



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:42 PM GMT

PDB ID : 4MFE
Title : Structure of the carboxyl transferase domain from Rhizobium etli pyruvate carboxylase with 3-hydroxypyruvate
Authors : Lietzan, A.D.; St. Maurice, M.
Deposited on : 2013-08-27
Resolution : 2.61 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

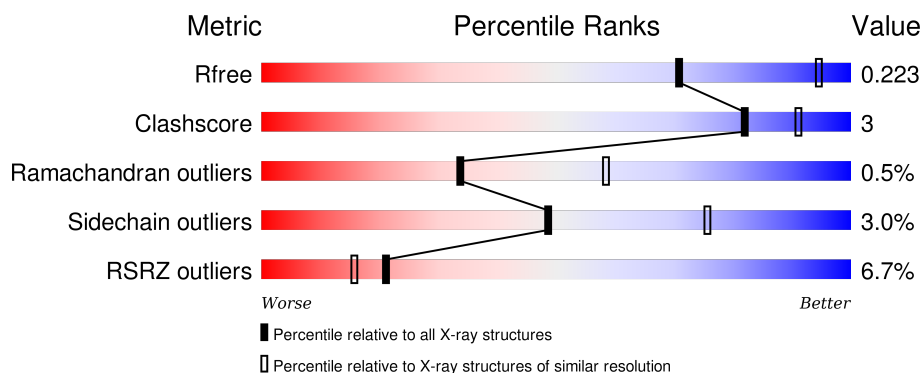
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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}	91344	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	632	<div> <div>10%</div> <div>83% 11% 6%</div> </div>
1	B	632	<div> <div>10%</div> <div>87% 7% 6%</div> </div>
1	C	632	<div> <div>4%</div> <div>86% 9% 6%</div> </div>
1	D	632	<div> <div>11%</div> <div>83% 11% 6%</div> </div>

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
5	MG	B	1104	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17744 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 PYRUVATE CARBOXYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	597	Total	C	N	O	S	0	1	0
			4497	2859	752	863	23			
1	B	594	Total	C	N	O	S	0	1	0
			4295	2720	720	832	23			
1	C	597	Total	C	N	O	S	0	2	0
			4416	2807	743	843	23			
1	D	594	Total	C	N	O	S	0	1	0
			4278	2708	727	820	23			

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	436	MET	-	EXPRESSION TAG	UNP Q2K340
A	437	GLY	-	EXPRESSION TAG	UNP Q2K340
A	438	SER	-	EXPRESSION TAG	UNP Q2K340
A	439	SER	-	EXPRESSION TAG	UNP Q2K340
A	440	HIS	-	EXPRESSION TAG	UNP Q2K340
A	441	HIS	-	EXPRESSION TAG	UNP Q2K340
A	442	HIS	-	EXPRESSION TAG	UNP Q2K340
A	443	HIS	-	EXPRESSION TAG	UNP Q2K340
A	444	HIS	-	EXPRESSION TAG	UNP Q2K340
A	445	HIS	-	EXPRESSION TAG	UNP Q2K340
A	446	HIS	-	EXPRESSION TAG	UNP Q2K340
A	447	HIS	-	EXPRESSION TAG	UNP Q2K340
A	448	ASP	-	EXPRESSION TAG	UNP Q2K340
A	449	TYR	-	EXPRESSION TAG	UNP Q2K340
A	450	ASP	-	EXPRESSION TAG	UNP Q2K340
A	451	ILE	-	EXPRESSION TAG	UNP Q2K340
A	452	PRO	-	EXPRESSION TAG	UNP Q2K340
A	453	THR	-	EXPRESSION TAG	UNP Q2K340
A	454	SER	-	EXPRESSION TAG	UNP Q2K340
A	455	GLU	-	EXPRESSION TAG	UNP Q2K340
A	456	ASN	-	EXPRESSION TAG	UNP Q2K340

