



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 26, 2023 – 07:22 PM EDT

PDB ID : 3PUO  
Title : Crystal structure of dihydrodipicolinate synthase from *Pseudomonas aeruginosa* (PsDHDPS) complexed with L-lysine at 2.65 Å resolution  
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Deposited on : 2010-12-06  
Resolution : 2.65 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](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.5 (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

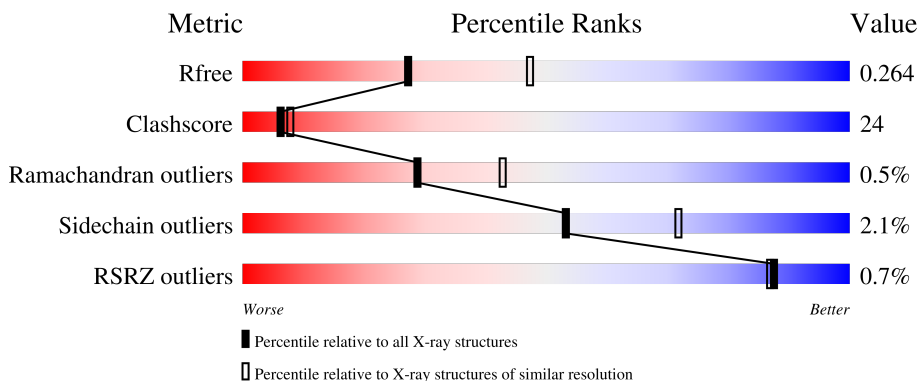
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	292	
1	B	292	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4762 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 Dihydrodipicolinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	292	2200	1382	392	412	14	0	0	0
1	B	292	2200	1382	392	412	14	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	ASP	GLU	engineered mutation	UNP D1MH64
A	60	VAL	ILE	engineered mutation	UNP D1MH64
A	234	ASP	GLU	engineered mutation	UNP D1MH64
A	279	ASP	GLU	engineered mutation	UNP D1MH64
B	34	ASP	GLU	engineered mutation	UNP D1MH64
B	60	VAL	ILE	engineered mutation	UNP D1MH64
B	234	ASP	GLU	engineered mutation	UNP D1MH64
B	279	ASP	GLU	engineered mutation	UNP D1MH64

- Molecule 2 is LYSINE (three-letter code: LYS) (formula: C<sub>6</sub>H<sub>15</sub>N<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total	C	N	O	0	0
			10	6	2	2		
2	A	1	Total	C	N	O	0	0
			10	6	2	2		
2	B	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	153	Total 153	O 153	0	0
4	B	173	Total 173	O 173	0	0

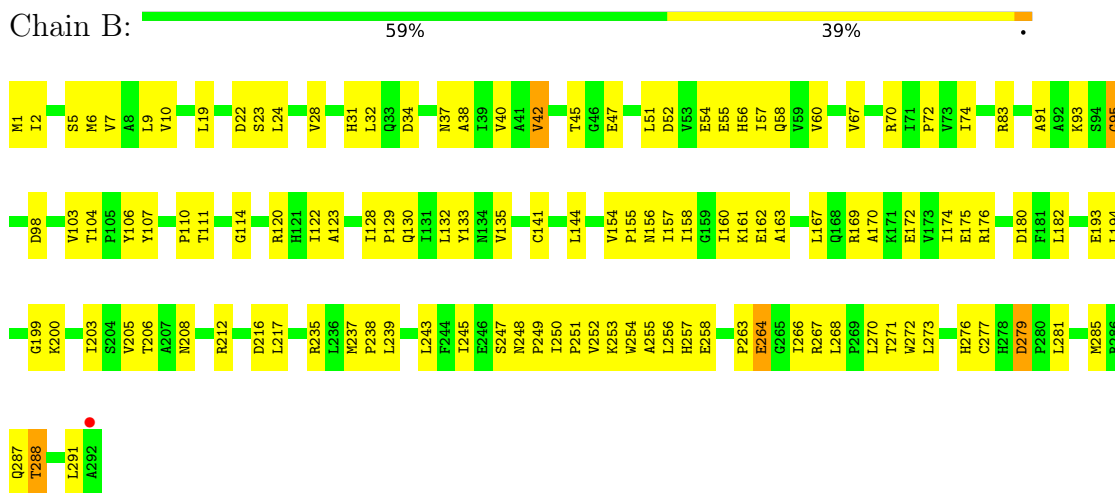
### 3 Residue-property plots [i](#)

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: Dihydrodipicolinate synthase



