



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:28 pm GMT

PDB ID : 3PBK
Title : Structural and Functional Studies of Fatty Acyl-Adenylate Ligases from *E. coli* and *L. pneumophila*
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Deposited on : 2010-10-20
Resolution : 3.00 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

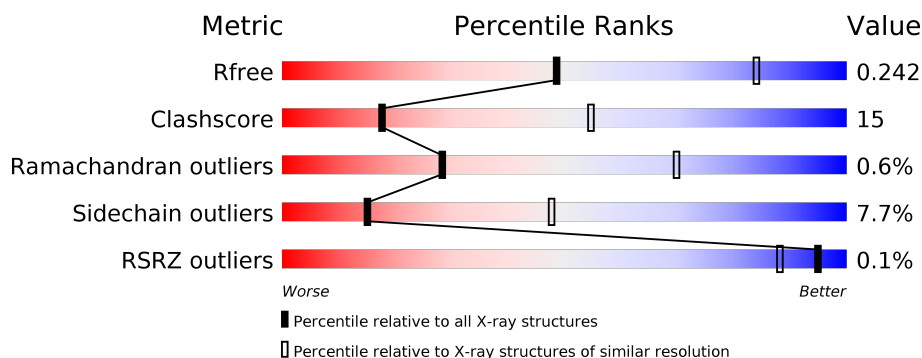
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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	583	 65% 27% • 5%
1	B	583	 64% 26% • 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8732 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.

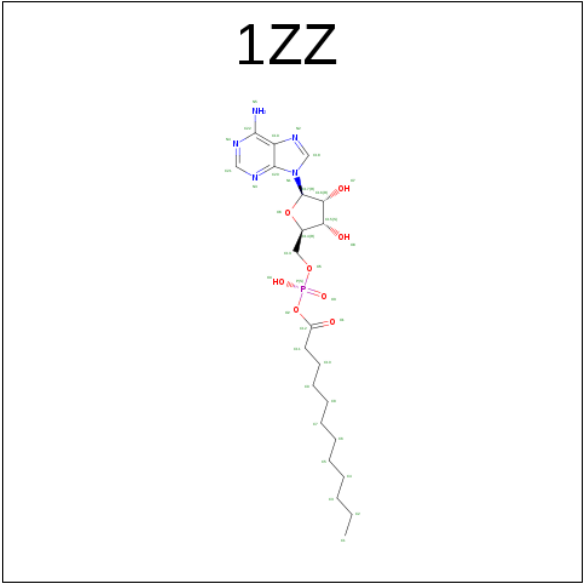
- Molecule 1 is a protein called Fatty Acyl-Adenylate Ligase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	Se	0	0	0
			4303	2729	750	804	11	9			
1	B	550	Total	C	N	O	S	Se	0	0	0
			4270	2713	744	794	11	8			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MSE	-	EXPRESSION TAG	UNP Q8FDN4
A	3	SER	-	EXPRESSION TAG	UNP Q8FDN4
A	4	LEU	-	EXPRESSION TAG	UNP Q8FDN4
A	577	GLU	-	EXPRESSION TAG	UNP Q8FDN4
A	578	GLY	-	EXPRESSION TAG	UNP Q8FDN4
A	579	HIS	-	EXPRESSION TAG	UNP Q8FDN4
A	580	HIS	-	EXPRESSION TAG	UNP Q8FDN4
A	581	HIS	-	EXPRESSION TAG	UNP Q8FDN4
A	582	HIS	-	EXPRESSION TAG	UNP Q8FDN4
A	583	HIS	-	EXPRESSION TAG	UNP Q8FDN4
A	584	HIS	-	EXPRESSION TAG	UNP Q8FDN4
B	2	MSE	-	EXPRESSION TAG	UNP Q8FDN4
B	3	SER	-	EXPRESSION TAG	UNP Q8FDN4
B	4	LEU	-	EXPRESSION TAG	UNP Q8FDN4
B	577	GLU	-	EXPRESSION TAG	UNP Q8FDN4
B	578	GLY	-	EXPRESSION TAG	UNP Q8FDN4
B	579	HIS	-	EXPRESSION TAG	UNP Q8FDN4
B	580	HIS	-	EXPRESSION TAG	UNP Q8FDN4
B	581	HIS	-	EXPRESSION TAG	UNP Q8FDN4
B	582	HIS	-	EXPRESSION TAG	UNP Q8FDN4
B	583	HIS	-	EXPRESSION TAG	UNP Q8FDN4
B	584	HIS	-	EXPRESSION TAG	UNP Q8FDN4