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Chain	Residue	Modelled	Actual	Comment	Reference
A	457	LEU	-	EXPRESSION TAG	UNP Q2K340
A	458	TYR	-	EXPRESSION TAG	UNP Q2K340
A	459	PHE	-	EXPRESSION TAG	UNP Q2K340
A	460	GLN	-	EXPRESSION TAG	UNP Q2K340
A	461	GLY	-	EXPRESSION TAG	UNP Q2K340
A	462	LEU	-	EXPRESSION TAG	UNP Q2K340
A	463	LEU	-	EXPRESSION TAG	UNP Q2K340
A	464	HIS	-	EXPRESSION TAG	UNP Q2K340
B	436	MET	-	EXPRESSION TAG	UNP Q2K340
B	437	GLY	-	EXPRESSION TAG	UNP Q2K340
B	438	SER	-	EXPRESSION TAG	UNP Q2K340
B	439	SER	-	EXPRESSION TAG	UNP Q2K340
B	440	HIS	-	EXPRESSION TAG	UNP Q2K340
B	441	HIS	-	EXPRESSION TAG	UNP Q2K340
B	442	HIS	-	EXPRESSION TAG	UNP Q2K340
B	443	HIS	-	EXPRESSION TAG	UNP Q2K340
B	444	HIS	-	EXPRESSION TAG	UNP Q2K340
B	445	HIS	-	EXPRESSION TAG	UNP Q2K340
B	446	HIS	-	EXPRESSION TAG	UNP Q2K340
B	447	HIS	-	EXPRESSION TAG	UNP Q2K340
B	448	ASP	-	EXPRESSION TAG	UNP Q2K340
B	449	TYR	-	EXPRESSION TAG	UNP Q2K340
B	450	ASP	-	EXPRESSION TAG	UNP Q2K340
B	451	ILE	-	EXPRESSION TAG	UNP Q2K340
B	452	PRO	-	EXPRESSION TAG	UNP Q2K340
B	453	THR	-	EXPRESSION TAG	UNP Q2K340
B	454	SER	-	EXPRESSION TAG	UNP Q2K340
B	455	GLU	-	EXPRESSION TAG	UNP Q2K340
B	456	ASN	-	EXPRESSION TAG	UNP Q2K340
B	457	LEU	-	EXPRESSION TAG	UNP Q2K340
B	458	TYR	-	EXPRESSION TAG	UNP Q2K340
B	459	PHE	-	EXPRESSION TAG	UNP Q2K340
B	460	GLN	-	EXPRESSION TAG	UNP Q2K340
B	461	GLY	-	EXPRESSION TAG	UNP Q2K340
B	462	LEU	-	EXPRESSION TAG	UNP Q2K340
B	463	LEU	-	EXPRESSION TAG	UNP Q2K340
B	464	HIS	-	EXPRESSION TAG	UNP Q2K340
C	436	MET	-	EXPRESSION TAG	UNP Q2K340
C	437	GLY	-	EXPRESSION TAG	UNP Q2K340
C	438	SER	-	EXPRESSION TAG	UNP Q2K340
C	439	SER	-	EXPRESSION TAG	UNP Q2K340
C	440	HIS	-	EXPRESSION TAG	UNP Q2K340

