



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 15, 2016 – 08:00 AM EDT

PDB ID : 5J4I  
Title : Crystal Structure of the L-arginine/agmatine antiporter from E. coli at 2.2 Angstrom resolution  
Authors : Jeckelmann, J.M.; Ilgue, H.; Fotiadis, D.  
Deposited on : 2016-04-01  
Resolution : 2.21 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

<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	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
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)	:	rb-20027939

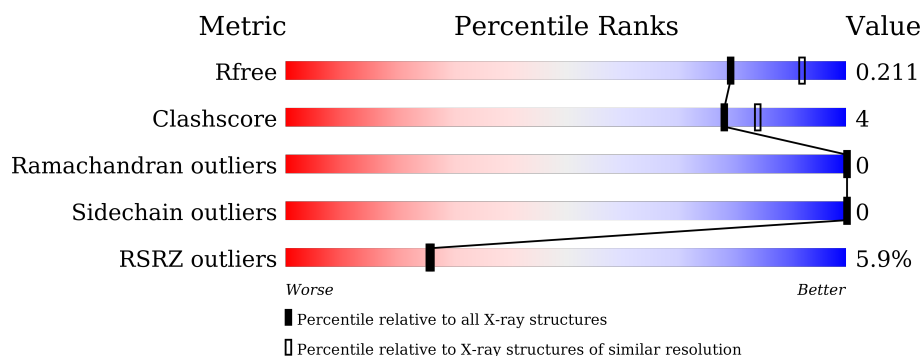
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.21 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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. 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	453	<div> <div>6%</div> <div>87%</div> <div>10%</div> <div>.</div> </div>
1	B	453	<div> <div>5%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6639 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 Arginine/agmatine antiporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3240	2149	518	551	22			
1	B	437	Total	C	N	O	S	0	0	0
			3240	2149	518	551	22			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	446	LEU	-	expression tag	UNP P60063
A	447	GLU	-	expression tag	UNP P60063
A	448	LEU	-	expression tag	UNP P60063
A	449	GLU	-	expression tag	UNP P60063
A	450	VAL	-	expression tag	UNP P60063
A	451	LEU	-	expression tag	UNP P60063
A	452	PHE	-	expression tag	UNP P60063
A	453	GLN	-	expression tag	UNP P60063
B	446	LEU	-	expression tag	UNP P60063
B	447	GLU	-	expression tag	UNP P60063
B	448	LEU	-	expression tag	UNP P60063
B	449	GLU	-	expression tag	UNP P60063
B	450	VAL	-	expression tag	UNP P60063
B	451	LEU	-	expression tag	UNP P60063
B	452	PHE	-	expression tag	UNP P60063
B	453	GLN	-	expression tag	UNP P60063

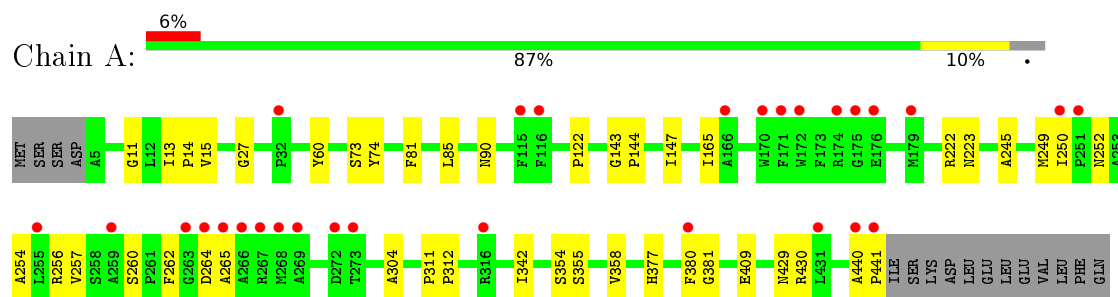
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	83	Total	O	0	0
			83	83		
2	B	76	Total	O	0	0
			76	76		

