



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 02:53 pm BST

PDB ID : 3TMM  
Title : TFAM imposes a U-turn on mitochondrial DNA  
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Deposited on : 2011-08-31  
Resolution : 2.50 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](mailto: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 ⓘ symbol.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

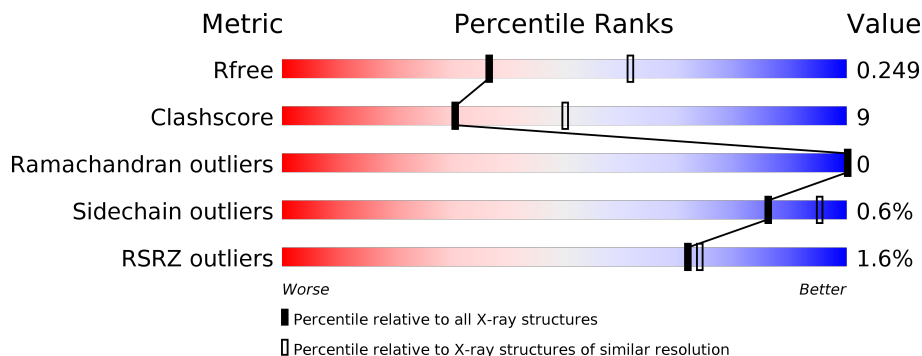
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 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  $\leq 5\%$ . 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	238	 2% 66% 16% 18%
2	B	28	 57% 43%
3	C	28	 43% 43% 14%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2869 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 Transcription factor A, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	195	1641	1037	296	302	1	5	0	0	0

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MSE	-	EXPRESSION TAG	UNP Q00059
A	-32	GLY	-	EXPRESSION TAG	UNP Q00059
A	-31	SER	-	EXPRESSION TAG	UNP Q00059
A	-30	SER	-	EXPRESSION TAG	UNP Q00059
A	-29	HIS	-	EXPRESSION TAG	UNP Q00059
A	-28	HIS	-	EXPRESSION TAG	UNP Q00059
A	-27	HIS	-	EXPRESSION TAG	UNP Q00059
A	-26	HIS	-	EXPRESSION TAG	UNP Q00059
A	-25	HIS	-	EXPRESSION TAG	UNP Q00059
A	-24	HIS	-	EXPRESSION TAG	UNP Q00059
A	-23	SER	-	EXPRESSION TAG	UNP Q00059
A	-22	SER	-	EXPRESSION TAG	UNP Q00059
A	-21	GLY	-	EXPRESSION TAG	UNP Q00059
A	-20	LEU	-	EXPRESSION TAG	UNP Q00059
A	-19	VAL	-	EXPRESSION TAG	UNP Q00059
A	-18	PRO	-	EXPRESSION TAG	UNP Q00059
A	-17	ARG	-	EXPRESSION TAG	UNP Q00059
A	-16	GLY	-	EXPRESSION TAG	UNP Q00059
A	-15	SER	-	EXPRESSION TAG	UNP Q00059
A	-14	HIS	-	EXPRESSION TAG	UNP Q00059
A	-13	MSE	-	EXPRESSION TAG	UNP Q00059
A	-12	ALA	-	EXPRESSION TAG	UNP Q00059
A	-11	SER	-	EXPRESSION TAG	UNP Q00059
A	-10	MSE	-	EXPRESSION TAG	UNP Q00059
A	-9	THR	-	EXPRESSION TAG	UNP Q00059
A	-8	GLY	-	EXPRESSION TAG	UNP Q00059
A	-7	GLY	-	EXPRESSION TAG	UNP Q00059

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLN	-	EXPRESSION TAG	UNP Q00059
A	-5	GLN	-	EXPRESSION TAG	UNP Q00059
A	-4	MSE	-	EXPRESSION TAG	UNP Q00059
A	-3	GLY	-	EXPRESSION TAG	UNP Q00059
A	-2	ARG	-	EXPRESSION TAG	UNP Q00059
A	-1	GLY	-	EXPRESSION TAG	UNP Q00059
A	0	SER	-	EXPRESSION TAG	UNP Q00059

- Molecule 2 is a DNA chain called DNA (28-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	28	587	279	108	172	28	0	0	0

- Molecule 3 is a DNA chain called DNA (28-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	C	28	561	269	100	164	28	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	51	Total	O	0	0
			51	51		
4	B	14	Total	O	0	0
			14	14		
4	C	15	Total	O	0	0
			15	15		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.44Å 81.91Å 161.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.19 – 2.50 24.19 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.5 (24.19-2.50) 90.9 (24.19-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 2.31Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.6 _289)	Depositor
R, $R_{free}$	0.195 , 0.248 0.190 , 0.249	Depositor DCC
$R_{free}$ test set	968 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.5	Xtrriage
Anisotropy	0.371	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 40.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2869	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.34% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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](#)

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	0.41	0/1667	0.50	0/2220
2	B	0.71	0/659	1.37	4/1019 (0.4%)
3	C	0.74	0/627	1.56	12/961 (1.2%)
All	All	0.57	0/2953	1.07	16/4200 (0.4%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	C	8	DA	O4'-C4'-C3'	-11.04	99.38	106.00
2	B	6	DG	O4'-C1'-N9	-7.10	103.03	108.00
3	C	20	DC	O4'-C1'-N1	7.01	112.91	108.00
3	C	28	DA	O4'-C1'-N9	6.80	112.76	108.00
3	C	8	DA	C1'-O4'-C4'	-6.11	103.99	110.10
3	C	3	DT	N3-C4-O4	5.70	123.32	119.90
3	C	8	DA	O4'-C1'-N9	5.59	111.91	108.00
2	B	18	DC	C1'-O4'-C4'	-5.53	104.57	110.10
2	B	1	DT	N3-C4-O4	5.53	123.22	119.90
3	C	16	DC	O4'-C1'-N1	-5.37	104.24	108.00
3	C	20	DC	O4'-C4'-C3'	-5.33	102.37	104.50
3	C	6	DT	O4'-C1'-C2'	-5.26	101.69	105.90
2	B	18	DC	O4'-C1'-C2'	-5.23	101.72	105.90
3	C	22	DA	O4'-C1'-N9	-5.11	104.42	108.00
3	C	9	DC	C6-N1-C2	5.01	122.31	120.30
3	C	15	DC	O4'-C1'-N1	5.01	111.51	108.00