- Molecule 2 is 5'-O-[(S)-(DODECANOYLOXY)(HYDROXY)PHOSPHORYL]ADENOSINE (three-letter code: 1ZZ) (formula: C₂₂H₃₆N₅O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			36	22	5	8	1		
2	B	1	Total	C	N	O	P	0	0
			36	22	5	8	1		

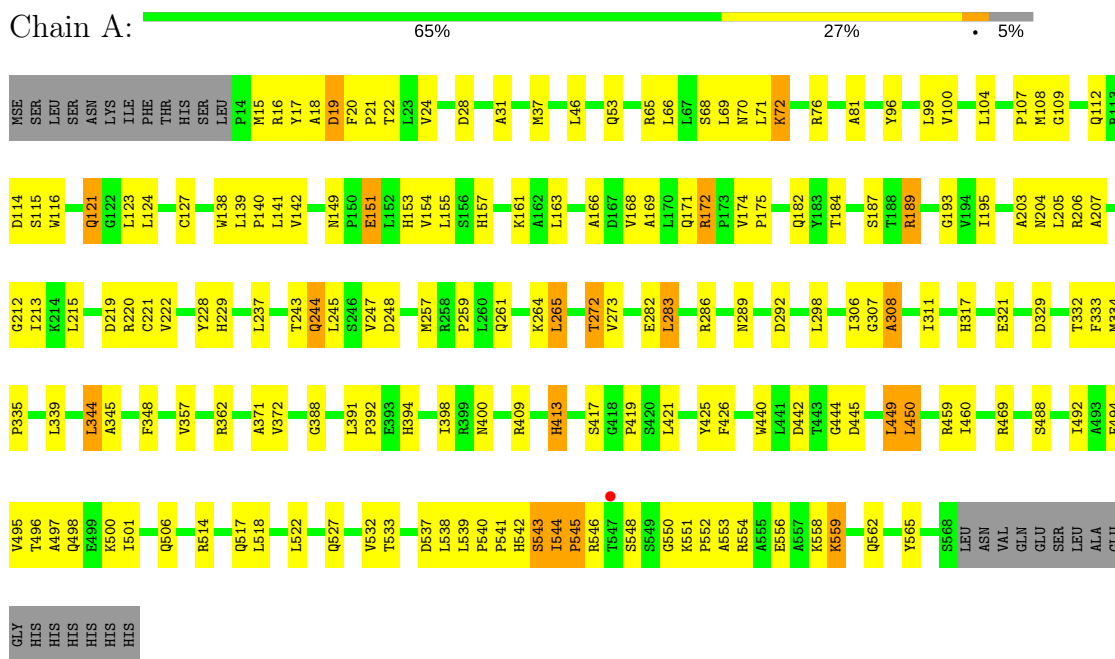
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	53	Total	O	0	0
			53	53		
3	B	34	Total	O	0	0
			34	34		

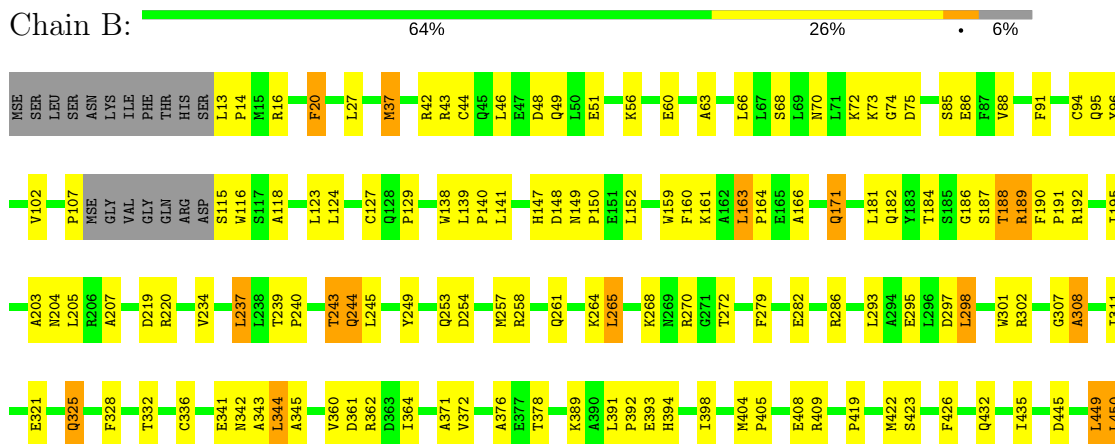
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Fatty Acyl-Adenylate Ligase



