



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:41 PM UTC

PDB ID : 4ONV / pdb_00004onv
Title : Crystal structure of YagE, a KDG aldolase protein in complex with 2-Keto-3-deoxy gluconate
Authors : Manoj Kumar, P.; Bhaskar, V.; Manicka, S.; Krishnaswamy, S.
Deposited on : 2014-01-29
Resolution : 2.57 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
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

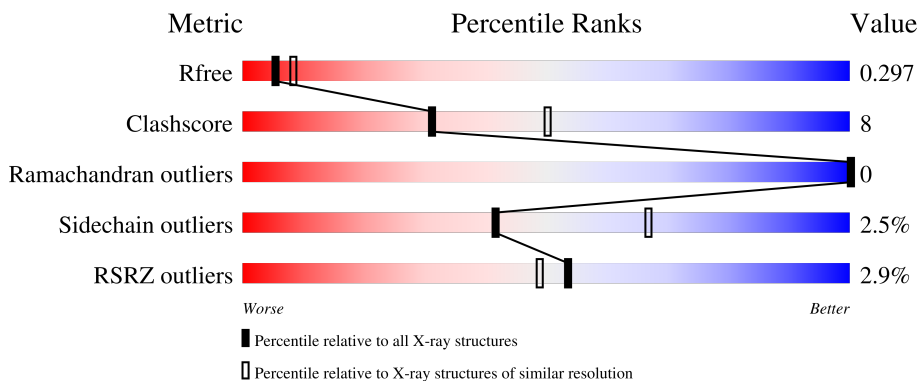
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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 $\leq 5\%$. 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	343	 4% 77% 10% 13%
1	B	343	 2% 75% 11% 13%
1	C	343	 2% 76% 10% 13%
1	D	343	 2% 77% 8% 13%

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	EDO	D	402	-	-	X	-
3	GOL	B	405	-	X	X	-
3	GOL	B	408	-	-	X	-
4	KDG	A	406	-	-	X	-
4	KDG	C	408	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9430 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 Probable 2-keto-3-deoxy-galactonate aldolase YagE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	298	2259	1446	386	421	6	0	0	0
1	B	298	2260	1447	387	420	6	0	0	0
1	C	298	2268	1451	389	422	6	0	1	0
1	D	298	2261	1447	387	421	6	0	0	0

There are 164 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	expression tag	UNP P75682
A	-16	GLY	-	expression tag	UNP P75682
A	-15	SER	-	expression tag	UNP P75682
A	-14	SER	-	expression tag	UNP P75682
A	-13	HIS	-	expression tag	UNP P75682
A	-12	HIS	-	expression tag	UNP P75682
A	-11	HIS	-	expression tag	UNP P75682
A	-10	HIS	-	expression tag	UNP P75682
A	-9	HIS	-	expression tag	UNP P75682
A	-8	HIS	-	expression tag	UNP P75682
A	-7	SER	-	expression tag	UNP P75682
A	-6	ALA	-	expression tag	UNP P75682
A	-5	GLY	-	expression tag	UNP P75682
A	-4	GLU	-	expression tag	UNP P75682
A	-3	ASN	-	expression tag	UNP P75682
A	-2	LEU	-	expression tag	UNP P75682
A	-1	TYR	-	expression tag	UNP P75682
A	0	PHE	-	expression tag	UNP P75682
A	1	GLN	-	expression tag	UNP P75682
A	2	GLY	-	expression tag	UNP P75682
A	3	GLN	-	expression tag	UNP P75682

