

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

Nov 5, 2023 – 10:46 pm GMT

PDB ID : 1DXF

Title : 2-dehydro-3-deoxy-galactarate aldolase from Escherichia coli in complex with

pyruvate

Authors: Izard, T.; Blackwell, N.C.

Deposited on : 2000-01-05

Resolution : 2.60 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 (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED

EDS : NOT EXECUTED

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

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

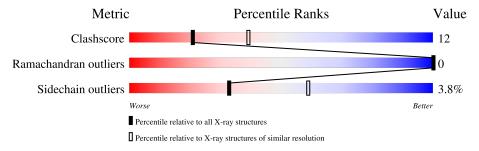
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

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

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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain				
1	A	256	71%	26%			
1	В	256	78%	19%	<del></del>		



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4080 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.

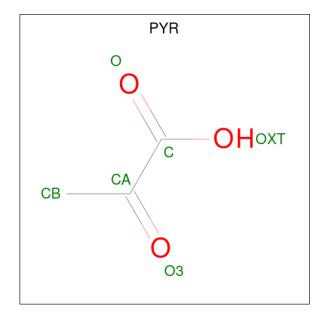
• Molecule 1 is a protein called 2-DEHYDRO-3-DEOXY-GALACTARATE ALDOLASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	A	253	Total 1911	C 1221	N 328	_	S 1	Se 2	0	0	0
1	В	253	Total 1911		N 328	_	S 1	Se 2	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	MSE	MET	modified residue	UNP P23522
A	131	MSE	MET	modified residue	UNP P23522
В	63	MSE	MET	modified residue	UNP P23522
В	131	MSE	MET	modified residue	UNP P23522

• Molecule 2 is PYRUVIC ACID (three-letter code: PYR) (formula: C<sub>3</sub>H<sub>4</sub>O<sub>3</sub>).





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

 $\bullet$  Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	В	1	Total Mg 1 1	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	118	Total O 118 118	0	0
4	В	126	Total O 126 126	0	0

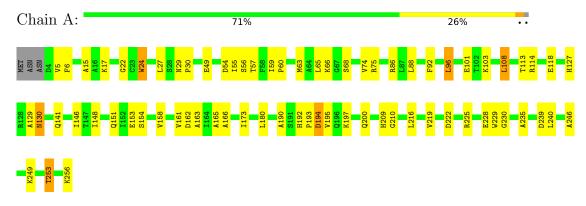


## 3 Residue-property plots (i)

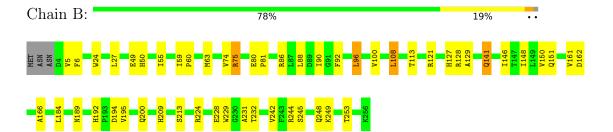
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: 2-DEHYDRO-3-DEOXY-GALACTARATE ALDOLASE



• Molecule 1: 2-DEHYDRO-3-DEOXY-GALACTARATE ALDOLASE





# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants	126.40Å 126.40Å 172.00Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	20.00 - 2.60	Depositor
% Data completeness	93.1 (20.00-2.60)	Depositor
(in resolution range)	30.1 (20.00 2.00)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
Refinement program	CNS 0.9	Depositor
$R, R_{free}$	0.173 , 0.233	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4080	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP



## 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: MG, PYR

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		RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.38	0/1952	0.60	0/2653
1	В	0.39	0/1952	0.59	0/2653
All	All	0.39	0/3904	0.60	0/5306

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	1911	0	1902	53	0
1	В	1911	0	1902	41	0
2	A	6	0	0	1	0
2	В	6	0	0	0	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	A	118	0	0	4	0
4	В	126	0	0	3	0
All	All	4080	0	3804	93	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 12.