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	1641	0	1695	30	0
2	B	587	0	319	11	0
3	C	561	0	315	10	0
4	A	51	0	0	2	0
4	B	14	0	0	0	0
4	C	15	0	0	1	0
All	All	2869	0	2329	46	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 9.

All (46) 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)
2:B:9:DG:H2''	2:B:10:DG:H5'	1.53	0.88
1:A:12:VAL:CG1	1:A:16:LEU:HB3	2.14	0.77
3:C:4:DT:H2''	3:C:5:DT:OP2	1.92	0.70
2:B:9:DG:C2'	2:B:10:DG:H5'	2.21	0.68
2:B:4:DT:H2'	2:B:5:DA:C8	2.31	0.66
2:B:24:DA:H1'	2:B:25:DA:H5''	1.79	0.65
3:C:14:DA:H2'	3:C:15:DC:O4'	1.97	0.63
1:A:193:ILE:HG22	1:A:194:LYS:H	1.66	0.60
1:A:49:LEU:O	1:A:54:LYS:HE3	2.02	0.59
1:A:144:LYS:HE2	3:C:21:DA:H4'	1.84	0.58
1:A:12:VAL:HG12	1:A:16:LEU:HB3	1.85	0.57
1:A:74:ARG:NE	4:A:215:HOH:O	2.37	0.57
1:A:98:ARG:HG3	2:B:16:DG:OP1	2.04	0.56
2:B:4:DT:H2''	2:B:5:DA:O5'	2.04	0.56
3:C:1:DA:H2''	3:C:2:DC:OP2	2.06	0.55
1:A:183:VAL:HG12	1:A:183:VAL:O	2.07	0.54
1:A:116:PRO:HG3	1:A:169:TYR:CD2	2.44	0.53
1:A:117:ARG:HD2	4:A:242:HOH:O	2.08	0.52
1:A:12:VAL:HG11	1:A:16:LEU:HB3	1.90	0.52
1:A:177:GLU:O	1:A:181:ILE:HG12	2.09	0.52
1:A:15:TYR:O	1:A:18:PHE:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:ILE:O	1:A:29:GLN:HG2	2.10	0.51
1:A:101:MSE:SE	2:B:15:DT:H4'	2.61	0.50
1:A:13:SER:HA	1:A:61:TYR:CD1	2.46	0.50
1:A:64:GLU:O	1:A:67:VAL:HG12	2.12	0.50
1:A:16:LEU:HD22	3:C:8:DA:N3	2.27	0.50
3:C:2:DC:H2''	3:C:3:DT:OP2	2.12	0.49
1:A:123:TYR:CE1	1:A:150:LEU:HD11	2.47	0.49
3:C:14:DA:C2'	3:C:15:DC:O4'	2.60	0.49
3:C:4:DT:H1'	3:C:5:DT:H5'	1.93	0.49
2:B:9:DG:H2''	2:B:10:DG:C5'	2.34	0.49
1:A:11:PRO:HB3	1:A:64:GLU:HB3	1.96	0.48
1:A:86:SER:O	1:A:90:GLU:HG3	2.13	0.48
2:B:25:DA:H2''	2:B:26:DA:C8	2.49	0.48
1:A:46:TRP:O	1:A:54:LYS:HE2	2.13	0.48
1:A:37:GLU:HA	1:A:37:GLU:OE1	2.14	0.47
1:A:131:ALA:O	1:A:139:LYS:HE3	2.15	0.46
2:B:4:DT:H4'	2:B:5:DA:OP1	2.16	0.46
3:C:4:DT:C2'	3:C:5:DT:OP2	2.64	0.45
1:A:193:ILE:HG22	1:A:194:LYS:N	2.29	0.45
1:A:21:GLU:O	1:A:24:PRO:HD2	2.16	0.44
1:A:139:LYS:O	1:A:143:VAL:HG23	2.18	0.44
3:C:27:DC:H2''	3:C:28:DA:O5'	2.18	0.44
1:A:125:ALA:HA	2:B:9:DG:H5'	2.02	0.42
1:A:139:LYS:HB3	1:A:139:LYS:HE2	1.91	0.41
1:A:104:LYS:HD3	4:C:50:HOH:O	2.20	0.40

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	193/238 (81%)	188 (97%)	5 (3%)	0	<a href="#">100</a> <a href="#">100</a>

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	Percentiles
1	A	181/205 (88%)	180 (99%)	1 (1%)	86 95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

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

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<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	A	190/238 (79%)	-0.23	4 (2%) 63 66	32, 55, 95, 137	0
2	B	28/28 (100%)	-0.67	0 100 100	41, 64, 100, 118	0
3	C	28/28 (100%)	-0.61	0 100 100	39, 67, 91, 117	0
All	All	246/294 (83%)	-0.32	4 (1%) 72 74	32, 57, 99, 137	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	194	LYS	4.6
1	A	193	ILE	3.8
1	A	195	LYS	3.6
1	A	1	SER	3.4

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

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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.