

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

#### Mar 9, 2024 – 09:28 AM EST

PDB ID : 3WGY

Title : Crystal structure of meso-dapdh Q154L/T173I/R199M/P248S/H249N/N276

S mutant with 4-methyl-2-oxovalerate of from Clostridium tetani E88

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Deposited on : 2013-08-19

Resolution : 2.00 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

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 : 1.8.5 (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)

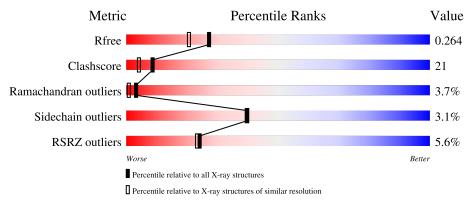
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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	326	66%	29%	
1	В	326	71%	24%	5% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	COI	В	400	-	-	X	X



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5961 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 Meso-diaminopimelate dehydrogenase.

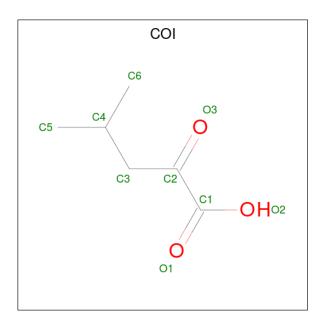
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	323	Total 2525	C 1591	N 437	O 487	S 10	0	0	0
1	В	324	Total 2531	C 1594	N 438	O 489	S 10	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	154	LEU	GLN	engineered mutation	UNP Q890V3
A	173	ILE	THR	engineered mutation	UNP Q890V3
A	199	MET	ARG	engineered mutation	UNP Q890V3
A	248	SER	PRO	engineered mutation	UNP Q890V3
A	249	ASN	HIS	engineered mutation	UNP Q890V3
A	276	SER	ASN	engineered mutation	UNP Q890V3
В	154	LEU	GLN	engineered mutation	UNP Q890V3
В	173	ILE	THR	engineered mutation	UNP Q890V3
В	199	MET	ARG	engineered mutation	UNP Q890V3
В	248	SER	PRO	engineered mutation	UNP Q890V3
В	249	ASN	HIS	engineered mutation	UNP Q890V3
В	276	SER	ASN	engineered mutation	UNP Q890V3

• Molecule 2 is 2-OXO-4-METHYLPENTANOIC ACID (three-letter code: COI) (formula:  $C_6H_{10}O_3$ ).





Mol	Chain	Residues	${f Atoms}$		ZeroOcc	AltConf
2	В	1	Total C 9 6	O 3	0	0

### • Molecule 3 is water.

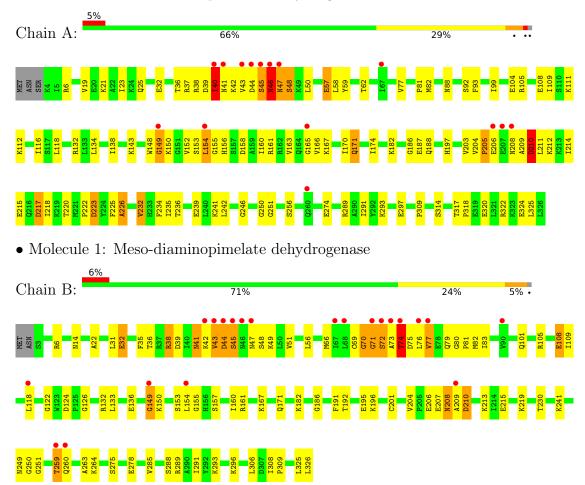
Mo	l Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	436	Total O 436 436	0	0
3	В	460	Total O 460 460	0	0



# 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: Meso-diaminopimelate dehydrogenase





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	47.19Å 135.54Å 60.79Å	Danagitan
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $110.54^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	24.40 - 2.00	Depositor
Resolution (A)	24.41 - 2.00	EDS
% Data completeness	95.5 (24.40-2.00)	Depositor
(in resolution range)	95.7 (24.41-2.00)	EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.29 (at 1.99Å)	Xtriage
Refinement program	CNS	Depositor
$R, R_{free}$	0.205 , $0.264$	Depositor
$\Pi,\ \Pi_{free}$	0.204 , $0.264$	DCC
$R_{free}$ test set	2294  reflections  (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.5	Xtriage
Anisotropy	0.509	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.31 , 58.6	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5961	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.32% 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: COI

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		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.36	0/2568	0.69	1/3456 (0.0%)	
1	В	0.35	0/2574	0.66	0/3464	
All	All	0.35	0/5142	0.67	1/6920 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	46	ASN	N-CA-C	-5.48	96.22	111.00

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	2525	0	2534	120	0
1	В	2531	0	2539	99	0
2	В	9	0	9	6	0
3	A	436	0	0	9	0
3	В	460	0	0	6	0
All	All	5961	0	5082	209	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 21.

The worst 5 of 209 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	$egin{aligned} \operatorname{Clash} \ \operatorname{overlap}\ (\mathring{\mathbf{A}}) \end{aligned}$
1:A:36:THR:HG22	1:A:38:ARG:H	1.31	0.93
1:B:186:GLY:HA3	1:B:264:LYS:HD3	1.56	0.85
1:A:163:VAL:O	1:A:166:VAL:HG22	1.77	0.83
1:A:40:ILE:H	1:A:40:ILE:HD12	1.42	0.82
1:B:154:LEU:HB3	2:B:400:COI:H4	1.63	0.81

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	321/326 (98%)	292 (91%)	18 (6%)	11 (3%)	3 1
1	В	322/326~(99%)	291 (90%)	18 (6%)	13 (4%)	3 1
All	All	643/652 (99%)	583 (91%)	36 (6%)	24 (4%)	3 1

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	SER
1	A	46	ASN
1	A	210	ASP
1	В	43	VAL
1	В	48	SER



#### 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	278/281 (99%)	270 (97%)	8 (3%)	42 43
1	В	279/281 (99%)	270 (97%)	9 (3%)	39 38
All	All	557/562 (99%)	540 (97%)	17 (3%)	40 40

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	108	GLU
1	В	241	LYS
1	A	232	VAL
1	В	32	GLU
1	В	38	ARG

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	В	208	ASN
1	В	188	GLN
1	В	41	ASN
1	В	164	GLN
1	A	258	ASN

#### 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).

Mol	Type	Chain	Dec	Link	B	ond leng	$\operatorname{gths}$	В	ond ang	gles
MIOI	Туре	Chain	nes	LIIIK	Counts   RMSZ   $\# Z  >$		# Z  > 2	Counts	RMSZ	# Z  > 2
2	COI	В	400	-	8,8,8	0.80	0	8,10,10	1.19	1 (12%)

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	COI	В	400	-	-	2/8/8/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	400	COI	O2-C1-C2	2.10	119.71	113.97

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	400	COI	C1-C2-C3-C4
2	В	400	COI	O3-C2-C3-C4

There are no ring outliers.



1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	400	COI	6	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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$\mathrm{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	323/326 (99%)	0.15	15 (4%) 32 3	31	24, 41, 73, 94	0
1	В	324/326 (99%)	0.14	21 (6%) 18 1	18	23, 40, 70, 93	0
All	All	647/652 (99%)	0.14	36 (5%) 24 2	23	23, 41, 73, 94	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	43	VAL	9.8
1	A	43	VAL	6.5
1	A	208	ASN	6.5
1	A	154	LEU	5.6
1	В	154	LEU	5.2

## 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,  $95^{th}$  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.



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
2	COI	В	400	9/9	0.38	0.46	104,105,106,107	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