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Chain	Residue	Modelled	Actual	Comment	Reference
C	441	HIS	-	EXPRESSION TAG	UNP Q2K340
C	442	HIS	-	EXPRESSION TAG	UNP Q2K340
C	443	HIS	-	EXPRESSION TAG	UNP Q2K340
C	444	HIS	-	EXPRESSION TAG	UNP Q2K340
C	445	HIS	-	EXPRESSION TAG	UNP Q2K340
C	446	HIS	-	EXPRESSION TAG	UNP Q2K340
C	447	HIS	-	EXPRESSION TAG	UNP Q2K340
C	448	ASP	-	EXPRESSION TAG	UNP Q2K340
C	449	TYR	-	EXPRESSION TAG	UNP Q2K340
C	450	ASP	-	EXPRESSION TAG	UNP Q2K340
C	451	ILE	-	EXPRESSION TAG	UNP Q2K340
C	452	PRO	-	EXPRESSION TAG	UNP Q2K340
C	453	THR	-	EXPRESSION TAG	UNP Q2K340
C	454	SER	-	EXPRESSION TAG	UNP Q2K340
C	455	GLU	-	EXPRESSION TAG	UNP Q2K340
C	456	ASN	-	EXPRESSION TAG	UNP Q2K340
C	457	LEU	-	EXPRESSION TAG	UNP Q2K340
C	458	TYR	-	EXPRESSION TAG	UNP Q2K340
C	459	PHE	-	EXPRESSION TAG	UNP Q2K340
C	460	GLN	-	EXPRESSION TAG	UNP Q2K340
C	461	GLY	-	EXPRESSION TAG	UNP Q2K340
C	462	LEU	-	EXPRESSION TAG	UNP Q2K340
C	463	LEU	-	EXPRESSION TAG	UNP Q2K340
C	464	HIS	-	EXPRESSION TAG	UNP Q2K340
D	436	MET	-	EXPRESSION TAG	UNP Q2K340
D	437	GLY	-	EXPRESSION TAG	UNP Q2K340
D	438	SER	-	EXPRESSION TAG	UNP Q2K340
D	439	SER	-	EXPRESSION TAG	UNP Q2K340
D	440	HIS	-	EXPRESSION TAG	UNP Q2K340
D	441	HIS	-	EXPRESSION TAG	UNP Q2K340
D	442	HIS	-	EXPRESSION TAG	UNP Q2K340
D	443	HIS	-	EXPRESSION TAG	UNP Q2K340
D	444	HIS	-	EXPRESSION TAG	UNP Q2K340
D	445	HIS	-	EXPRESSION TAG	UNP Q2K340
D	446	HIS	-	EXPRESSION TAG	UNP Q2K340
D	447	HIS	-	EXPRESSION TAG	UNP Q2K340
D	448	ASP	-	EXPRESSION TAG	UNP Q2K340
D	449	TYR	-	EXPRESSION TAG	UNP Q2K340
D	450	ASP	-	EXPRESSION TAG	UNP Q2K340
D	451	ILE	-	EXPRESSION TAG	UNP Q2K340
D	452	PRO	-	EXPRESSION TAG	UNP Q2K340
D	453	THR	-	EXPRESSION TAG	UNP Q2K340

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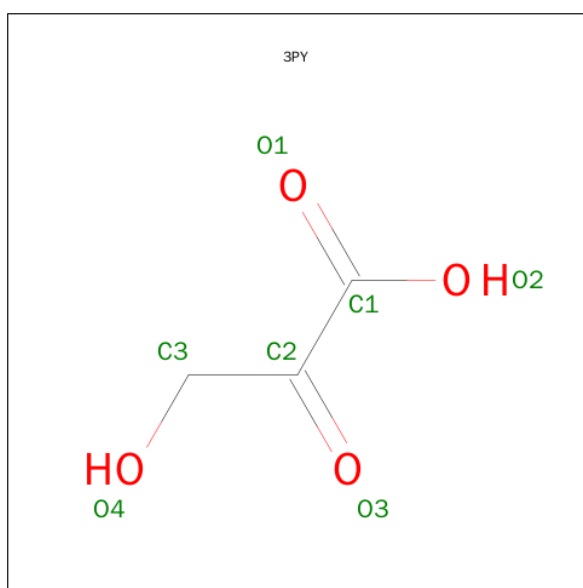
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Chain	Residue	Modelled	Actual	Comment	Reference
D	454	SER	-	EXPRESSION TAG	UNP Q2K340
D	455	GLU	-	EXPRESSION TAG	UNP Q2K340
D	456	ASN	-	EXPRESSION TAG	UNP Q2K340
D	457	LEU	-	EXPRESSION TAG	UNP Q2K340
D	458	TYR	-	EXPRESSION TAG	UNP Q2K340
D	459	PHE	-	EXPRESSION TAG	UNP Q2K340
D	460	GLN	-	EXPRESSION TAG	UNP Q2K340
D	461	GLY	-	EXPRESSION TAG	UNP Q2K340
D	462	LEU	-	EXPRESSION TAG	UNP Q2K340
D	463	LEU	-	EXPRESSION TAG	UNP Q2K340
D	464	HIS	-	EXPRESSION TAG	UNP Q2K340

