



# wwPDB X-ray Structure Validation Summary Report

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PDB ID : 1X2G  
Title : Crystal Structure of Lipate-Protein Ligase A from Escherichia coli  
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Deposited on : 2005-04-23  
Resolution : 2.40 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

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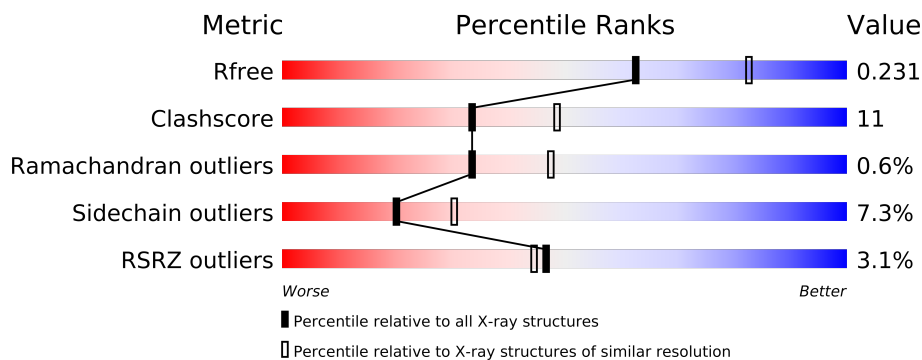
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.40 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))
$R_{free}$	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	337	
1	B	337	
1	C	337	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8425 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Lipoate-protein ligase A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	Se	0	0	0
			2618	1646	467	494	6	5			
1	B	330	Total	C	N	O	S	Se	0	0	0
			2614	1644	466	493	6	5			
1	C	337	Total	C	N	O	S	Se	0	0	0
			2663	1673	476	503	6	5			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	177	Total	O	0	0
			177	177		
2	B	175	Total	O	0	0
			175	175		
2	C	178	Total	O	0	0
			178	178		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.00Å 112.80Å 289.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.60 – 2.40 43.61 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (43.60-2.40) 99.6 (43.61-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.71 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.171 , 0.233 0.170 , 0.231	Depositor DCC
$R_{free}$ test set	2686 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.0	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 37.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 52725 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8425	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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	1.03	4/2669 (0.1%)	0.94	3/3606 (0.1%)
1	B	0.98	2/2665 (0.1%)	0.95	5/3601 (0.1%)
1	C	1.04	8/2715 (0.3%)	0.93	6/3670 (0.2%)
All	All	1.02	14/8049 (0.2%)	0.94	14/10877 (0.1%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	54	GLU	CB-CG	11.49	1.74	1.52
1	C	54	GLU	CD-OE2	9.15	1.35	1.25
1	B	265	GLU	CD-OE1	8.82	1.35	1.25
1	C	265	GLU	CD-OE1	8.79	1.35	1.25
1	A	265	GLU	CD-OE1	8.69	1.35	1.25

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	4	ARG	NE-CZ-NH2	-10.57	115.01	120.30
1	B	4	ARG	NE-CZ-NH1	7.81	124.20	120.30
1	C	160	ARG	NE-CZ-NH1	7.77	124.19	120.30
1	C	160	ARG	NE-CZ-NH2	-7.68	116.46	120.30
1	A	160	ARG	NE-CZ-NH2	-7.32	116.64	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2618	0	2554	56	0
1	B	2614	0	2551	43	0
1	C	2663	0	2605	78	0
2	A	177	0	0	7	0
2	B	175	0	0	8	0
2	C	178	0	0	16	0
All	All	8425	0	7710	171	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

The worst 5 of 171 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:89:MSE:HE2	1:C:145:ARG:HB2	1.31	1.11
1:C:169:LYS:HD3	1:C:169:LYS:H	1.01	1.08
1:C:337:ARG:HG2	2:C:515:HOH:O	1.56	1.05
1:C:126:LYS:HG3	1:C:130:GLY:O	1.58	1.04
1:C:142:THR:HG22	1:C:144:ASP:H	1.26	1.00

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	327/337 (97%)	318 (97%)	9 (3%)	0	100	100
1	B	326/337 (97%)	313 (96%)	12 (4%)	1 (0%)	50	68
1	C	335/337 (99%)	314 (94%)	16 (5%)	5 (2%)	15	20
All	All	988/1011 (98%)	945 (96%)	37 (4%)	6 (1%)	33	47

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	191	LEU
1	B	192	PRO
1	C	130	GLY
1	C	186	ASN
1	C	192	PRO

### 5.3.2 Protein sidechains ⓘ

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	276/277 (100%)	259 (94%)	17 (6%)	26	39
1	B	276/277 (100%)	254 (92%)	22 (8%)	17	26
1	C	282/277 (102%)	260 (92%)	22 (8%)	18	27
All	All	834/831 (100%)	773 (93%)	61 (7%)	20	30

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	158	LEU
1	B	194	ILE
1	C	190	LEU
1	B	169	LYS
1	B	183	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	223	ASN
1	B	244	ASN
1	C	253	HIS
1	B	230	ASN
1	B	279	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.



## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

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 ⓘ

### 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	331/337 (98%)	-0.17	10 (3%) 48 45	26, 41, 66, 97	0
1	B	330/337 (97%)	-0.14	14 (4%) 35 32	27, 42, 87, 99	0
1	C	337/337 (100%)	0.04	7 (2%) 60 58	29, 48, 88, 98	0
All	All	998/1011 (98%)	-0.09	31 (3%) 47 44	26, 43, 86, 99	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	GLY	5.2
1	A	175	LYS	3.8
1	A	174	ALA	3.7
1	A	173	ALA	3.3
1	A	120	ARG	3.3

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.