



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:52 PM GMT

PDB ID : 4MYC
Title : Structure of the mitochondrial ABC transporter, Atm1
Authors : Srinivasan, V.
Deposited on : 2013-09-27
Resolution : 3.06 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

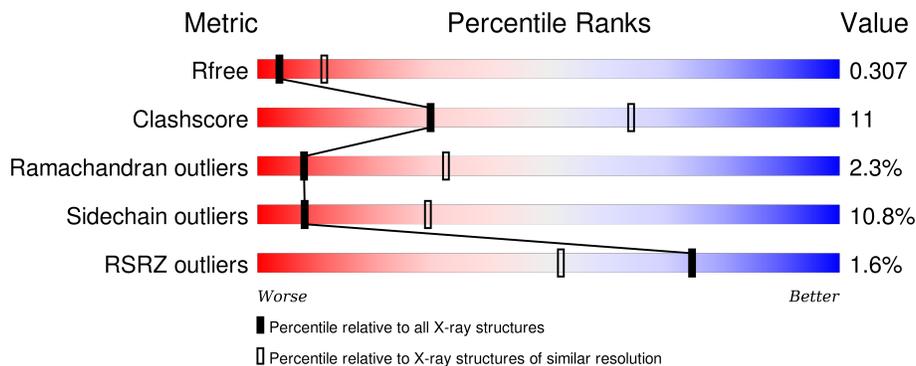
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.06 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}	91344	1191 (3.10-3.02)
Clashscore	102246	1303 (3.10-3.02)
Ramachandran outliers	100387	1254 (3.10-3.02)
Sidechain outliers	100360	1254 (3.10-3.02)
RSRZ outliers	91569	1197 (3.10-3.02)

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. 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	598	
1	B	598	
1	C	598	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14028 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 Iron-sulfur clusters transporter ATM1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	598	4676	3002	802	855	17	0	0	0
1	C	598	4676	3002	802	855	17	0	0	0
1	B	598	4676	3002	802	855	17	0	0	0

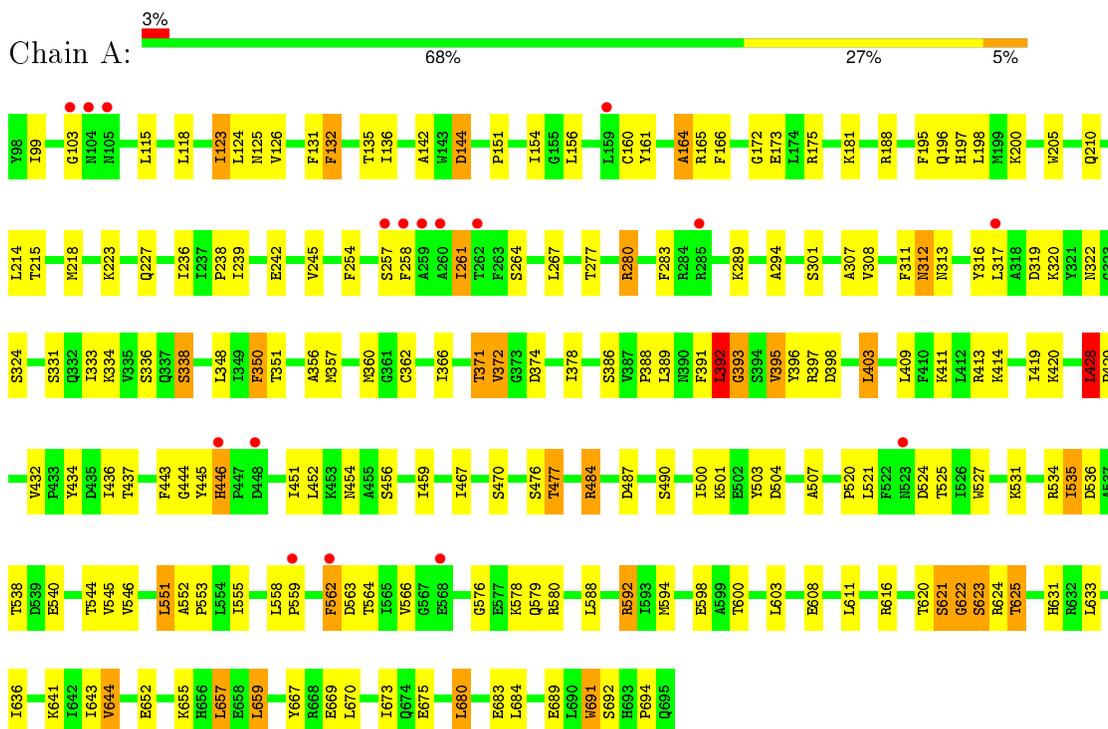
There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	691	TRP	-	EXPRESSION TAG	UNP P40416
A	692	SER	-	EXPRESSION TAG	UNP P40416
A	693	HIS	-	EXPRESSION TAG	UNP P40416
A	694	PRO	-	EXPRESSION TAG	UNP P40416
A	695	GLN	-	EXPRESSION TAG	UNP P40416
C	691	TRP	-	EXPRESSION TAG	UNP P40416
C	692	SER	-	EXPRESSION TAG	UNP P40416
C	693	HIS	-	EXPRESSION TAG	UNP P40416
C	694	PRO	-	EXPRESSION TAG	UNP P40416
C	695	GLN	-	EXPRESSION TAG	UNP P40416
B	691	TRP	-	EXPRESSION TAG	UNP P40416
B	692	SER	-	EXPRESSION TAG	UNP P40416
B	693	HIS	-	EXPRESSION TAG	UNP P40416
B	694	PRO	-	EXPRESSION TAG	UNP P40416
B	695	GLN	-	EXPRESSION TAG	UNP P40416

