

wwPDB X-ray Structure Validation Summary Report (i)

Oct 23, 2021 – 02:12 PM EDT

PDB ID : 5TTR

Title : LEU 55 PRO TRANSTHYRETIN CRYSTAL STRUCTURE

Authors : Sebastiao, M.P.; Saraiva, M.J.; Damas, A.M.

Deposited on : 1998-04-30

Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

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

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

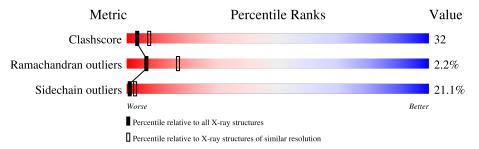
Validation Pipeline (wwPDB-VP) : 2.23.2

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 2.70 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)

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%

Note EDS was not executed.

Mol	Chain	Length		Quality of cha	iin		
1	A	127	24%	47%	17%	•	9%
1	В	127	28%	31%	26%	6%	9%
1	С	127	28%	40%	17%	6%	9%
1	D	127	28%	33%	26%	5%	9%
1	E	127		_			
			33%	31%	20%	8%	9%
1	F	127	28%	35%	24%	5%	9%
1	G	127	30%	34%	21%	6%	9%
1	Н	127	29%	36%	20%	6%	9%



2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 7147 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	A	116	Total	С	N	О	S	4	0	0
1	A	110	895	572	147	174	2	4	U	0
1	В	116	Total	С	N	О	S	18	0	0
1	Ъ	110	890	569	145	174	2	10		0
1	С	116	Total	С	N	О	S	7	0	0
1		110	895	572	147	174	2	1	0	
1	D	116	Total	С	N	О	S	0	0	0
1	D	110	891	570	147	172	2	U	U	0
1	Е	116	Total	С	N	О	S	11	0	0
1	Ľ	110	895	572	147	174	2	11	0	
1	F	116	Total	С	N	O	S	0	0	0
1	I.	110	895	572	147	174	2	0		0
1	G	116	Total	С	N	Ο	S	7	0	0
1	G	110	891	570	147	172	2	1	U	U
1	Н	116	Total	С	N	О	S	4	0	0
1	11	110	895	572	147	174	2	4	0	U

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	55	PRO	LEU	engineered mutation	UNP P02766
В	55	PRO	LEU	engineered mutation	UNP P02766
С	55	PRO	LEU	engineered mutation	UNP P02766
D	55	PRO	LEU	engineered mutation	UNP P02766
E	55	PRO	LEU	engineered mutation	UNP P02766
F	55	PRO	LEU	engineered mutation	UNP P02766
G	55	PRO	LEU	engineered mutation	UNP P02766
Н	55	PRO	LEU	engineered mutation	UNP P02766

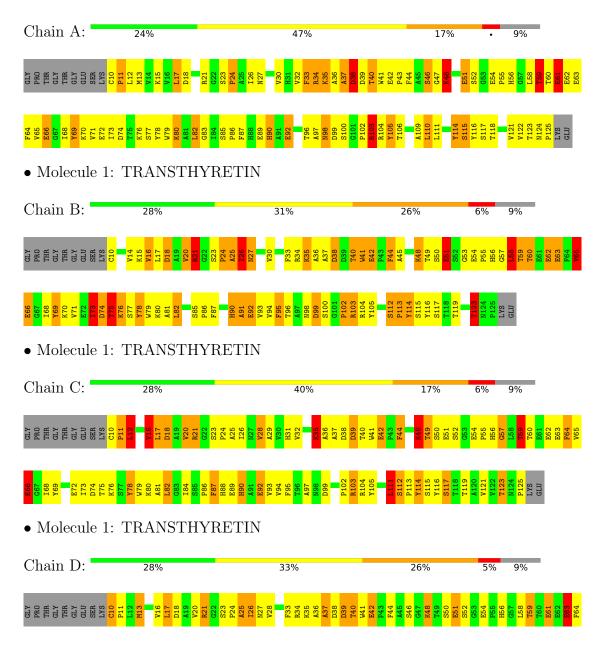


3 Residue-property plots (i)

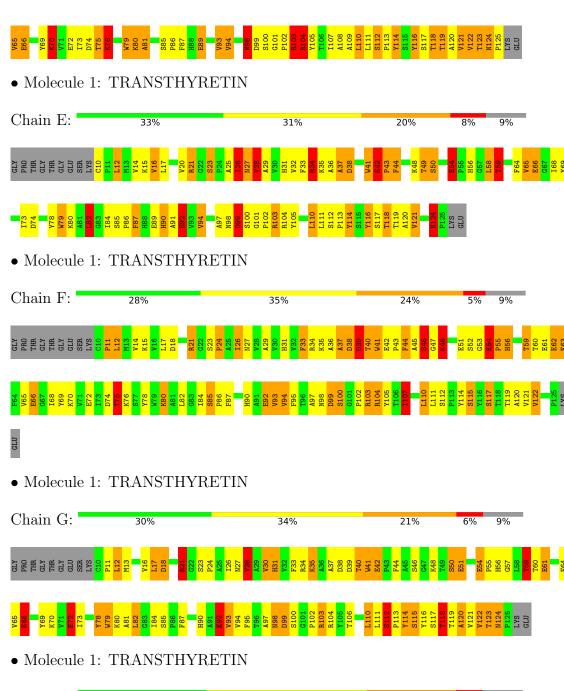
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

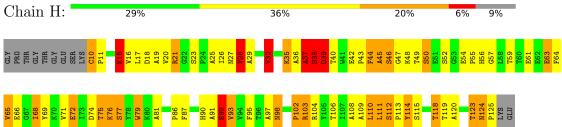
Note EDS was not executed.

