

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 5, 2023 – 09:44 pm GMT

PDB ID : 5M47

Title : Crystal structure of DapF from Corynebacterium glutamicum in complex with

D,L-diaminopimelate

Authors : Sagong, H.-Y.; Kim, K.-J.

Deposited on : 2016-10-18

Resolution : 2.59 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*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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

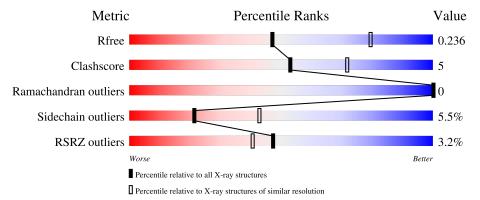
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 2.59 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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		
			3%		
1	A	283	81%	15%	••



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2154 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.

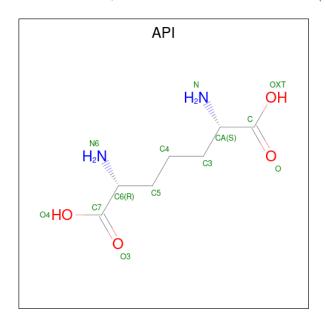
• Molecule 1 is a protein called Diaminopimelate epimerase.

Mol	Chain	Residues		Atoms					AltConf	Trace
1	Λ	280	Total	С	N	О	S	0	0	0
1	A	200	2073	1288	361	409	15	0	0	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	278	HIS	-	expression tag	UNP Q8NP73
A	279	HIS	-	expression tag	UNP Q8NP73
A	280	HIS	-	expression tag	UNP Q8NP73
A	281	HIS	-	expression tag	UNP Q8NP73
A	282	HIS	-	expression tag	UNP Q8NP73
A	283	HIS	-	expression tag	UNP Q8NP73

• Molecule 2 is 2,6-DIAMINOPIMELIC ACID (three-letter code: API) (formula: C<sub>7</sub>H<sub>14</sub>N<sub>2</sub>O<sub>4</sub>).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 13 7 2 4	0	0

#### • Molecule 3 is water.

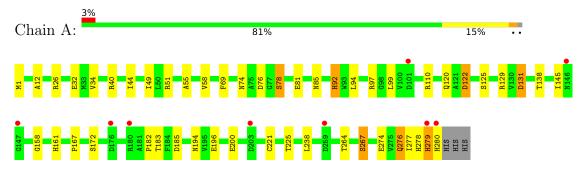
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	68	Total O 68 68	0	0



## 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: Diaminopimelate epimerase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 3 2	Depositor
Cell constants	155.69Å 155.69Å 155.69Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	110.09 - 2.59	Depositor
Resolution (A)	37.76 - 2.59	EDS
% Data completeness	97.5 (110.09-2.59)	Depositor
(in resolution range)	97.5 (37.76-2.59)	EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.34	Depositor
$< I/\sigma(I) > 1$	4.93 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
D D.	0.191 , 0.229	Depositor
$R, R_{free}$	0.199 , 0.236	DCC
$R_{free}$ test set	976 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 40.1	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.42, < L^2>=0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2154	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.54% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: API

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	Bo	nd lengths	Во	ond angles
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.92	2/2110 (0.1%)	1.13	$12/2872 \ (0.4\%)$

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$Ideal(\AA)$
1	A	274	GLU	CD-OE1	5.77	1.31	1.25
1	A	110	ARG	CZ-NH1	5.09	1.39	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	110	ARG	NE-CZ-NH2	-9.80	115.40	120.30
1	A	40	ARG	NE-CZ-NH1	7.09	123.85	120.30
1	A	131	ASP	CB-CG-OD1	-6.81	112.17	118.30
1	A	122	ASP	CB-CA-C	-5.74	98.93	110.40
1	A	110	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	A	185	ASP	CB-CG-OD2	-5.51	113.34	118.30
1	A	51	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	97	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	A	26	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	A	78	SER	N-CA-CB	-5.27	102.59	110.50
1	A	51	ARG	NE-CZ-NH1	5.22	122.91	120.30

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I	Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^o)$
	1	A	44	ILE	CB-CA-C	-5.04	101.52	111.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	278	HIS	Peptide
1	A	279	HIS	Peptide

#### 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	2073	0	2007	22	0
2	A	13	0	7	1	0
3	A	68	0	0	1	0
All	All	2154	0	2014	22	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 5.