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Chain	Residue	Modelled	Actual	Comment	Reference
A	4	GLN	-	expression tag	UNP P75682
A	5	GLY	-	expression tag	UNP P75682
A	6	ASP	-	expression tag	UNP P75682
A	7	LEU	-	expression tag	UNP P75682
A	310	CYS	-	expression tag	UNP P75682
A	311	GLY	-	expression tag	UNP P75682
A	312	ARG	-	expression tag	UNP P75682
A	313	THR	-	expression tag	UNP P75682
A	314	ARG	-	expression tag	UNP P75682
A	315	ALA	-	expression tag	UNP P75682
A	316	PRO	-	expression tag	UNP P75682
A	317	PRO	-	expression tag	UNP P75682
A	318	PRO	-	expression tag	UNP P75682
A	319	PRO	-	expression tag	UNP P75682
A	320	PRO	-	expression tag	UNP P75682
A	321	LEU	-	expression tag	UNP P75682
A	322	ARG	-	expression tag	UNP P75682
A	323	SER	-	expression tag	UNP P75682
A	324	GLY	-	expression tag	UNP P75682
A	325	CYS	-	expression tag	UNP P75682
B	-17	MET	-	expression tag	UNP P75682
B	-16	GLY	-	expression tag	UNP P75682
B	-15	SER	-	expression tag	UNP P75682
B	-14	SER	-	expression tag	UNP P75682
B	-13	HIS	-	expression tag	UNP P75682
B	-12	HIS	-	expression tag	UNP P75682
B	-11	HIS	-	expression tag	UNP P75682
B	-10	HIS	-	expression tag	UNP P75682
B	-9	HIS	-	expression tag	UNP P75682
B	-8	HIS	-	expression tag	UNP P75682
B	-7	SER	-	expression tag	UNP P75682
B	-6	ALA	-	expression tag	UNP P75682
B	-5	GLY	-	expression tag	UNP P75682
B	-4	GLU	-	expression tag	UNP P75682
B	-3	ASN	-	expression tag	UNP P75682
B	-2	LEU	-	expression tag	UNP P75682
B	-1	TYR	-	expression tag	UNP P75682
B	0	PHE	-	expression tag	UNP P75682
B	1	GLN	-	expression tag	UNP P75682
B	2	GLY	-	expression tag	UNP P75682
B	3	GLN	-	expression tag	UNP P75682
B	4	GLN	-	expression tag	UNP P75682

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	GLY	-	expression tag	UNP P75682
B	6	ASP	-	expression tag	UNP P75682
B	7	LEU	-	expression tag	UNP P75682
B	310	CYS	-	expression tag	UNP P75682
B	311	GLY	-	expression tag	UNP P75682
B	312	ARG	-	expression tag	UNP P75682
B	313	THR	-	expression tag	UNP P75682
B	314	ARG	-	expression tag	UNP P75682
B	315	ALA	-	expression tag	UNP P75682
B	316	PRO	-	expression tag	UNP P75682
B	317	PRO	-	expression tag	UNP P75682
B	318	PRO	-	expression tag	UNP P75682
B	319	PRO	-	expression tag	UNP P75682
B	320	PRO	-	expression tag	UNP P75682
B	321	LEU	-	expression tag	UNP P75682
B	322	ARG	-	expression tag	UNP P75682
B	323	SER	-	expression tag	UNP P75682
B	324	GLY	-	expression tag	UNP P75682
B	325	CYS	-	expression tag	UNP P75682
C	-17	MET	-	expression tag	UNP P75682
C	-16	GLY	-	expression tag	UNP P75682
C	-15	SER	-	expression tag	UNP P75682
C	-14	SER	-	expression tag	UNP P75682
C	-13	HIS	-	expression tag	UNP P75682
C	-12	HIS	-	expression tag	UNP P75682
C	-11	HIS	-	expression tag	UNP P75682
C	-10	HIS	-	expression tag	UNP P75682
C	-9	HIS	-	expression tag	UNP P75682
C	-8	HIS	-	expression tag	UNP P75682
C	-7	SER	-	expression tag	UNP P75682
C	-6	ALA	-	expression tag	UNP P75682
C	-5	GLY	-	expression tag	UNP P75682
C	-4	GLU	-	expression tag	UNP P75682
C	-3	ASN	-	expression tag	UNP P75682
C	-2	LEU	-	expression tag	UNP P75682
C	-1	TYR	-	expression tag	UNP P75682
C	0	PHE	-	expression tag	UNP P75682
C	1	GLN	-	expression tag	UNP P75682
C	2	GLY	-	expression tag	UNP P75682
C	3	GLN	-	expression tag	UNP P75682
C	4	GLN	-	expression tag	UNP P75682
C	5	GLY	-	expression tag	UNP P75682

