wwPDB X-ray Structure Validation Summary Report (i)

Mar 9, 2026 – 04:58 AM UTC

PDB ID	:	3EH0 / pdb_00003eh0
Title	:	Crystal Structure of LpxD from Escherichia coli
Authors	:	Bartling, C.M.; Raetz, C.R.H.
Deposited on	:	2008-09-11
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:

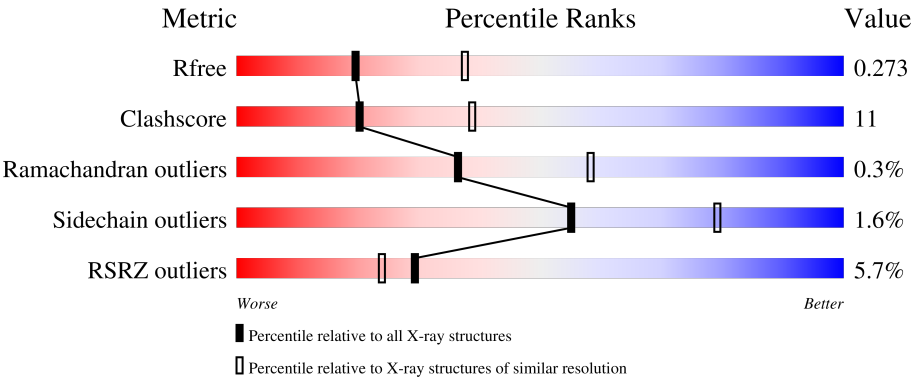
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (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	341	9% 74% 24%
1	B	341	2% 81% 18%
1	C	341	6% 73% 23%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7918 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 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	1	0
			2523	1571	449	483	20			
1	B	341	Total	C	N	O	S	0	0	0
			2515	1567	447	481	20			
1	C	341	Total	C	N	O	S	0	0	0
			2515	1567	447	481	20			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	PRO	engineered mutation	UNP P21645
B	2	ALA	PRO	engineered mutation	UNP P21645
C	2	ALA	PRO	engineered mutation	UNP P21645

- Molecule 2 is water.

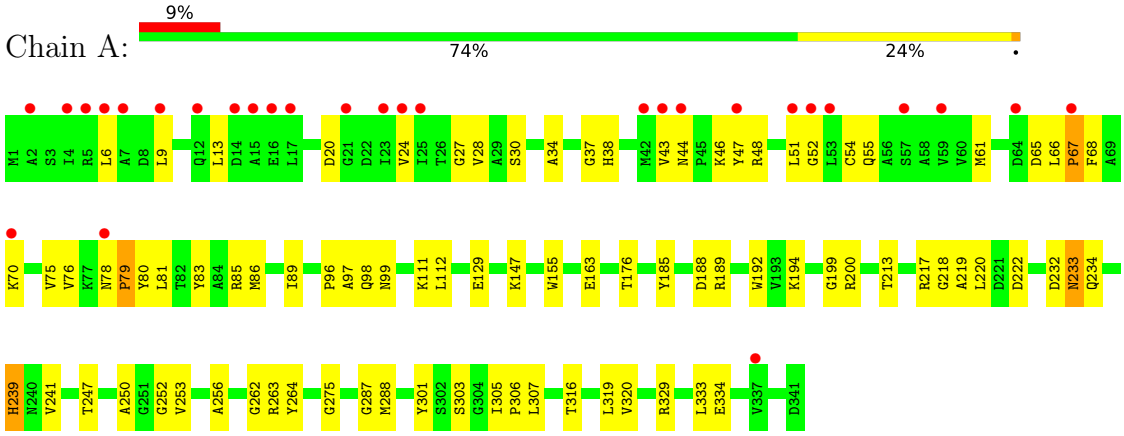
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	120	Total	O	0	0
			120	120		
2	B	123	Total	O	0	0
			123	123		
2	C	122	Total	O	0	0
			122	122		

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.