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

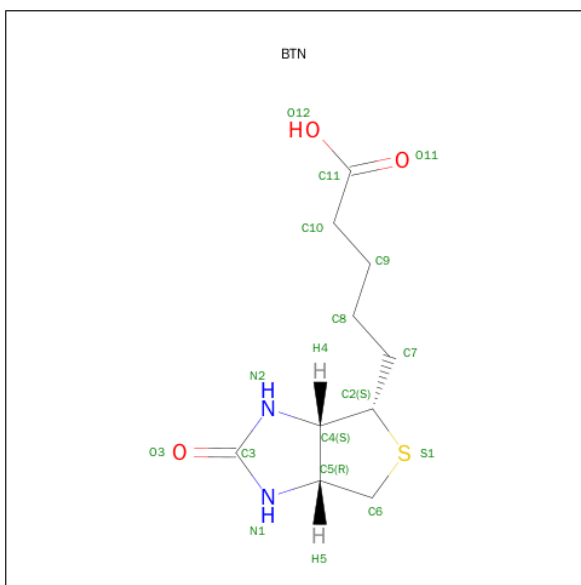
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0

- Molecule 3 is 3-HYDROXYPYRUVIC ACID (three-letter code: 3PY) (formula: C₃H₄O₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 3 4	0	0
3	B	1	Total C O 7 3 4	0	0
3	C	1	Total C O 7 3 4	0	0
3	D	1	Total C O 7 3 4	0	0

- Molecule 4 is BIOTIN (three-letter code: BTN) (formula: C₁₀H₁₆N₂O₃S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O S 9 5 2 1 1	0	0
4	B	1	Total C N O S 10 6 2 1 1	0	0
4	C	1	Total C N O S 10 6 2 1 1	0	0
4	D	1	Total C N O S 9 5 2 1 1	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Mg 1 1	0	0
5	A	1	Total Mg 1 1	0	0

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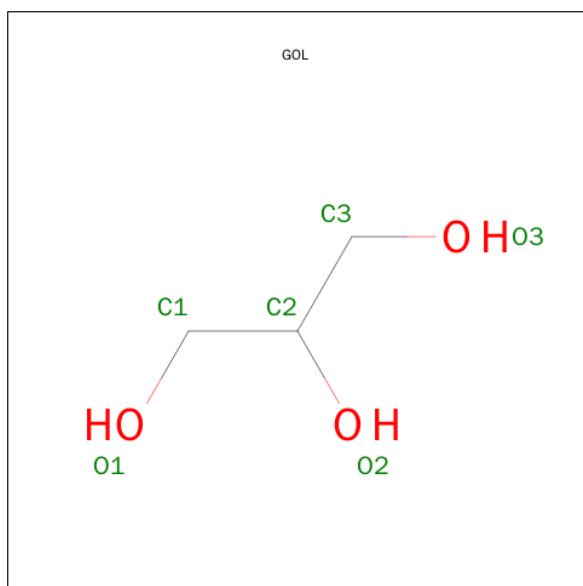
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		
6	A	1	Total	Cl	0	0
			1	1		
6	C	1	Total	Cl	0	0
			1	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