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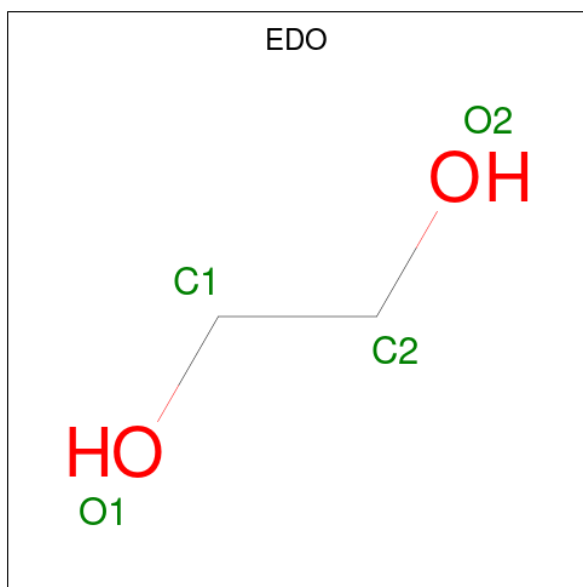
Chain	Residue	Modelled	Actual	Comment	Reference
C	6	ASP	-	expression tag	UNP P75682
C	7	LEU	-	expression tag	UNP P75682
C	310	CYS	-	expression tag	UNP P75682
C	311	GLY	-	expression tag	UNP P75682
C	312	ARG	-	expression tag	UNP P75682
C	313	THR	-	expression tag	UNP P75682
C	314	ARG	-	expression tag	UNP P75682
C	315	ALA	-	expression tag	UNP P75682
C	316	PRO	-	expression tag	UNP P75682
C	317	PRO	-	expression tag	UNP P75682
C	318	PRO	-	expression tag	UNP P75682
C	319	PRO	-	expression tag	UNP P75682
C	320	PRO	-	expression tag	UNP P75682
C	321	LEU	-	expression tag	UNP P75682
C	322	ARG	-	expression tag	UNP P75682
C	323	SER	-	expression tag	UNP P75682
C	324	GLY	-	expression tag	UNP P75682
C	325	CYS	-	expression tag	UNP P75682
D	-17	MET	-	expression tag	UNP P75682
D	-16	GLY	-	expression tag	UNP P75682
D	-15	SER	-	expression tag	UNP P75682
D	-14	SER	-	expression tag	UNP P75682
D	-13	HIS	-	expression tag	UNP P75682
D	-12	HIS	-	expression tag	UNP P75682
D	-11	HIS	-	expression tag	UNP P75682
D	-10	HIS	-	expression tag	UNP P75682
D	-9	HIS	-	expression tag	UNP P75682
D	-8	HIS	-	expression tag	UNP P75682
D	-7	SER	-	expression tag	UNP P75682
D	-6	ALA	-	expression tag	UNP P75682
D	-5	GLY	-	expression tag	UNP P75682
D	-4	GLU	-	expression tag	UNP P75682
D	-3	ASN	-	expression tag	UNP P75682
D	-2	LEU	-	expression tag	UNP P75682
D	-1	TYR	-	expression tag	UNP P75682
D	0	PHE	-	expression tag	UNP P75682
D	1	GLN	-	expression tag	UNP P75682
D	2	GLY	-	expression tag	UNP P75682
D	3	GLN	-	expression tag	UNP P75682
D	4	GLN	-	expression tag	UNP P75682
D	5	GLY	-	expression tag	UNP P75682
D	6	ASP	-	expression tag	UNP P75682

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Chain	Residue	Modelled	Actual	Comment	Reference
D	7	LEU	-	expression tag	UNP P75682
D	310	CYS	-	expression tag	UNP P75682
D	311	GLY	-	expression tag	UNP P75682
D	312	ARG	-	expression tag	UNP P75682
D	313	THR	-	expression tag	UNP P75682
D	314	ARG	-	expression tag	UNP P75682
D	315	ALA	-	expression tag	UNP P75682
D	316	PRO	-	expression tag	UNP P75682
D	317	PRO	-	expression tag	UNP P75682
D	318	PRO	-	expression tag	UNP P75682
D	319	PRO	-	expression tag	UNP P75682
D	320	PRO	-	expression tag	UNP P75682
D	321	LEU	-	expression tag	UNP P75682
D	322	ARG	-	expression tag	UNP P75682
D	323	SER	-	expression tag	UNP P75682
D	324	GLY	-	expression tag	UNP P75682
D	325	CYS	-	expression tag	UNP P75682