All (93) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:225:ARG:O	1:A:228:GLU:HG2	1.80	0.82	
1:A:192:HIS:ND1	1:A:194:ASP:HB2	1.99	0.77	
1:A:88:LEU:HD11	1:A:113:THR:HA	1.70	0.74	
1:B:244:ARG:HH12	1:B:248:GLN:HE21	1.32	0.73	
1:B:88:LEU:HD11	1:B:113:THR:HA	1.70	0.72	
1:A:219:VAL:HB	1:A:222:ASP:OD2	1.89	0.71	
1:A:75:ARG:HG2	1:A:96:LEU:HB3	1.70	0.71	
1:B:244:ARG:HH12	1:B:248:GLN:NE2	1.91	0.68	
1:B:75:ARG:HG2	1:B:96:LEU:HB3	1.75	0.68	
1:A:103:LYS:NZ	1:A:103:LYS:HB3	2.10	0.67	
1:B:50:HIS:HE1	4:B:2105:HOH:O	1.77	0.66	
1:B:166:ALA:HB2	1:B:209:HIS:CD2	2.30	0.66	
1:A:166:ALA:HB2	1:A:209:HIS:CD2	2.31	0.65	
1:A:166:ALA:HB2	1:A:209:HIS:HD2	1.62	0.65	
1:B:127:HIS:CE1	1:B:129:ALA:HB3	2.32	0.65	
1:A:113:THR:HB	1:A:146:ILE:HG21	1.81	0.61	
1:B:245:SER:O	1:B:249:LYS:HD3	1.99	0.61	
1:A:153:GLU:HA	1:A:180:LEU:HD23	1.81	0.61	
1:B:127:HIS:ND1	1:B:129:ALA:HB3	2.16	0.60	
1:A:130:ASN:HD22	1:A:130:ASN:C	2.05	0.60	
1:A:230:GLY:HA3	4:A:2111:HOH:O	2.02	0.59	
1:B:249:LYS:O	1:B:253:THR:HG23	2.02	0.59	
1:B:108:LEU:HD22	4:B:2053:HOH:O	2.05	0.57	
1:B:90:ILE:O	1:B:128:ARG:NH1	2.34	0.57	
1:A:24:TRP:HZ2	1:A:75:ARG:NH1	2.03	0.56	
1:A:192:HIS:CE1	1:A:194:ASP:HB2	2.40	0.55	
1:B:141:GLN:OE1	1:B:141:GLN:HA	2.07	0.54	
1:B:75:ARG:HH11	1:B:151:GLN:HE22	1.54	0.54	
1:B:49:GLU:HB3	1:B:75:ARG:HE	1.73	0.53	
1:B:24:TRP:HZ2	1:B:75:ARG:NH1	2.06	0.53	
1:B:200:GLN:HG2	1:B:229:TRP:CE3	2.44	0.52	
1:A:103:LYS:HD3	1:A:163:ALA:HB1	1.91	0.51	
1:A:127:HIS:CE1	1:A:129:ALA:HB3	2.46	0.51	
1:A:239:ASP:OD1	1:A:240:LEU:N	2.44	0.51	
1:B:59:ILE:HB	1:B:60:PRO:HD3	1.93	0.51	
1:A:75:ARG:HH11	1:A:151:GLN:HE22	1.57	0.51	
1:A:162:ASP:HB2	4:A:2090:HOH:O	2.11	0.50	
1:A:113:THR:HG21	1:A:148:ILE:HD11	1.94	0.50	
1:A:55:ILE:HG12	4:A:2034:HOH:O	2.12	0.49	
1:B:244:ARG:NH1	1:B:248:GLN:HE21	2.08	0.48	

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Continued from previ		Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \ ({\rm \AA})$	overlap (Å)
1:A:108:LEU:HD22	4:A:2050:HOH:O	2.14	0.48
1:A:114:ARG:HD3	1:A:118:GLU:OE2	2.12	0.48
1:A:154:SER:O	1:A:158:VAL:HG23	2.12	0.48
1:B:213:SER:OG	1:B:231:ALA:HA	2.14	0.48
1:A:193:PRO:O	1:A:197:LYS:HG3	2.14	0.48
1:A:103:LYS:HB3	1:A:103:LYS:HZ2	1.77	0.48
1:B:113:THR:HG21	1:B:148:ILE:HD11	1.96	0.47
1:B:192:HIS:CD2	1:B:194:ASP:H	2.33	0.47
1:B:232:THR:HG23	4:B:2122:HOH:O	2.15	0.47
1:A:127:HIS:H	1:A:130:ASN:HD21	1.62	0.47
1:B:224:ARG:HG2	1:B:224:ARG:NH1	2.29	0.47
1:A:130:ASN:C	1:A:130:ASN:ND2	2.68	0.46
1:B:59:ILE:CG2	1:B:63:MSE:HE3	2.45	0.46
1:A:65:LEU:O	1:A:68:SER:HB3	2.16	0.46
1:A:74:VAL:HB	1:A:92:PHE:CE1	2.51	0.45
1:B:184:LEU:HD12	1:B:195:VAL:HG22	1.98	0.45
1:A:49:GLU:HB3	1:A:75:ARG:HE	1.81	0.45
1:A:6:PHE:CD2	1:A:141:GLN:HB3	2.51	0.45
1:A:57:THR:O	1:A:60:PRO:HD2	2.16	0.45
1:A:59:ILE:HB	1:A:60:PRO:HD3	1.98	0.45
1:A:5:VAL:HG12	1:A:6:PHE:CD1	2.52	0.44
1:B:74:VAL:HB	1:B:92:PHE:CE1	2.53	0.44
1:B:75:ARG:HD3	1:B:151:GLN:HE22	1.82	0.44
1:A:15:ALA:C	1:A:17:LYS:H	2.22	0.44
1:B:81:PRO:HG3	1:B:108:LEU:HD21	2.00	0.44
1:B:113:THR:HB	1:B:146:ILE:HG21	2.01	0.43
1:A:103:LYS:NZ	1:A:103:LYS:CB	2.81	0.43
1:A:54:ASP:OD1	1:A:56:SER:OG	2.33	0.43
1:A:59:ILE:O	1:A:63:MSE:HG3	2.19	0.43
1:B:88:LEU:HD13	1:B:121:ARG:CD	2.49	0.43
1:A:190:ALA:O	1:A:195:VAL:HB	2.18	0.43
1:A:200:GLN:HB2	1:A:229:TRP:CZ3	2.54	0.43
1:B:192:HIS:HD2	1:B:194:ASP:HB2	1.84	0.42
1:B:5:VAL:HG12	1:B:6:PHE:CD1	2.54	0.42
1:A:103:LYS:HB3	1:A:103:LYS:HZ3	1.81	0.42
1:A:249:LYS:O	1:A:253:THR:CG2	2.67	0.42
1:A:55:ILE:HG13	1:A:86:ARG:NH2	2.34	0.42
1:A:216:LEU:HD23	2:A:501:PYR:CB	2.50	0.42
1:A:29:ASN:HB2	1:A:30:PRO:HD2	2.02	0.41
1:A:165:ALA:HA	1:A:173:ILE:HD11	2.02	0.41
1:B:27:LEU:HD23	1:B:27:LEU:HA	1.90	0.41