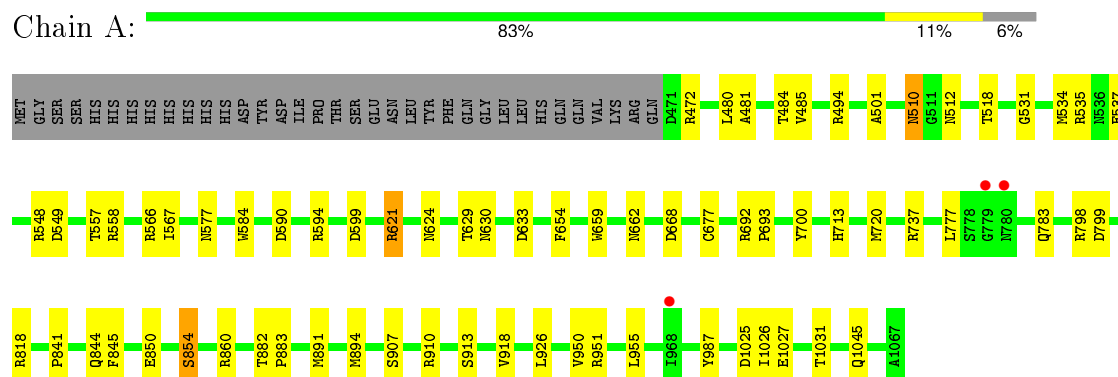
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	62	Total 62	O 62	0	0
8	B	35	Total 35	O 35	0	0
8	C	40	Total 40	O 40	0	0
8	D	32	Total 32	O 32	0	0

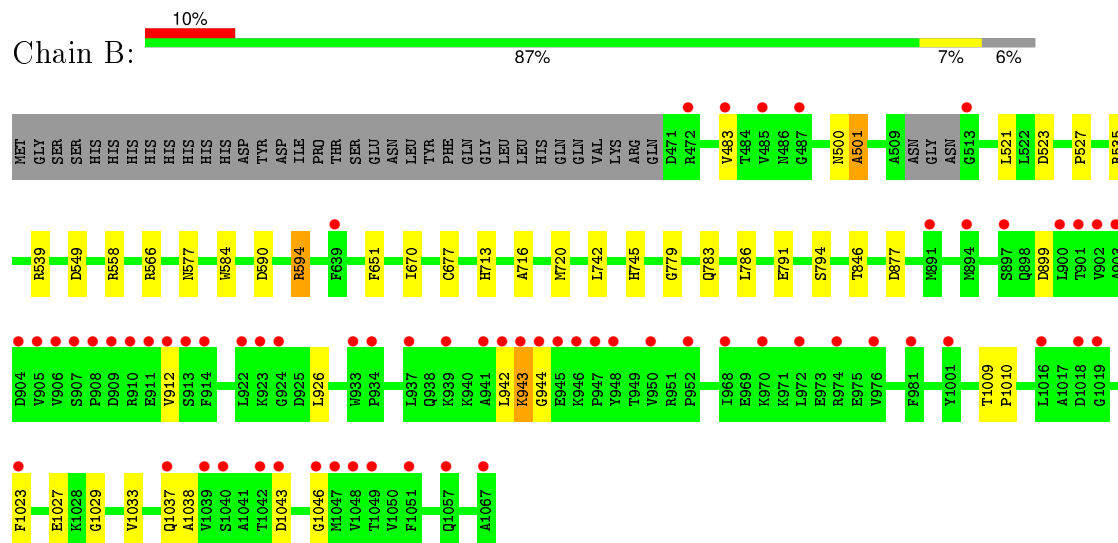
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