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



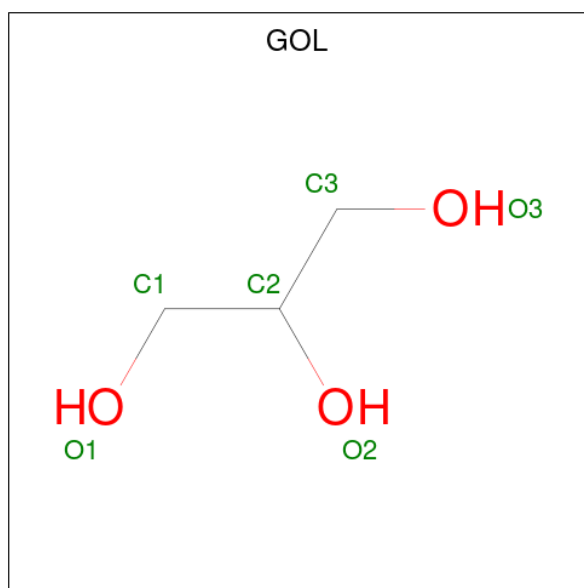
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

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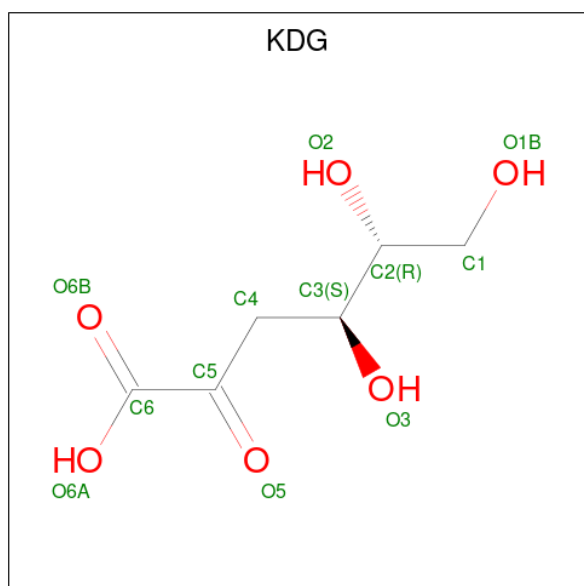
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is 2-KETO-3-DEOXYGLUCONATE (CCD ID: KDG) (formula: C₆H₁₀O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		

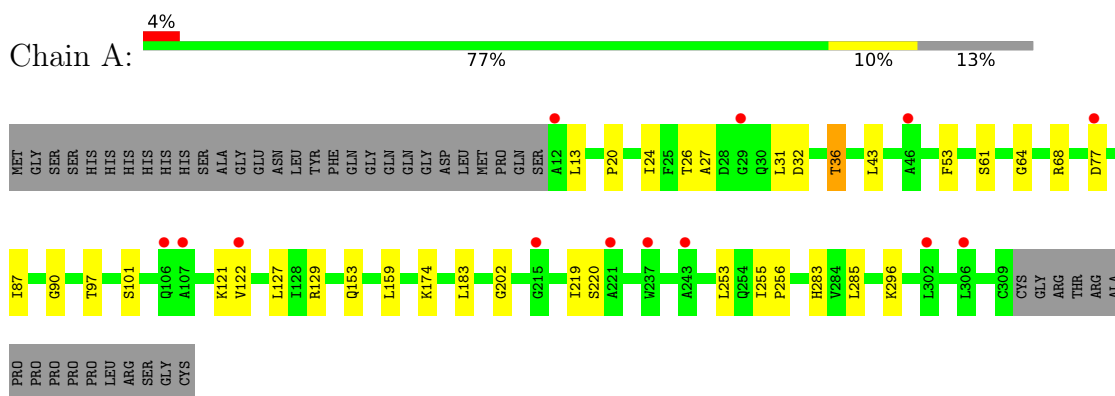
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	48	Total	O	0	0
			48	48		
5	B	59	Total	O	0	0
			59	59		
5	C	41	Total	O	0	0
			41	41		
5	D	52	Total	O	0	0
			52	52		

