	1.85	2 (33%)													

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
1	OCS	A	10	1	-	1/4/7/9	-
1	OCS	В	10	1	_	1/4/7/9	-

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	${ m Observed}({ m \AA})$	$Ideal(\AA)$
1	В	10	OCS	CB-CA	-3.00	1.50	1.53
1	A	10	OCS	OD1-SG	-2.79	1.36	1.45

#### All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	ype Atoms		$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	В	10	OCS	OD2-SG-CB	-2.46	101.82	105.74
1	В	10	OCS	OD3-SG-OD1	2.41	122.29	113.95
1	A	10	OCS	OD3-SG-OD1	2.24	121.71	113.95

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	10	OCS	N-CA-CB-SG
1	В	10	OCS	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.



## 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry (i)

There are no ligands in this entry.

### 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	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	115/125~(92%)	0.16	7 (6%) 21 19	17, 24, 48, 63	0
1	В	114/125 (91%)	-0.06	2 (1%) 68 67	15, 21, 39, 46	0
All	All	229/250 (91%)	0.05	9 (3%) 39 36	15, 22, 45, 63	0

All (9) RSRZ outliers are listed below:

Mol	Chain	${f Res}$	Type	RSRZ
1	A	15	TRP	5.4
1	В	15[A]	TRP	4.8
1	A	37	ALA	4.2
1	A	102	PRO	3.5
1	A	100	SER	2.6
1	В	84	ILE	2.4
1	A	38	ASP	2.3
1	A	103	ARG	2.2
1	A	101	GLY	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains (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	${f B-factors}({f \AA}^2)$	Q<0.9
1	OCS	A	10	9/10	0.84	0.29	26,32,34,35	9
1	OCS	В	10	9/10	0.88	0.27	19,21,23,25	9



## 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

# 6.4 Ligands (i)

There are no ligands in this entry.

## 6.5 Other polymers (i)

There are no such residues in this entry.