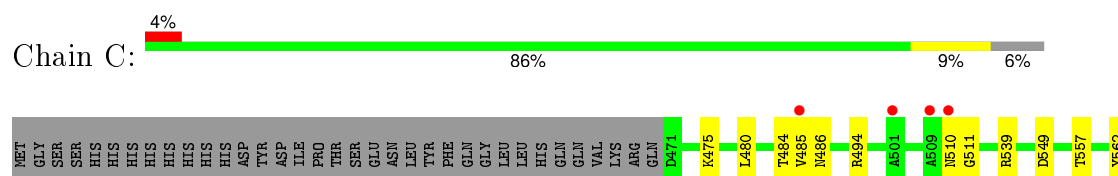
• Molecule 1: PYRUVATE CARBOXYLASE

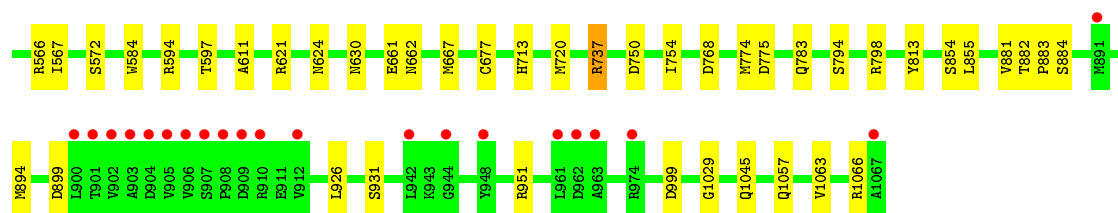


• Molecule 1: PYRUVATE CARBOXYLASE

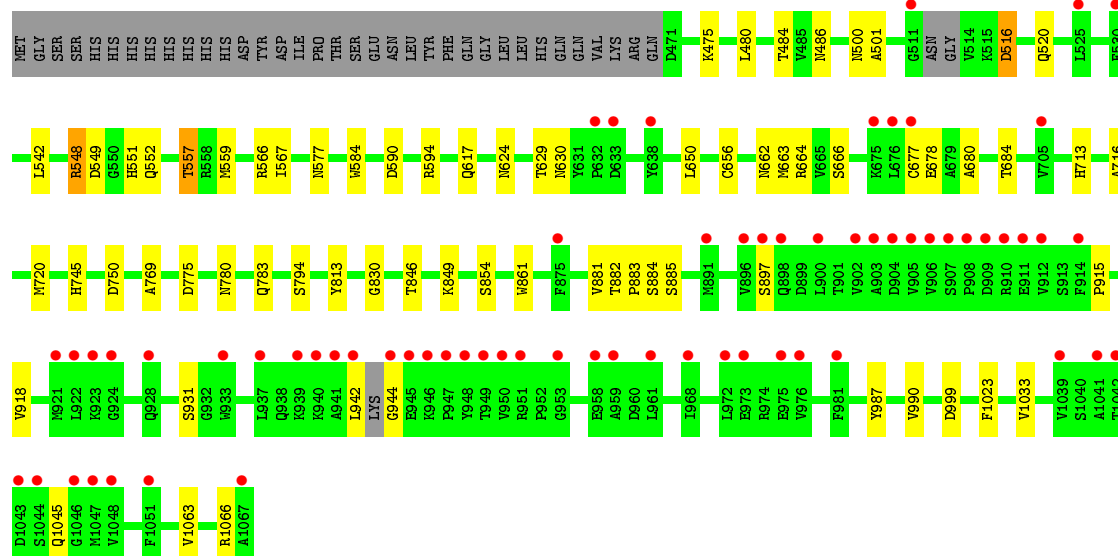
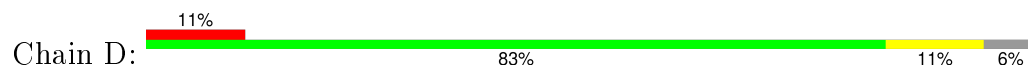


• Molecule 1: PYRUVATE CARBOXYLASE





• Molecule 1: PYRUVATE CARBOXYLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.25Å 157.85Å 243.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.37 – 2.61 49.32 – 2.61	Depositor EDS
% Data completeness (in resolution range)	95.7 (49.37-2.61) 95.7 (49.32-2.61)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.81 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.177 , 0.225 0.180 , 0.223	Depositor DCC
R_{free} test set	4777 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	63.5	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 45.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 95679 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17744	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 3PY, ZN, GOL, CL, MG, BTN, KCX

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	0.89	4/4583 (0.1%)	0.94	9/6245 (0.1%)
1	B	0.71	1/4380 (0.0%)	0.82	6/5991 (0.1%)
1	C	0.74	0/4507	0.88	8/6156 (0.1%)
1	D	0.65	0/4362	0.76	1/5967 (0.0%)
All	All	0.75	5/17832 (0.0%)	0.85	24/24359 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	854	SER	CB-OG	-5.64	1.34	1.42
1	A	700	TYR	CE1-CZ	-5.62	1.31	1.38
1	B	791	GLU	CD-OE2	5.50	1.31	1.25
1	A	845	PHE	CB-CG	-5.46	1.42	1.51
1	A	659	TRP	CZ3-CH2	5.25	1.48	1.40