All (22) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)
1:A:76:ASP:OD1	1:A:78:SER:HB3	1.84	0.77
1:A:81:GLU:HG3	1:A:158:GLY:O	1.94	0.67
1:A:32:GLU:N	1:A:32:GLU:OE2	2.38	0.56
1:A:76:ASP:OD1	1:A:78:SER:CB	2.55	0.53
1:A:183:THR:HG22	3:A:444:HOH:O	2.08	0.53
1:A:58:VAL:HG21	1:A:69:PHE:CE1	2.45	0.52
1:A:161:HIS:HD2	1:A:196:GLU:OE2	1.94	0.51
1:A:74:ASN:HD21	2:A:301:API:H6	1.77	0.50
1:A:167:PRO:HA	1:A:200:GLU:OE2	2.12	0.50
1:A:34:VAL:HG13	1:A:49:ILE:HD12	1.93	0.49
1:A:276:GLN:NE2	1:A:276:GLN:CA	2.74	0.49

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Atom-1	Atom-2	Interatomic	Clash
7100111 1	7100111 2	$\operatorname{distance}\left(\mathrm{\AA}\right)$	overlap (Å)
1:A:12:ALA:HB3	1:A:85:ASN:HB3	1.96	0.47
1:A:276:GLN:NE2	1:A:276:GLN:HA	2.29	0.47
1:A:94:LEU:HD23	1:A:99:LEU:HD12	1.97	0.46
1:A:129:ARG:HG3	1:A:264:THR:OG1	2.16	0.45
1:A:122:ASP:HB2	1:A:125:SER:H	1.80	0.45
1:A:145:ILE:HG12	1:A:182:PRO:HB3	1.99	0.45
1:A:221:CYS:O	1:A:225:THR:HG23	2.17	0.44
1:A:276:GLN:CA	1:A:276:GLN:HE21	2.29	0.44
1:A:92:HIS:HD2	1:A:267:SER:OG	2.01	0.43
1:A:161:HIS:CD2	1:A:194:ASN:HB2	2.54	0.43
1:A:55:ALA:HA	1:A:58:VAL:CG1	2.50	0.41

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	278/283 (98%)	265 (95%)	13 (5%)	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	220/223 (99%)	208 (94%)	12 (6%)	21 43

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	92	HIS
1	A	120	GLN
1	A	131	ASP
1	A	138	THR
1	A	172	SER
1	A	238	LEU
1	A	267	SER
1	A	276	GLN
1	A	277	ILE
1	A	279	HIS
1	A	280	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	92	HIS
1	A	120	GLN
1	A	161	HIS
1	A	186	GLN
1	A	276	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)

1 ligand is 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).

7	/[a]	Type	Chain	Pog	Link	Bo	ond leng	$ ag{ths}$	В	ond ang	les
1	VIOI	туре	Chain	rtes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
	2	API	A	301	-	10,12,12	1.01	1 (10%)	13,15,15	1.72	5 (38%)

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	API	A	301	-	-	10/14/14/14	-

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(Å)	$\operatorname{Ideal}( ext{\AA})$
2	A	301	API	OXT-C	-2.15	1.23	1.30

#### All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
2	A	301	API	O4-C7-C6	3.01	123.63	113.38
2	A	301	API	OXT-C-CA	2.94	123.40	113.38
2	A	301	API	C5-C4-C3	-2.57	101.42	113.24
2	A	301	API	O3-C7-C6	-2.28	114.08	122.14
2	A	301	API	OXT-C-O	-2.19	119.12	124.09

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	API	C4-C3-CA-C
2	A	301	API	C5-C6-C7-O4

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Mol	Chain	Res	Type	Atoms
2	A	301	API	N6-C6-C7-O4
2	A	301	API	C5-C6-C7-O3
2	A	301	API	O-C-CA-C3
2	A	301	API	OXT-C-CA-C3
2	A	301	API	C3-C4-C5-C6
2	A	301	API	N6-C6-C7-O3
2	A	301	API	O-C-CA-N
2	A	301	API	OXT-C-CA-N

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	API	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,  $95^{th}$  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 $>$	$\# \mathrm{RSRZ}{>}2$		$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	280/283 (98%)	-0.36	9 (3%) 47	40	17, 31, 59, 105	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	280	HIS	3.1
1	A	203	ASP	2.5
1	A	101	ASP	2.3
1	A	147	GLY	2.2
1	A	279	HIS	2.1
1	A	176	ASP	2.1
1	A	146	ASN	2.1
1	A	180	ARG	2.0
1	A	259	ASP	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 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,  $95^{th}$  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.



Mo	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
2	API	A	301	13/13	0.98	0.12	24,28,36,41	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