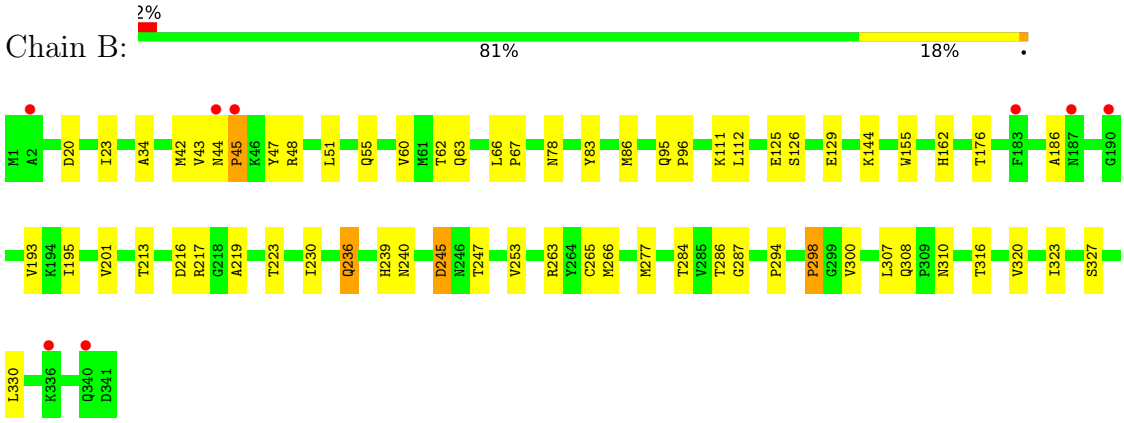
• Molecule 1: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase

Chain A:



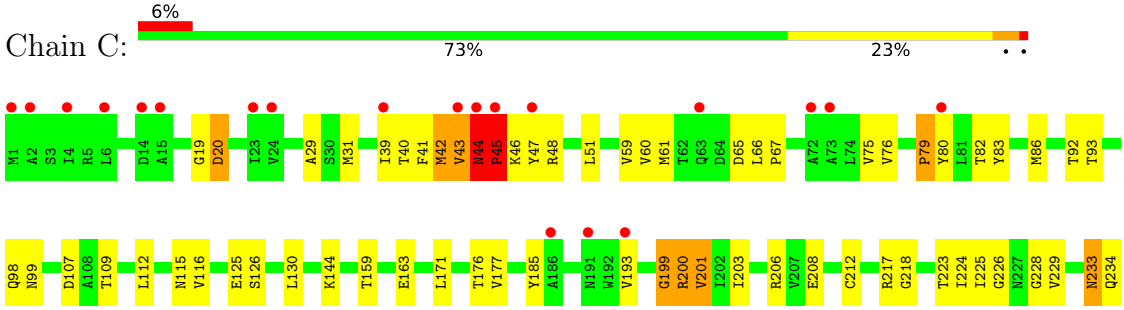
• Molecule 1: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase

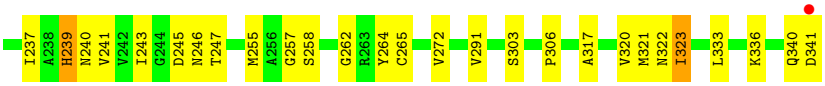
Chain B:



• Molecule 1: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase

Chain C:




I237
A238
H239
N240
V241
V242
I243
G244
D245
N246
T247
M255
A256
G257
S258
G262
R263
Y264
C265
V272
V291
S303
P306
A317
V320
M321
N322
I323
L333
K336
Q340
D341

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	157.95Å 94.17Å 103.66Å 90.00° 126.50° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60 20.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.5 (20.00-2.60) 98.3 (20.00-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.17	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 2.59Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.214 , 0.279 0.206 , 0.273	Depositor DCC
R_{free} test set	1871 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	31.4	Xtriage
Anisotropy	0.453	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7918	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.66% 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