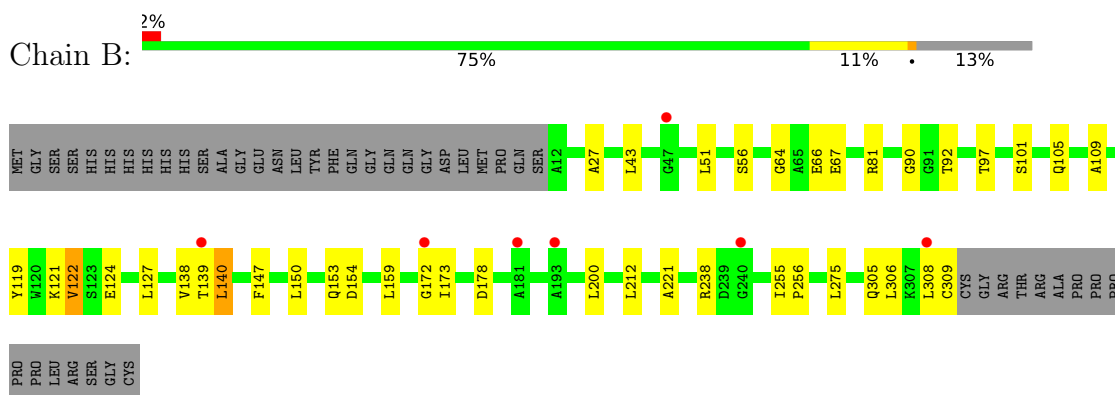
3 Residue-property plots [i](#)

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.

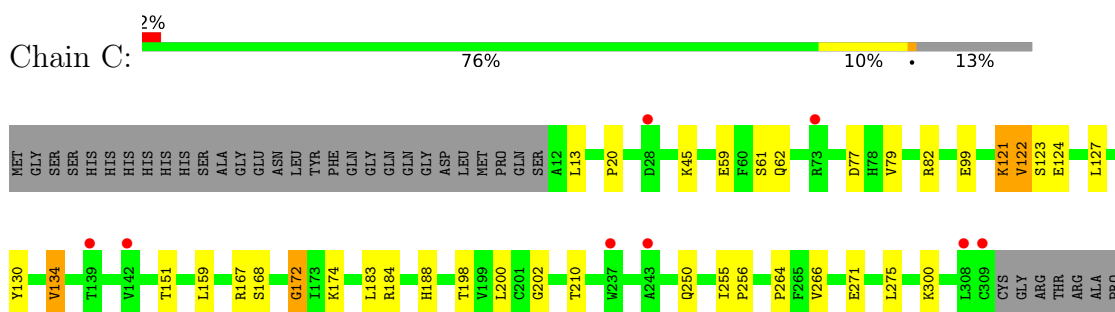
- Molecule 1: Probable 2-keto-3-deoxy-galactonate aldolase YagE



- Molecule 1: Probable 2-keto-3-deoxy-galactonate aldolase YagE




- Molecule 1: Probable 2-keto-3-deoxy-galactonate aldolase YagE



PRO
PRO
PRO
PRO
LEU
ARG
SER
GLY
CYS

- Molecule 1: Probable 2-keto-3-deoxy-galactonate aldolase YagE

Chain D: 

MET
GLY
SER
SER
HIS
HIS
HIS
HIS
HIS
HIS
HIS
HIS
ALA
GLY
GLU
ASM
LEU
TYR
PHE
GLN
GLY
GLM
GLN
GLY
ASP
LEU
MET
PRO
GLN
SER
A12
P20
L43
E69
A72
R73
T92
S101
A109
P117
Y118
Y119
W120
K121
V122
S123
E124
L127
Y130
V134

L140
T151
G152
L159
S168
G172
I173
K174
S195
T198
A226
R238
A243
Q250
I255
P256
Y259
P264
L285
K300
Q304
C309
CYS
GLY
ARG
THR
ARG
ALA
PRO
PRO
PRO
PRO
PRO
LEU
ARG
SER
GLY
CYS

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	141.17Å 155.41Å 55.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.79 – 2.57 19.79 – 2.57	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.79-2.57) 98.9 (19.79-2.57)	Depositor EDS
R_{merge}	0.41	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.56Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.247 , 0.284 0.256 , 0.297	Depositor DCC
R_{free} test set	1970 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtrriage
Anisotropy	0.210	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9430	wwPDB-VP
Average B, all atoms (Å ²)	22.0	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 45.08 % 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 1.3923e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: EDO, GOL, KDG