• Molecule 1: Fatty Acyl-Adenylate Ligase



G451	G452	Y453	T460	K461	I464	T485	I486	R469	E477	E481	I492	V495	T496	A497	Q498	R508	R514	Q517	L518	L519	Q527	T533	I536	D537	L538	I544	P545	R546	G550	K551	P552	A553	R554	A555	E556	R560	Y561	Q562	S568	L569	ASN	VAL	
GLN	GLU	SER	LEU	ALA	GLU	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.47Å 118.34Å 137.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.82 – 3.00 89.82 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (89.82-3.00) 99.7 (89.82-2.60)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.62Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.190 , 0.251 0.184 , 0.242	Depositor DCC
R_{free} test set	1556 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 26.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8732	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
1ZZ

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	0.40	0/4389	0.55	0/5948
1	B	0.40	0/4356	0.54	0/5906
All	All	0.40	0/8745	0.54	0/11854

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 [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	4303	0	4257	141	0
1	B	4270	0	4235	122	0
2	A	36	0	34	4	0
2	B	36	0	33	10	0
3	A	53	0	0	1	0
3	B	34	0	0	3	0
All	All	8732	0	8559	263	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 15.

The worst 5 of 263 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:243:THR:HG22	1:A:245:LEU:HG	1.37	1.05
1:A:16:ARG:HH21	1:A:19:ASP:HB3	1.20	1.03
1:A:259:PRO:HG3	1:A:283:LEU:HD13	1.39	1.02
1:B:219:ASP:OD1	1:B:272:THR:HG21	1.62	0.99
1:A:189:ARG:HH11	1:A:189:ARG:HG3	1.23	0.99

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	553/583 (95%)	522 (94%)	27 (5%)	4 (1%)	25	67
1	B	546/583 (94%)	512 (94%)	31 (6%)	3 (0%)	32	74
All	All	1099/1166 (94%)	1034 (94%)	58 (5%)	7 (1%)	28	70

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ASP
1	A	545	PRO
1	B	147	HIS
1	A	308	ALA
1	B	188	THR

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	450/467 (96%)	414 (92%)	36 (8%)	14	45
1	B	447/467 (96%)	414 (93%)	33 (7%)	16	49
All	All	897/934 (96%)	828 (92%)	69 (8%)	15	48

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	538	LEU
1	B	46	LEU
1	B	517	GLN
1	A	543	SER
1	A	565	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	394	HIS
1	A	562	GLN
1	B	517	GLN
1	A	517	GLN
1	B	95	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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

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
2	1ZZ	A	1	-	34,38,38	1.59	8 (23%)	34,52,52	2.65	11 (32%)
2	1ZZ	B	585	-	34,38,38	1.75	10 (29%)	34,52,52	2.87	12 (35%)

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
2	1ZZ	A	1	-	-	0/20/42/42	0/3/3/3
2	1ZZ	B	585	-	-	0/20/42/42	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	585	1ZZ	C19-C20	-4.13	1.31	1.40
2	A	1	1ZZ	C19-C20	-4.00	1.31	1.40
2	B	585	1ZZ	P-O4	-3.61	1.37	1.55
2	A	1	1ZZ	P-O4	-3.43	1.37	1.55
2	B	585	1ZZ	C21-N4	-3.38	1.27	1.33

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	585	1ZZ	N3-C21-N4	-11.31	119.01	128.86
2	A	1	1ZZ	N3-C21-N4	-8.94	121.07	128.86
2	A	1	1ZZ	O6-C14-C15	-4.47	96.29	105.17
2	A	1	1ZZ	O1-C12-C11	-3.76	108.83	123.68
2	B	585	1ZZ	O4-P-O3	-2.05	101.65	112.28

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	1ZZ	4	0
2	B	585	1ZZ	10	0

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	546/583 (93%)	-0.60	1 (0%) 94 85	14, 24, 47, 66	0
1	B	542/583 (92%)	-0.66	0 100 100	15, 25, 48, 70	0
All	All	1088/1166 (93%)	-0.63	1 (0%) 95 88	14, 25, 48, 70	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	547	THR	2.3

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	1ZZ	B	585	36/36	0.95	0.18	0.71	16,19,22,23	0
2	1ZZ	A	1	36/36	0.94	0.21	0.42	15,21,25,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.