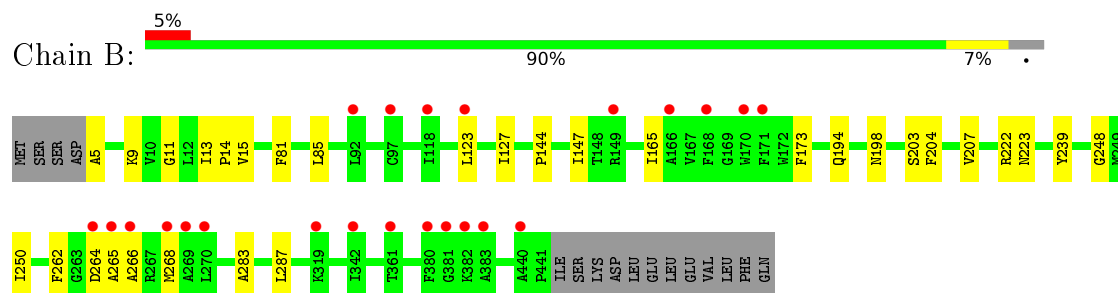
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Arginine/agmatine antiporter



#### • Molecule 1: Arginine/agmatine antiporter



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.74Å 175.42Å 73.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.51 – 2.21 49.51 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.51-2.21) 99.3 (49.51-2.21)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.26 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.197 , 0.210 0.200 , 0.211	Depositor DCC
$R_{free}$ test set	3406 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	47.7	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 59.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6639	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% 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

### 5.1 Standard geometry

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	0.43	0/3326	0.51	0/4553
1	B	0.31	0/3326	0.46	0/4553
All	All	0.37	0/6652	0.49	0/9106

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	3240	0	3355	27	0
1	B	3240	0	3355	20	0
2	A	83	0	0	5	0
2	B	76	0	0	0	0
All	All	6639	0	6710	47	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 4.

All (47) 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:A:250:ILE:HD11	1:A:265:ALA:HB2	1.39	1.01