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	0.82	0/2307	0.95	2/3144 (0.1%)
1	B	0.82	0/2308	0.95	2/3145 (0.1%)
1	C	0.82	0/2316	0.96	1/3155 (0.0%)
1	D	0.84	0/2309	0.98	5/3147 (0.2%)
All	All	0.82	0/9240	0.96	10/12591 (0.1%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	300	LYS	CA-CB-CG	6.75	127.60	114.10
1	D	285	LEU	CA-C-N	-5.42	114.80	120.38
1	D	285	LEU	C-N-CA	-5.42	114.80	120.38
1	B	173	ILE	N-CA-C	5.37	114.94	108.06
1	D	173	ILE	N-CA-C	5.37	114.93	108.06

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	2259	0	2272	36	0
1	B	2260	0	2283	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2268	0	2286	36	0
1	D	2261	0	2280	33	0
2	A	4	0	6	2	0
2	B	16	0	24	5	0
2	C	24	0	36	4	0
2	D	16	0	24	7	0
3	A	24	0	32	1	0
3	B	24	0	32	14	0
3	C	6	0	8	3	0
3	D	24	0	32	5	0
4	A	11	0	9	11	0
4	B	11	0	9	5	0
4	C	11	0	9	9	0
4	D	11	0	9	2	0
5	A	48	0	0	9	0
5	B	59	0	0	12	0
5	C	41	0	0	8	0
5	D	52	0	0	10	0
All	All	9430	0	9351	153	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 8.

The worst 5 of 153 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:A:87:ILE:HD13	5:A:528:HOH:O	1.41	1.17
1:C:61:SER:O	1:D:92:THR:HG23	1.42	1.16
1:A:53:PHE:HB2	5:A:528:HOH:O	1.56	1.03
1:A:174:LYS:HE2	4:A:406:KDG:O3	1.62	0.99
1:C:121:LYS:HE2	1:C:151:THR:O	1.71	0.91

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	296/343 (86%)	290 (98%)	6 (2%)	0	100	100
1	B	296/343 (86%)	289 (98%)	7 (2%)	0	100	100
1	C	297/343 (87%)	290 (98%)	7 (2%)	0	100	100
1	D	296/343 (86%)	289 (98%)	7 (2%)	0	100	100
All	All	1185/1372 (86%)	1158 (98%)	27 (2%)	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	240/280 (86%)	235 (98%)	5 (2%)	47	71
1	B	242/280 (86%)	236 (98%)	6 (2%)	42	67
1	C	242/280 (86%)	234 (97%)	8 (3%)	33	59
1	D	242/280 (86%)	237 (98%)	5 (2%)	47	71
All	All	966/1120 (86%)	942 (98%)	24 (2%)	42	67

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	121	LYS
1	C	200	LEU
1	C	134	VAL
1	C	250	GLN
1	B	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	188	HIS
1	B	209	ASN
1	D	257	GLN
1	C	298	GLN
1	D	102	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](#)