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	737	ARG	NE-CZ-NH2	12.93	126.77	120.30
1	A	737	ARG	NE-CZ-NH1	-8.58	116.01	120.30
1	C	737	ARG	NE-CZ-NH1	-7.68	116.46	120.30
1	C	594	ARG	NE-CZ-NH2	7.09	123.85	120.30
1	A	737	ARG	NE-CZ-NH2	6.75	123.67	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	4497	0	4328	35	0
1	B	4295	0	3918	21	0
1	C	4416	0	4162	24	0
1	D	4278	0	3903	29	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	7	0	3	0	0
3	B	7	0	3	0	0
3	C	7	0	3	1	0
3	D	7	0	3	0	0
4	A	9	0	6	0	0
4	B	10	0	7	0	0
4	C	10	0	7	0	0
4	D	9	0	6	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
7	A	6	0	8	3	0
7	D	6	0	8	1	0
8	A	62	0	0	0	0
8	B	35	0	0	2	0
8	C	40	0	0	0	0
8	D	32	0	0	0	0
All	All	17744	0	16365	110	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 3.

The worst 5 of 110 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:481:ALA:O	1:A:485:VAL:HG23	1.46	1.15
1:B:500:ASN:OD1	1:B:501:ALA:N	1.94	1.00
1:A:480:LEU:O	1:A:484:THR:OG1	1.79	0.99
1:C:480:LEU:O	1:C:484:THR:OG1	1.91	0.88
1:D:942:LEU:C	1:D:944:GLY:N	2.26	0.88

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	595/632 (94%)	573 (96%)	21 (4%)	1 (0%)	52	76
1	B	590/632 (93%)	556 (94%)	29 (5%)	5 (1%)	24	44
1	C	596/632 (94%)	557 (94%)	35 (6%)	4 (1%)	26	49
1	D	588/632 (93%)	558 (95%)	28 (5%)	2 (0%)	46	70
All	All	2369/2528 (94%)	2244 (95%)	113 (5%)	12 (0%)	34	58

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	510	ASN
1	D	501	ALA
1	A	501	ALA
1	B	501	ALA
1	C	511	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	451/519 (87%)	440 (98%)	11 (2%)	57	81
1	B	401/519 (77%)	392 (98%)	9 (2%)	60	83
1	C	430/519 (83%)	417 (97%)	13 (3%)	48	75
1	D	397/519 (76%)	379 (96%)	18 (4%)	34	61
All	All	1679/2076 (81%)	1628 (97%)	51 (3%)	48	75

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	597	THR
1	C	855	LEU
1	D	854	SER
1	C	720	MET
1	C	899	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	783	GLN
1	C	577	ASN
1	D	713	HIS
1	B	873	GLN
1	C	624	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	KCX	A	718	1,2	7,11,12	0.89	1 (14%)	7,12,14	2.61	2 (28%)
1	KCX	B	718	1,2	7,11,12	0.46	0	7,12,14	1.22	0
1	KCX	C	718	1,2	7,11,12	0.80	0	7,12,14	1.03	0
1	KCX	D	718	1,2	7,11,12	0.54	0	7,12,14	3.70	2 (28%)