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Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:63:MSE:HA	1:A:66:LYS:HD2	2.01	0.41
1:B:88:LEU:HD13	1:B:121:ARG:HD2	2.02	0.41
1:B:55:ILE:HD12	1:B:86:ARG:NH2	2.35	0.41
1:B:75:ARG:HD3	1:B:151:GLN:NE2	2.35	0.41
1:A:17:LYS:HE3	1:A:210:GLY:O	2.21	0.41
1:A:22:GLY:O	1:A:235:ALA:HA	2.20	0.41
1:A:27:LEU:HD23	1:A:27:LEU:HA	1.96	0.40
1:B:224:ARG:HG2	1:B:224:ARG:HH11	1.85	0.40
1:A:246:ALA:HB1	1:B:242:VAL:HG13	2.04	0.40
1:A:161:VAL:HG13	1:A:162:ASP:N	2.36	0.40
1:B:100:VAL:HG21	1:B:150:VAL:HB	2.04	0.40
1:B:161:VAL:HG13	1:B:162:ASP:N	2.36	0.40

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	Perce	ntiles
1	A	251/256 (98%)	233 (93%)	18 (7%)	0	100	100
1	В	251/256 (98%)	241 (96%)	10 (4%)	0	100	100
All	All	502/512 (98%)	474 (94%)	28 (6%)	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	200/201 (100%)	192 (96%)	8 (4%)	31	57	
1	В	200/201 (100%)	193 (96%)	7 (4%)	36	62	
All	All	400/402 (100%)	385 (96%)	15 (4%)	33	59	

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	TRP
1	A	96	LEU
1	A	101	GLU
1	A	108	LEU
1	A	130	ASN
1	A	194	ASP
1	A	253	THR
1	A	256	LYS
1	В	75	ARG
1	В	80	GLU
1	В	96	LEU
1	В	108	LEU
1	В	141	GLN
1	В	189	ASN
1	В	228	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	29	ASN
1	A	130	ASN
1	A	151	GLN
1	A	156	GLN
1	A	200	GLN
1	A	204	ASN
1	A	209	HIS
1	A	248	GLN
1	В	50	HIS
1	В	151	GLN
1	В	156	GLN
1	В	160	ASN

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Mol	Chain	Res	Type
1	В	189	ASN
1	В	192	HIS
1	В	209	HIS
1	В	248	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)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	Tuno	Chain	in Res Link		В	ond leng	${ m gths}$	В	ond ang	gles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PYR	A	501	3	5,5,5	1.50	1 (20%)	3,6,6	1.68	1 (33%)
2	PYR	В	501	3	5,5,5	1.42	1 (20%)	3,6,6	1.60	1 (33%)

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	PYR	A	501	3	-	0/4/4/4	-
2	PYR	В	501	3	-	0/4/4/4	=

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

Mol	Chain	$\operatorname{Res}$	Type	Atoms	$\mathbf{Z}$	Observed(A)	$\operatorname{Ideal}( ext{\AA})$
2	A	501	PYR	OXT-C	-2.70	1.22	1.30
2	В	501	PYR	OXT-C	-2.52	1.23	1.30

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

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	501	PYR	OXT-C-CA	2.35	120.41	113.97
2	В	501	PYR	OXT-C-CA	2.23	120.07	113.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	PYR	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)

EDS was not executed - this section is therefore empty.

#### 6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

#### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