32 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	EDO	C	402	-	3,3,3	0.58	0	2,2,2	0.25	0
3	GOL	A	404	-	5,5,5	0.66	0	5,5,5	0.46	0
4	KDG	D	409	1	10,10,11	0.93	0	12,12,14	1.64	2 (16%)
3	GOL	D	406	-	5,5,5	0.69	0	5,5,5	0.70	0
2	EDO	B	404	-	3,3,3	0.51	0	2,2,2	0.23	0
2	EDO	C	407	-	3,3,3	0.42	0	2,2,2	0.37	0
2	EDO	C	401	-	3,3,3	0.36	0	2,2,2	0.28	0
2	EDO	D	402	-	3,3,3	0.41	0	2,2,2	0.37	0
4	KDG	C	408	1	10,10,11	0.82	0	12,12,14	1.69	3 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	B	407	-	5,5,5	0.65	0	5,5,5	0.74	0
2	EDO	D	403	-	3,3,3	0.27	0	2,2,2	0.46	0
2	EDO	D	405	-	3,3,3	0.68	0	2,2,2	0.19	0
2	EDO	D	401	-	3,3,3	0.56	0	2,2,2	0.60	0
3	GOL	B	408	-	5,5,5	0.64	0	5,5,5	1.77	2 (40%)
3	GOL	D	404	-	5,5,5	0.56	0	5,5,5	0.64	0
3	GOL	A	402	-	5,5,5	0.59	0	5,5,5	0.50	0
2	EDO	B	402	-	3,3,3	0.24	0	2,2,2	1.11	0
3	GOL	B	406	-	5,5,5	0.41	0	5,5,5	0.29	0
4	KDG	A	406	1	10,10,11	0.93	0	12,12,14	1.37	1 (8%)
2	EDO	C	405	-	3,3,3	0.71	0	2,2,2	0.04	0
3	GOL	B	405	-	5,5,5	0.52	0	5,5,5	1.63	2 (40%)
3	GOL	C	406	-	5,5,5	0.62	0	5,5,5	0.86	0
2	EDO	C	403	-	3,3,3	0.46	0	2,2,2	0.11	0
2	EDO	C	404	-	3,3,3	0.54	0	2,2,2	0.25	0
2	EDO	B	403	-	3,3,3	0.55	0	2,2,2	0.59	0
3	GOL	A	405	-	5,5,5	0.77	0	5,5,5	0.90	0
3	GOL	D	407	-	5,5,5	0.58	0	5,5,5	0.80	0
4	KDG	B	409	1	10,10,11	0.89	0	12,12,14	1.39	3 (25%)
3	GOL	D	408	-	5,5,5	0.61	0	5,5,5	0.82	0
2	EDO	B	401	-	3,3,3	0.54	0	2,2,2	0.38	0
3	GOL	A	403	-	5,5,5	0.96	0	5,5,5	1.37	1 (20%)
2	EDO	A	401	-	3,3,3	0.30	0	2,2,2	0.51	0

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. ^{1,2} means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	C	402	-	-	1/1/1/1	-
3	GOL	A	404	-	-	4/4/4/4	-
4	KDG	D	409	1	-	8/11/11/14	-
3	GOL	D	406	-	-	4/4/4/4	-
2	EDO	B	404	-	-	1/1/1/1	-
2	EDO	C	407	-	-	1/1/1/1	-
2	EDO	C	401	-	-	1/1/1/1	-
2	EDO	D	402	-	-	1/1/1/1	-
4	KDG	C	408	1	-	8/11/11/14	-
3	GOL	B	407	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	D	403	-	-	1/1/1/1	-
2	EDO	D	405	-	-	1/1/1/1	-
2	EDO	D	401	-	-	1/1/1/1	-
3	GOL	B	408	-	-	3/4/4/4	-
3	GOL	D	404	-	-	0/4/4/4	-
3	GOL	A	402	-	-	4/4/4/4	-
2	EDO	B	402	-	-	1/1/1/1	-
3	GOL	B	406	-	-	4/4/4/4	-
4	KDG	A	406	1	-	4/11/11/14	-
2	EDO	C	405	-	-	1/1/1/1	-
3	GOL	B	405	-	-	4/4/4/4	-
3	GOL	C	406	-	-	4/4/4/4	-
2	EDO	C	403	-	-	1/1/1/1	-
2	EDO	C	404	-	-	1/1/1/1	-
2	EDO	B	403	-	-	1/1/1/1	-
3	GOL	A	405	-	-	4/4/4/4	-
3	GOL	D	407	-	-	0/4/4/4	-
4	KDG	B	409	1	-	4/11/11/14	-
3	GOL	D	408	-	-	4/4/4/4	-
2	EDO	B	401	-	-	1/1/1/1	-
3	GOL	A	403	-	-	2/4/4/4	-
2	EDO	A	401	-	-	1/1/1/1	-

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	409	KDG	C5-C4-C3	-4.45	105.68	114.81
4	C	408	KDG	C4-C5-C6	3.13	120.84	112.49
4	C	408	KDG	O6A-C6-C5	2.54	122.02	114.00
3	B	405	GOL	C3-C2-C1	2.54	121.11	111.80
4	C	408	KDG	C5-C4-C3	-2.50	109.67	114.81

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	GOL	C1-C2-C3-O3
3	A	402	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	404	GOL	C1-C2-C3-O3
3	A	405	GOL	O1-C1-C2-C3
3	B	405	GOL	C1-C2-C3-O3

There are no ring outliers.

