wwPDB X-ray Structure Validation Summary Report (i)

Oct 30, 2023 – 07:31 PM JST

PDB ID	:	4YMT
Title	:	Crystal structure of an amino acid ABC transporter complex with arginines
Authors	:	Ge, J.; Yu, J.; Yang, M.
Deposited on	:	2015-03-07
Resolution	:	2.60 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

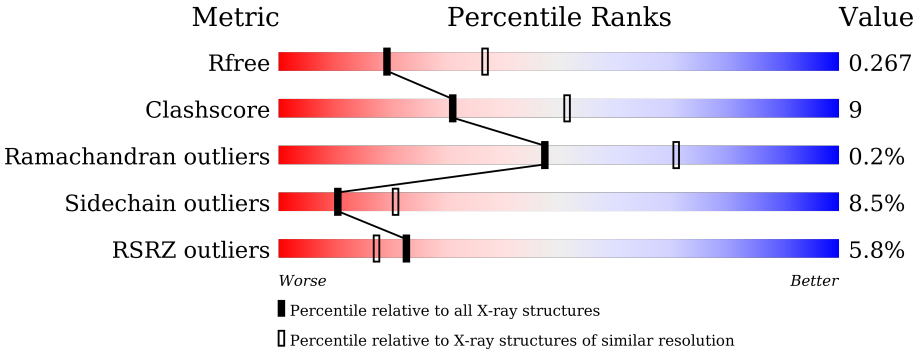
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.60 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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% 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	240	4% 80% 17% •
1	J	240	.% 81% 17% •
2	B	220	8% 70% 24% • •
2	C	220	11% 68% 25% 5% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7142 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.

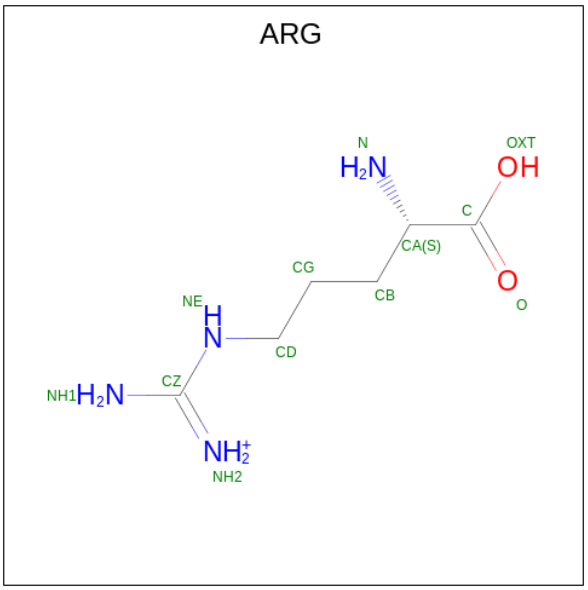
- Molecule 1 is a protein called ABC-type polar amino acid transport system, ATPase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	J	240	1872	1198	317	345	12	0	0	0
1	A	240	1872	1198	317	345	12	0	0	0

- Molecule 2 is a protein called ABC-type amino acid transport system, permease component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	215	1659	1096	264	286	13	0	0	0
2	B	215	1659	1096	264	286	13	0	0	0

- Molecule 3 is ARGININE (three-letter code: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	C	1	12	6	4	2	0	0
			Total	C	N	O		
3	B	1	12	6	4	2	0	0

- Molecule 4 is water.

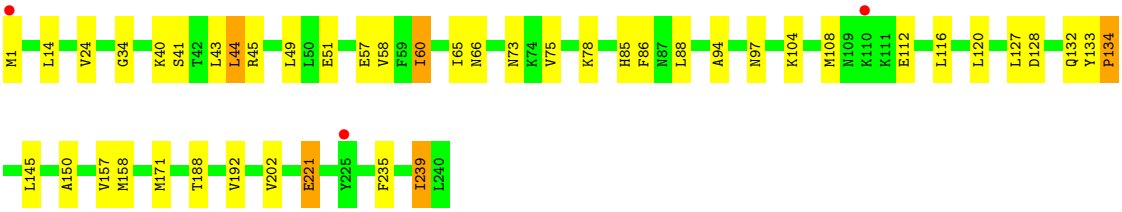
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	J	20	20	20	0	0
			Total	O		
4	A	17	17	17	0	0
			Total	O		
4	C	10	10	10	0	0
			Total	O		
4	B	9	9	9	0	0

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 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.