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	5/2556 (0.2%)	1.06	9/3466 (0.3%)
1	B	0.86	4/2548 (0.2%)	1.10	10/3455 (0.3%)
1	C	0.95	7/2548 (0.3%)	1.14	14/3455 (0.4%)
All	All	0.95	16/7652 (0.2%)	1.10	33/10376 (0.3%)

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	B	0	1
1	C	0	2
All	All	0	3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	262	GLY	C-N	-27.14	0.94	1.33
1	C	199	GLY	C-N	-24.65	1.01	1.33
1	A	79	PRO	N-CD	-14.19	1.27	1.47
1	C	45	PRO	N-CD	7.94	1.58	1.47
1	B	45	PRO	N-CD	7.84	1.58	1.47

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	43	VAL	N-CA-C	-9.75	100.33	113.00
1	A	79	PRO	CA-N-CD	-9.69	98.43	112.00
1	C	306	PRO	CA-N-CD	-9.46	98.75	112.00
1	C	79	PRO	CA-N-CD	-8.70	99.82	112.00
1	C	45	PRO	CA-N-CD	-8.65	99.89	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	45	PRO	Peptide
1	C	42	MET	Peptide
1	C	44	ASN	Mainchain

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	2523	0	2558	58	1
1	B	2515	0	2554	49	1
1	C	2515	0	2553	78	0
2	A	120	0	0	0	0
2	B	123	0	0	0	1
2	C	122	0	0	0	1
All	All	7918	0	7665	172	2

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 172 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:44:ASN:HB3	1:C:47:TYR:CD2	2.01	0.95
1:B:186:ALA:HB3	1:B:193:VAL:HB	1.50	0.94
1:C:60:VAL:HG21	1:C:86:MET:HE1	1.50	0.93
1:A:44:ASN:ND2	1:A:47:TYR:CD2	2.39	0.91
1:C:243:ILE:HD11	1:C:255:MET:HE1	1.52	0.89

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:LYS:NZ	1:B:284:THR:CG2[4_546]	1.92	0.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:426:HOH:O	2:C:434:HOH:O[4_556]	2.07	0.13

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	340/341 (100%)	328 (96%)	12 (4%)	0	100	100
1	B	339/341 (99%)	327 (96%)	11 (3%)	1 (0%)	36	58
1	C	339/341 (99%)	319 (94%)	18 (5%)	2 (1%)	21	42
All	All	1018/1023 (100%)	974 (96%)	41 (4%)	3 (0%)	36	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	44	ASN
1	B	298	PRO
1	C	45	PRO

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	270/269 (100%)	265 (98%)	5 (2%)	50	75
1	B	269/269 (100%)	265 (98%)	4 (2%)	57	80
1	C	269/269 (100%)	265 (98%)	4 (2%)	57	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	808/807 (100%)	795 (98%)	13 (2%)	55 79

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	236	GLN
1	B	308	GLN
1	C	322	ASN
1	C	176	THR
1	C	203	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	173	GLN
1	C	133	ASN
1	B	239	HIS
1	C	115	ASN
1	B	173	GLN

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 oligosaccharides 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	199:GLY	C	200:ARG	N	1.01
1	A	262:GLY	C	263:ARG	N	0.94

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^{th} 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	341/341 (100%)	0.07	29 (8%)	16	13	16, 30, 110, 119	1 (0%)
1	B	341/341 (100%)	-0.39	8 (2%)	61	55	17, 31, 69, 114	0
1	C	341/341 (100%)	0.01	21 (6%)	26	21	16, 34, 93, 120	0
All	All	1023/1023 (100%)	-0.10	58 (5%)	29	24	16, 31, 97, 120	1 (0%)

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	44	ASN	6.7
1	C	44	ASN	6.2
1	B	44	ASN	5.5
1	A	70	LYS	4.9
1	A	78	ASN	4.1

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 oligosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.