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:ILE:HD11	1:A:265:ALA:CB	2.02	0.88
1:B:204:PHE:O	1:B:207:VAL:HG23	1.74	0.86
1:B:250:ILE:HD11	1:B:265:ALA:CB	2.10	0.82
1:A:250:ILE:CD1	1:A:265:ALA:HB2	2.12	0.79
1:B:264:ASP:O	1:B:268:MET:HG2	1.91	0.70
1:B:250:ILE:HD11	1:B:265:ALA:HB1	1.72	0.68
1:A:222:ARG:NH1	1:A:223:ASN:OD1	2.26	0.68
1:B:250:ILE:HD11	1:B:265:ALA:HB2	1.83	0.61
1:B:5:ALA:HA	1:B:9:LYS:HD2	1.84	0.60
1:B:250:ILE:CD1	1:B:265:ALA:HB2	2.32	0.58
1:A:144:PRO:HA	1:A:147:ILE:HG22	1.86	0.57
1:A:254:ALA:O	1:A:257:VAL:HG12	2.05	0.57
1:B:144:PRO:HA	1:B:147:ILE:HG22	1.87	0.56
1:A:13:ILE:HB	1:A:14:PRO:HD3	1.88	0.55
1:A:355:SER:HB3	1:A:409:GLU:HG2	1.89	0.53
1:B:13:ILE:HB	1:B:14:PRO:HD3	1.91	0.53
1:A:60:TYR:OH	1:A:73:SER:OG	2.24	0.51
1:A:354:SER:O	1:A:358:VAL:HG23	2.11	0.49
1:A:252:ASN:OD1	1:A:256:ARG:HD2	2.13	0.49
1:B:173:PHE:CE2	1:B:248:GLY:HA3	2.49	0.48
1:B:222:ARG:NH1	1:B:223:ASN:OD1	2.47	0.47
1:B:81:PHE:HB3	1:B:85:LEU:HD12	1.96	0.47
1:A:81:PHE:HB3	1:A:85:LEU:HD12	1.96	0.47
1:A:222:ARG:NH2	2:A:501:HOH:O	2.34	0.46
1:A:74:TYR:CZ	1:A:304:ALA:HA	2.51	0.46
1:A:27:GLY:HA3	2:A:513:HOH:O	2.15	0.46
1:A:11:GLY:O	1:A:15:VAL:HG23	2.16	0.46
1:B:173:PHE:CD2	1:B:248:GLY:HA3	2.52	0.45
1:A:311:PRO:HA	1:A:312:PRO:HD3	1.88	0.44
1:B:123:LEU:O	1:B:127:ILE:HG12	2.18	0.43
1:B:11:GLY:O	1:B:15:VAL:HG23	2.18	0.43
1:A:440:ALA:HA	1:A:441:PRO:HD2	1.79	0.43
1:B:165:ILE:HD12	1:B:262:PHE:CD2	2.53	0.42
1:B:283:ALA:O	1:B:287:LEU:HG	2.19	0.42
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.54	0.42
1:A:165:ILE:HD12	1:A:262:PHE:CD2	2.54	0.42
1:A:260:SER:O	1:A:264:ASP:N	2.38	0.42
1:A:381:GLY:N	2:A:505:HOH:O	2.53	0.42
1:A:429:ASN:O	1:A:430:ARG:HB2	2.19	0.41
1:A:143:GLY:HA3	2:A:562:HOH:O	2.19	0.41
1:A:245:ALA:O	1:A:249:MET:HG3	2.21	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:GLN:NE2	1:B:198:ASN:OD1	2.53	0.41
1:A:122:PRO:HB2	1:A:342:ILE:O	2.21	0.41
1:B:262:PHE:O	1:B:266:ALA:HB2	2.21	0.41
1:B:203:SER:HB3	1:B:239:TYR:CE2	2.56	0.40
1:A:90:ASN:HB3	2:A:528:HOH:O	2.21	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	435/453 (96%)	434 (100%)	1 (0%)	0	100	100
1	B	435/453 (96%)	433 (100%)	2 (0%)	0	100	100
All	All	870/906 (96%)	867 (100%)	3 (0%)	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	Percentiles	
1	A	335/351 (95%)	335 (100%)	0	100	100
1	B	335/351 (95%)	335 (100%)	0	100	100
All	All	670/702 (95%)	670 (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. 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 [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	437/453 (96%)	0.21	29 (6%)	22 21	39, 53, 101, 155	0
1	B	437/453 (96%)	0.24	23 (5%)	30 29	39, 55, 95, 161	0
All	All	874/906 (96%)	0.23	52 (5%)	26 25	39, 54, 99, 161	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	268	MET	8.2
1	A	266	ALA	7.8
1	A	440	ALA	7.4
1	A	264	ASP	6.6
1	A	441	PRO	5.5
1	B	381	GLY	4.6
1	B	382	LYS	4.0
1	A	171	PHE	4.0
1	B	269	ALA	4.0
1	B	268	MET	3.9
1	B	440	ALA	3.8
1	A	175	GLY	3.8
1	A	269	ALA	3.8
1	A	170	TRP	3.8
1	A	116	PHE	3.7
1	B	170	TRP	3.7
1	A	179	MET	3.6
1	B	118	ILE	3.6
1	A	265	ALA	3.6
1	A	172	TRP	3.6
1	B	171	PHE	3.5
1	A	263	GLY	3.4
1	B	168	PHE	3.1
1	B	97	CYS	3.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	431	LEU	3.1
1	A	267	ARG	3.1
1	B	264	ASP	3.0
1	A	176	GLU	3.0
1	A	115	PHE	3.0
1	A	250	ILE	3.0
1	A	32	PRO	3.0
1	A	174	ARG	3.0
1	B	166	ALA	2.9
1	A	259	ALA	2.8
1	B	342	ILE	2.8
1	B	270	LEU	2.8
1	A	273	THR	2.7
1	A	255	LEU	2.6
1	B	266	ALA	2.6
1	A	272	ASP	2.6
1	B	92	LEU	2.5
1	A	251	PRO	2.4
1	A	166	ALA	2.3
1	A	316	ARG	2.2
1	B	361	THR	2.2
1	B	265	ALA	2.2
1	B	383	ALA	2.1
1	A	380	PHE	2.1
1	B	149	ARG	2.1
1	B	123	LEU	2.1
1	B	319	LYS	2.1
1	B	380	PHE	2.0

## 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.