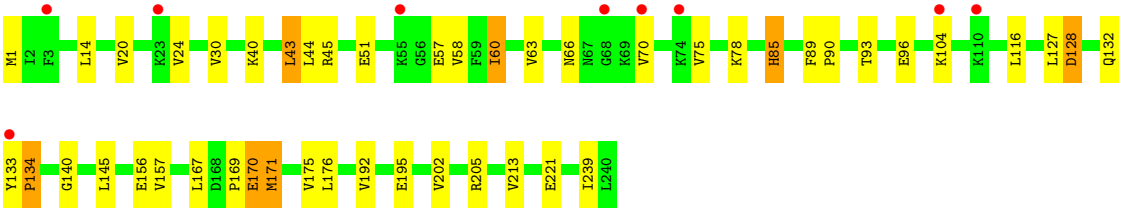
• Molecule 1: ABC-type polar amino acid transport system, ATPase component

Chain J:



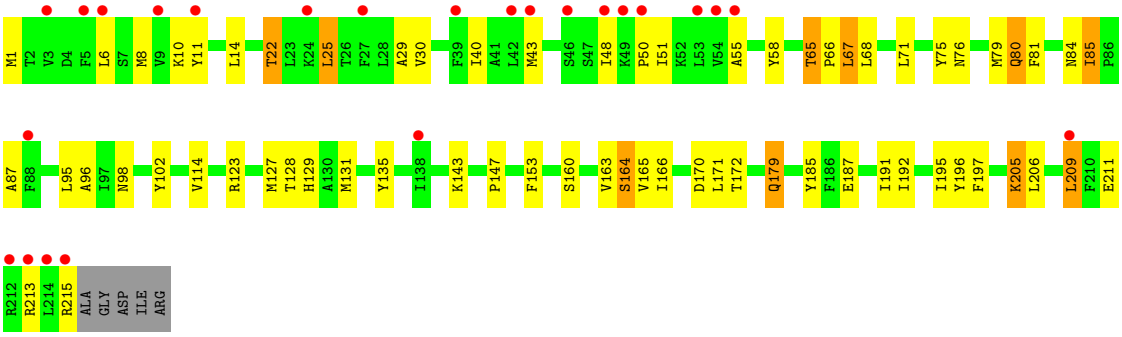
• Molecule 1: ABC-type polar amino acid transport system, ATPase component

Chain A:



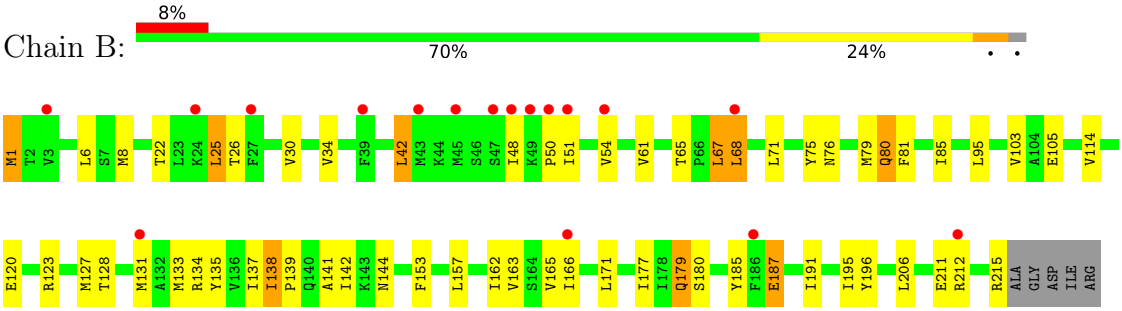
• Molecule 2: ABC-type amino acid transport system, permease component

Chain C:



• Molecule 2: ABC-type amino acid transport system, permease component

Chain B:


8%
70%
24%
M1 T2 V3 L6 S7 M8 T22 L23 K24 L25 T26 F27 V30 V34 F39 L42 M43 K44 M45 S46 S47 I48 K49 P50 I51 V54 V61 T65 P66 L67 L68 L71 Y75 N76 M79 Q80 F81 I85 L95 V103 A104 E105 V114
E120 R123 M127 T128 M131 A132 M133 R134 Y135 V136 I137 I138 P139 Q140 A141 I142 K143 N144 F153 L157 I162 V163 S164 V165 I166 L171 I177 I178 Q179 S180 Y185 F186 E187 I191 I195 Y196 L206 E211 R212 R215 ALA GLY ASP ILE ARG

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	96.38Å 114.78Å 300.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.78 – 2.60 49.78 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.6 (49.78-2.60) 94.6 (49.78-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.18 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.222 , 0.264 0.226 , 0.267	Depositor DCC
R_{free} test set	2503 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	61.2	Xtriage
Anisotropy	0.681	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 55.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7142	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]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.