• Molecule 1: TRANSTHYRETIN











4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	149.99Å 78.74Å 98.95Å	Depositor	
a, b, c, α , β , γ	90.00° 100.50° 90.00°	Depositor	
Resolution (Å)	8.00 - 2.70	Depositor	
% Data completeness	98.0 (8.00-2.70)	Depositor	
(in resolution range)	30.0 (0.00 2.10)		
R_{merge}	0.06	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	PROLSQ	Depositor	
R, R_{free}	0.199 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	7147	wwPDB-VP	
Average B, all atoms (Å ²)	31.0	wwPDB-VP	



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	Boı	nd lengths	Е	Bond angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	1.10	0/920	3.12	70/1257~(5.6%)
1	В	1.16	1/914 (0.1%)	2.93	88/1249 (7.0%)
1	С	1.42	1/920 (0.1%)	2.77	87/1257 (6.9%)
1	D	1.07	0/916	3.04	82/1252~(6.5%)
1	Е	1.11	1/920 (0.1%)	2.76	75/1257 (6.0%)
1	F	1.06	1/920 (0.1%)	2.87	80/1257 (6.4%)
1	G	1.06	$2/916 \ (0.2\%)$	3.24	82/1252 (6.5%)
1	Н	1.10	1/920 (0.1%)	2.73	80/1257 (6.4%)
All	All	1.14	7/7346 (0.1%)	2.94	644/10038 (6.4%)

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	С	1	0
1	Е	0	1
1	G	0	1
All	All	1	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(A)
1	С	125	PRO	CA-C	27.92	2.08	1.52
1	В	123	THR	C-N	15.14	1.68	1.34
1	G	124	ASN	C-N	11.03	1.55	1.34
1	Е	92	GLU	CD-OE1	6.22	1.32	1.25
1	G	39	ASP	C-O	5.92	1.34	1.23

The worst 5 of 644 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	G	124	ASN	O-C-N	-50.10	25.90	121.10
1	A	21	ARG	CD-NE-CZ	40.18	179.85	123.60
1	D	103	ARG	NE-CZ-NH1	29.44	135.02	120.30
1	D	103	ARG	NE-CZ-NH2	-27.97	106.31	120.30
1	Е	21	ARG	NE-CZ-NH2	-26.89	106.86	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Chain Res		Atom
1	С	125	PRO	CA

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Е	124	ASN	Peptide
1	G	124	ASN	Mainchain

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	895	0	865	68	0
1	В	890	0	860	71	0
1	С	895	0	863	50	0
1	D	891	0	861	72	0
1	Е	895	0	865	55	0
1	F	895	0	865	49	0
1	G	891	0	859	56	0
1	Н	895	0	865	55	0
All	All	7147	0	6903	449	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 32.

The worst 5 of 449 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)	
1:D:26:ILE:CD1	1:D:51:GLU:HA	1.24	1.62	
1:C:21:ARG:NH2	1:C:82:LEU:HD11	1.29	1.48	
1:C:21:ARG:NH2	1:C:82:LEU:CD1	1.82	1.42	
1:F:44:PHE:CZ	1:F:59:THR:HG21	1.63	1.33	
1:C:44:PHE:CZ	1:C:59:THR:HG21	1.63	1.32	

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	114/127~(90%)	107 (94%)	4 (4%)	3 (3%)	5 13
1	В	114/127~(90%)	105 (92%)	5 (4%)	4 (4%)	3 8
1	C	114/127 (90%)	109 (96%)	2 (2%)	3 (3%)	5 13
1	D	114/127~(90%)	108 (95%)	4 (4%)	2 (2%)	8 21
1	E	114/127 (90%)	103 (90%)	8 (7%)	3 (3%)	5 13
1	F	114/127 (90%)	105 (92%)	7 (6%)	2 (2%)	8 21
1	G	114/127 (90%)	106 (93%)	7 (6%)	1 (1%)	17 40
1	Н	114/127 (90%)	109 (96%)	3 (3%)	2 (2%)	8 21
All	All	912/1016 (90%)	852 (93%)	40 (4%)	20 (2%)	6 17

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	37	ALA
1	Н	37	ALA
1	D	39	ASP
1	Е	56	HIS
1	F	37	ALA



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	Analysed Rotameric Outliers		Percentiles		
1	A	97/105~(92%)	78 (80%)	19 (20%)	1	3	
1	В	96/105 (91%)	77 (80%)	19 (20%)	1	3	
1	С	97/105 (92%)	78 (80%)	19 (20%)	1	3	
1	D	96/105 (91%)	71 (74%)	25 (26%)	0	1	
1	E	97/105 (92%)	75 (77%)	22 (23%)	1	2	
1	F	97/105 (92%)	75 (77%)	22 (23%)	1	2	
1	G	96/105 (91%)	74 (77%)	22 (23%)	1	2	
1	Н	97/105~(92%)	82 (84%)	15 (16%)	2	7	
All	All	773/840 (92%)	610 (79%)	163 (21%)	1	3	

5 of 163 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	62	GLU
1	G	100	SER
1	F	85	SER
1	G	30	VAL
1	Н	21	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	fol Chain Res		Type	
1	G	27 ASI		
1	G	90	HIS	
1	1 H		HIS	
1	1 D		ASN	
1	Е	124	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 monosaccharides 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	В	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	В	123:THR	С	124:ASN	N	1.68



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