- Molecule 1: Dihydrodipicolinate synthase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.34Å 81.84Å 81.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.27 – 2.65 33.27 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.1 (33.27-2.65) 99.2 (33.27-2.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.54 (at 2.65Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.216 , 0.255 0.227 , 0.264	Depositor DCC
$R_{free}$ test set	830 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtrriage
Anisotropy	0.348	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 59.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.000 for -h,l,k 0.000 for -k,-h,l 0.000 for l,-k,h 0.000 for l,h,k 0.000 for k,l,h	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4762	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.81 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.1392e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.68	5/2239 (0.2%)	0.77	4/3043 (0.1%)
1	B	0.71	5/2239 (0.2%)	0.77	2/3043 (0.1%)
All	All	0.70	10/4478 (0.2%)	0.77	6/6086 (0.1%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	106	TYR	CD2-CE2	-8.37	1.26	1.39
1	B	106	TYR	CD1-CE1	-6.84	1.29	1.39
1	A	106	TYR	CD1-CE1	-6.79	1.29	1.39
1	B	106	TYR	CD2-CE2	-6.39	1.29	1.39
1	B	107	TYR	CD2-CE2	-6.35	1.29	1.39

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	279	ASP	CB-CG-OD1	6.85	124.47	118.30
1	A	106	TYR	N-CA-C	6.62	128.88	111.00
1	A	138	ARG	O-C-N	6.52	133.14	122.70
1	A	138	ARG	C-N-CA	-6.03	106.62	121.70
1	A	138	ARG	CA-C-N	-5.23	105.69	117.20

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	2200	0	2235	111	0
1	B	2200	0	2235	109	0
2	A	20	0	24	2	0
2	B	10	0	12	0	0
3	A	6	0	8	1	0
4	A	153	0	0	8	0
4	B	173	0	0	7	0
All	All	4762	0	4514	217	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 24.

The worst 5 of 217 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:B:5:SER:N	1:B:37:ASN:HD22	1.44	1.14
1:B:5:SER:H	1:B:37:ASN:ND2	1.47	1.12
1:B:111:THR:HG23	1:B:114:GLY:H	1.24	1.03
1:A:237:MET:HG3	1:A:241:LYS:HE3	1.48	0.95
1:A:103:VAL:HA	1:A:133:TYR:HB3	1.49	0.94

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	290/292 (99%)	273 (94%)	16 (6%)	1 (0%)	41	56
1	B	290/292 (99%)	278 (96%)	10 (3%)	2 (1%)	22	33
All	All	580/584 (99%)	551 (95%)	26 (4%)	3 (0%)	29	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	GLY
1	B	42	VAL
1	B	95	GLY

### 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	232/232 (100%)	227 (98%)	5 (2%)	52	70
1	B	232/232 (100%)	227 (98%)	5 (2%)	52	70
All	All	464/464 (100%)	454 (98%)	10 (2%)	53	70

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	180	ASP
1	B	279	ASP
1	B	288	THR
1	A	182	LEU
1	A	279	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	31	HIS
1	B	37	ASN
1	B	287	GLN
1	B	276	HIS
1	B	283	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

4 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	LYS	B	293	-	8,9,9	1.12	1 (12%)	9,10,10	1.07	2 (22%)
3	GOL	A	294	-	5,5,5	0.32	0	5,5,5	0.35	0
2	LYS	A	293	-	8,9,9	0.70	0	9,10,10	0.62	0
2	LYS	A	295	-	8,9,9	1.31	2 (25%)	9,10,10	1.02	1 (11%)

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	LYS	B	293	-	-	1/9/9/9	-
3	GOL	A	294	-	-	4/4/4/4	-
2	LYS	A	293	-	-	5/9/9/9	-
2	LYS	A	295	-	-	4/9/9/9	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	295	LYS	OXT-C	-2.57	1.22	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	293	LYS	OXT-C	-2.38	1.22	1.30
2	A	295	LYS	O-C	2.18	1.28	1.22

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	295	LYS	OXT-C-O	-2.54	118.33	124.09
2	B	293	LYS	OXT-C-CA	2.25	121.06	113.38
2	B	293	LYS	OXT-C-O	-2.09	119.33	124.09

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	295	LYS	C-CA-CB-CG
3	A	294	GOL	C1-C2-C3-O3
3	A	294	GOL	O2-C2-C3-O3
2	A	295	LYS	CE-CD-CG-CB
2	A	293	LYS	CE-CD-CG-CB

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	294	GOL	1	0
2	A	293	LYS	1	0
2	A	295	LYS	1	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, 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	292/292 (100%)	-0.13	3 (1%) 82 81	5, 20, 36, 48	0
1	B	292/292 (100%)	-0.14	1 (0%) 94 95	6, 19, 33, 43	0
All	All	584/584 (100%)	-0.13	4 (0%) 87 87	5, 20, 34, 48	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	276	HIS	2.5
1	A	168	GLN	2.3
1	B	292	ALA	2.3
1	A	180	ASP	2.2

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	LYS	A	295	10/10	0.66	0.36	15,24,29,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	LYS	B	293	10/10	0.77	0.25	30,33,34,35	0
3	GOL	A	294	6/6	0.79	0.34	28,28,29,30	0
2	LYS	A	293	10/10	0.80	0.25	33,33,34,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.