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	0.57	1/1897 (0.1%)	0.65	2/2552 (0.1%)
1	J	0.59	1/1897 (0.1%)	0.69	2/2552 (0.1%)
2	B	0.47	1/1688 (0.1%)	0.57	1/2288 (0.0%)
2	C	0.41	0/1688	0.57	0/2288
All	All	0.52	3/7170 (0.0%)	0.63	5/9680 (0.1%)

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	134	PRO	N-CD	5.30	1.55	1.47
1	A	134	PRO	N-CD	5.18	1.55	1.47
2	B	139	PRO	N-CD	5.14	1.55	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	138	ILE	C-N-CD	5.62	140.21	128.40
1	J	133	TYR	C-N-CD	5.51	139.98	128.40
1	A	133	TYR	C-N-CD	5.39	139.72	128.40
1	J	85	HIS	N-CA-C	-5.33	96.61	111.00
1	A	85	HIS	N-CA-C	-5.29	96.71	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	85	HIS	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	1872	0	1960	23	0
1	J	1872	0	1960	22	0
2	B	1659	0	1774	52	0
2	C	1659	0	1774	54	0
3	B	12	0	12	0	0
3	C	12	0	12	0	0
4	A	17	0	0	0	0
4	B	9	0	0	5	0
4	C	10	0	0	5	0
4	J	20	0	0	1	0
All	All	7142	0	7492	133	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.

The worst 5 of 133 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:C:29:ALA:HB1	4:C:407:HOH:O	1.15	1.25
2:C:96:ALA:N	4:C:407:HOH:O	1.85	1.07
2:B:105:GLU:OE1	4:B:404:HOH:O	1.83	0.95
2:B:1:MET:SD	4:B:401:HOH:O	2.32	0.85
2:B:1:MET:HA	4:B:401:HOH:O	1.81	0.80

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	238/240 (99%)	232 (98%)	6 (2%)	0	100	100
1	J	238/240 (99%)	232 (98%)	6 (2%)	0	100	100
2	B	213/220 (97%)	203 (95%)	9 (4%)	1 (0%)	29	52
2	C	213/220 (97%)	204 (96%)	8 (4%)	1 (0%)	29	52
All	All	902/920 (98%)	871 (97%)	29 (3%)	2 (0%)	47	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	80	GLN
2	C	80	GLN

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	208/209 (100%)	188 (90%)	20 (10%)	8	16
1	J	208/209 (100%)	189 (91%)	19 (9%)	9	18
2	B	180/184 (98%)	167 (93%)	13 (7%)	14	29
2	C	180/184 (98%)	166 (92%)	14 (8%)	12	25
All	All	776/786 (99%)	710 (92%)	66 (8%)	10	21

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	67	LEU
2	B	71	LEU
2	B	206	LEU
1	A	60	ILE
1	A	58	VAL

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands 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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	ARG	C	301	-	10,11,11	0.67	0	11,13,13	0.99	2 (18%)
3	ARG	B	301	-	10,11,11	0.71	1 (10%)	11,13,13	1.16	2 (18%)

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
3	ARG	C	301	-	-	1/11/11/11	-
3	ARG	B	301	-	-	0/11/11/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	ARG	OXT-C	-2.04	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	301	ARG	OXT-C-O	-2.72	117.91	124.09
3	B	301	ARG	OXT-C-CA	2.45	121.74	113.38
3	C	301	ARG	OXT-C-O	-2.23	119.02	124.09
3	C	301	ARG	OXT-C-CA	2.11	120.57	113.38

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	301	ARG	O-C-CA-N

There are no ring outliers.

No monomer is involved in short contacts.

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	240/240 (100%)	0.52	9 (3%)	40	33	47, 66, 94, 119	0
1	J	240/240 (100%)	0.27	3 (1%)	77	73	44, 60, 85, 113	0
2	B	215/220 (97%)	0.66	17 (7%)	12	9	57, 87, 119, 146	0
2	C	215/220 (97%)	0.79	24 (11%)	5	3	52, 81, 114, 145	0
All	All	910/920 (98%)	0.55	53 (5%)	23	17	44, 74, 109, 146	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	50	PRO	6.5
2	C	49	LYS	4.7
2	C	214	LEU	4.2
2	B	51	ILE	4.2
2	B	54	VAL	4.1

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 monosaccharides in this entry.

6.4 Ligands (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, 95th 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	B-factors(Å^2)	Q<0.9
3	ARG	C	301	12/12	0.93	0.18	70,77,81,82	0
3	ARG	B	301	12/12	0.96	0.16	70,78,84,86	0

6.5 Other polymers (i)

There are no such residues in this entry.