21 monomers are involved in 68 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	409	KDG	2	0
3	D	406	GOL	1	0
2	B	404	EDO	1	0
2	D	402	EDO	5	0
4	C	408	KDG	9	0
2	D	405	EDO	2	0
3	B	408	GOL	4	0
3	D	404	GOL	2	0
2	B	402	EDO	2	0
3	B	406	GOL	1	0
4	A	406	KDG	11	0
2	C	405	EDO	1	0
3	B	405	GOL	9	0
3	C	406	GOL	3	0
2	C	403	EDO	3	0
2	B	403	EDO	2	0
3	D	407	GOL	1	0
4	B	409	KDG	5	0
3	D	408	GOL	1	0
3	A	403	GOL	1	0
2	A	401	EDO	2	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, 95th 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	298/343 (86%)	0.61	13 (4%) 39 34	14, 23, 37, 43	0
1	B	298/343 (86%)	0.46	7 (2%) 61 56	13, 20, 32, 45	0
1	C	298/343 (86%)	0.59	8 (2%) 56 52	10, 22, 38, 57	1 (0%)
1	D	298/343 (86%)	0.56	7 (2%) 61 56	12, 21, 34, 47	0
All	All	1192/1372 (86%)	0.55	35 (2%) 53 49	10, 21, 36, 57	1 (0%)

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	29	GLY	3.3
1	D	243	ALA	3.1
1	C	243	ALA	2.9
1	A	302	LEU	2.8
1	B	308	LEU	2.7

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 oligosaccharides 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, 95th 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(\AA^2)	Q<0.9
3	GOL	D	407	6/6	0.66	0.17	31,35,38,40	0
3	GOL	D	408	6/6	0.66	0.17	37,43,43,46	0
3	GOL	A	403	6/6	0.67	0.22	29,31,32,32	0
3	GOL	A	402	6/6	0.70	0.15	37,39,40,40	0
3	GOL	B	405	6/6	0.71	0.21	25,31,31,33	0
3	GOL	B	407	6/6	0.73	0.16	40,41,42,43	0
3	GOL	D	404	6/6	0.73	0.15	36,39,41,42	0
4	KDG	A	406	11/12	0.73	0.21	15,17,18,18	11
2	EDO	D	405	4/4	0.75	0.17	19,19,19,20	0
4	KDG	B	409	11/12	0.76	0.16	30,35,39,42	0
3	GOL	A	404	6/6	0.77	0.15	28,31,34,35	0
3	GOL	D	406	6/6	0.77	0.15	35,37,40,40	0
4	KDG	C	408	11/12	0.77	0.20	17,19,20,20	11
3	GOL	C	406	6/6	0.79	0.18	32,33,34,34	0
4	KDG	D	409	11/12	0.80	0.14	25,29,31,33	0
2	EDO	C	407	4/4	0.81	0.14	32,33,35,36	0
2	EDO	B	401	4/4	0.83	0.12	27,27,28,28	0
2	EDO	B	403	4/4	0.83	0.15	25,26,27,28	0
2	EDO	D	402	4/4	0.84	0.27	18,19,19,19	0
2	EDO	B	402	4/4	0.84	0.14	16,17,17,18	0
2	EDO	D	401	4/4	0.85	0.12	25,25,26,27	0
3	GOL	B	406	6/6	0.85	0.12	29,31,35,37	0
2	EDO	C	404	4/4	0.85	0.11	31,34,35,35	0
2	EDO	C	403	4/4	0.85	0.10	31,32,32,33	0
2	EDO	C	405	4/4	0.86	0.11	24,24,25,26	0
3	GOL	A	405	6/6	0.86	0.11	35,37,39,39	0
3	GOL	B	408	6/6	0.87	0.10	20,20,21,21	0
2	EDO	C	402	4/4	0.88	0.16	19,19,20,20	0
2	EDO	D	403	4/4	0.89	0.12	24,24,26,29	0
2	EDO	B	404	4/4	0.91	0.14	33,34,35,36	0
2	EDO	A	401	4/4	0.92	0.10	26,27,28,28	0
2	EDO	C	401	4/4	0.93	0.08	23,23,23,25	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.