3 Residue-property plots

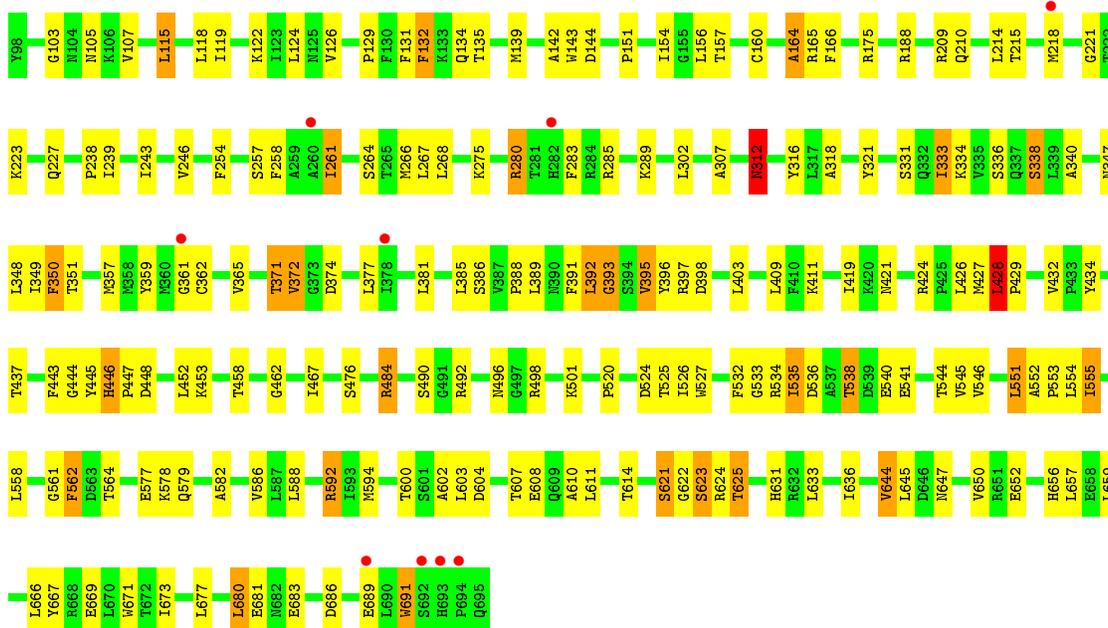
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Iron-sulfur clusters transporter ATM1, mitochondrial





● Molecule 1: Iron-sulfur clusters transporter ATM1, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	156.62Å 156.62Å 520.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.60 – 3.06 48.60 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.60-3.06) 99.7 (48.60-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 3.01Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.251 , 0.298 0.259 , 0.307	Depositor DCC
R_{free} test set	3611 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	71.7	Xtrriage
Anisotropy	0.115	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 19.8	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Outliers	2 of 76585 reflections (0.003%)	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	14028	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.51	0/4763	0.65	0/6451
1	B	0.52	0/4763	0.67	1/6451 (0.0%)
1	C	0.53	0/4763	0.67	0/6451
All	All	0.52	0/14289	0.66	1/19353 (0.0%)

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	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	428	LEU	C-N-CD	-6.17	107.02	120.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	428	LEU	Peptide
1	B	428	LEU	Peptide
1	C	428	LEU	Peptide

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	4676	0	4738	130	0
1	B	4676	0	4738	125	0
1	C	4676	0	4738	95	0
All	All	14028	0	14214	317	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 11.

The worst 5 of 317 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:C:453:LYS:NZ	1:C:647:ASN:OD1	2.04	0.90
1:A:546:VAL:HG13	1:A:551:LEU:HB3	1.57	0.86
1:B:526:ILE:HD11	1:B:558:LEU:HD12	1.57	0.86
1:A:631:HIS:HB2	1:B:691:TRP:HH2	1.47	0.80
1:C:261:ILE:HD11	1:C:357:MET:HG3	1.64	0.78

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	596/598 (100%)	540 (91%)	42 (7%)	14 (2%)	8	32
1	B	596/598 (100%)	540 (91%)	42 (7%)	14 (2%)	8	32
1	C	596/598 (100%)	544 (91%)	38 (6%)	14 (2%)	8	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1788/1794 (100%)	1624 (91%)	122 (7%)	42 (2%)	8	32

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	312	ASN
1	A	392	LEU
1	A	395	VAL
1	A	396	TYR
1	A	603	LEU

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	501/514 (98%)	444 (89%)	57 (11%)	7	26
1	B	501/514 (98%)	449 (90%)	52 (10%)	9	31
1	C	501/514 (98%)	447 (89%)	54 (11%)	8	29
All	All	1503/1542 (98%)	1340 (89%)	163 (11%)	8	29

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

Mol	Chain	Res	Type
1	C	280	ARG
1	C	476	SER
1	B	538	THR
1	C	289	LYS
1	C	371	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	ASN
1	B	140	ASN

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Mol	Chain	Res	Type
1	B	379	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 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, 95th 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 ²)	Q<0.9
1	A	598/598 (100%)	-0.06	17 (2%) 56 30	5, 41, 61, 87	0
1	B	598/598 (100%)	-0.15	9 (1%) 76 55	4, 37, 57, 77	0
1	C	598/598 (100%)	-0.20	3 (0%) 91 81	4, 28, 49, 69	0
All	All	1794/1794 (100%)	-0.14	29 (1%) 74 52	4, 33, 57, 87	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	104	ASN	7.8
1	A	103	GLY	5.7
1	B	692	SER	5.7
1	A	105	ASN	4.9
1	B	694	PRO	4.0

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

There are no such residues in this entry.