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
1	KCX	A	718	1,2	-	0/6/10/12	0/0/0/0
1	KCX	B	718	1,2	-	0/6/10/12	0/0/0/0
1	KCX	C	718	1,2	-	0/6/10/12	0/0/0/0
1	KCX	D	718	1,2	-	0/6/10/12	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	718	KCX	CB-CA	2.03	1.55	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	718	KCX	CD-CE-NZ	2.85	119.18	111.46
1	D	718	KCX	CD-CE-NZ	4.40	123.38	111.46
1	A	718	KCX	CE-NZ-CX	5.79	130.05	123.49
1	D	718	KCX	CE-NZ-CX	8.49	133.11	123.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 21 ligands modelled in this entry, 11 are monoatomic - leaving 10 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	3PY	A	1102	-	2,6,6	0.25	0	2,7,7	1.06	0
4	BTN	A	1103	-	8,10,17	1.17	2 (25%)	7,14,23	1.58	1 (14%)
7	GOL	A	1106	-	5,5,5	0.28	0	5,5,5	0.99	0
3	3PY	B	1102	-	2,6,6	0.17	0	2,7,7	2.10	1 (50%)
4	BTN	B	1103	-	9,11,17	0.61	0	8,16,23	0.97	0
3	3PY	C	1102	-	2,6,6	0.25	0	2,7,7	1.53	0
4	BTN	C	1103	-	9,11,17	0.97	0	8,16,23	1.36	2 (25%)
7	GOL	D	1101	-	5,5,5	0.47	0	5,5,5	1.46	1 (20%)
3	3PY	D	1103	-	2,6,6	0.78	0	2,7,7	0.24	0
4	BTN	D	1104	-	8,10,17	0.89	0	7,14,23	0.88	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	3PY	A	1102	-	-	0/2/6/6	0/0/0/0
4	BTN	A	1103	-	-	0/0/18/28	0/2/2/2
7	GOL	A	1106	-	-	0/4/4/4	0/0/0/0
3	3PY	B	1102	-	-	0/2/6/6	0/0/0/0
4	BTN	B	1103	-	-	0/0/21/28	0/2/2/2
3	3PY	C	1102	-	-	0/2/6/6	0/0/0/0
4	BTN	C	1103	-	-	0/0/21/28	0/2/2/2
7	GOL	D	1101	-	-	0/4/4/4	0/0/0/0
3	3PY	D	1103	-	-	0/2/6/6	0/0/0/0
4	BTN	D	1104	-	-	0/0/18/28	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1103	BTN	C6-S1	-2.45	1.75	1.81
4	A	1103	BTN	C3-N1	-2.09	1.32	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1102	3PY	O4-C3-C2	-2.76	106.04	112.33
4	C	1103	BTN	C5-C4-N2	-2.11	100.39	102.52
7	D	1101	GOL	O2-C2-C1	2.10	118.30	108.65
4	C	1103	BTN	C4-N2-C3	2.22	114.78	112.66
4	A	1103	BTN	C4-N2-C3	2.53	114.38	112.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1106	GOL	3	0
3	C	1102	3PY	1	0
7	D	1101	GOL	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	596/632 (94%)	-0.21	3 (0%) 91 90	34, 56, 84, 138	13 (2%)
1	B	593/632 (93%)	0.41	64 (10%) 8 4	40, 86, 160, 212	5 (0%)
1	C	596/632 (94%)	0.03	25 (4%) 40 33	45, 70, 120, 158	10 (1%)
1	D	593/632 (93%)	0.37	67 (11%) 7 4	45, 88, 146, 188	8 (1%)
All	All	2378/2528 (94%)	0.15	159 (6%) 21 16	34, 72, 140, 212	36 (1%)

The worst 5 of 159 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	912	VAL	7.4
1	D	944	GLY	6.9
1	D	907	SER	6.0
1	D	941	ALA	5.8
1	D	908	PRO	5.5

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	KCX	D	718	12/13	0.96	0.19	-	68,72,87,90	0
1	KCX	A	718	12/13	0.99	0.18	-	40,42,44,46	0
1	KCX	C	718	12/13	0.97	0.22	-	48,51,61,62	0
1	KCX	B	718	12/13	0.96	0.17	-	59,60,65,68	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	MG	B	1104	1/1	0.92	0.18	2.59	60,60,60,60	0
7	GOL	D	1101	6/6	0.92	0.28	1.66	53,62,68,68	0
7	GOL	A	1106	6/6	0.95	0.31	1.10	58,63,67,72	0
5	MG	D	1105	1/1	0.78	0.21	1.02	66,66,66,66	0
4	BTN	D	1104	9/16	0.91	0.22	1.00	76,81,86,89	0
3	3PY	A	1102	7/7	0.97	0.21	0.97	44,48,52,62	0
3	3PY	C	1102	7/7	0.97	0.20	0.68	53,59,60,68	0
4	BTN	B	1103	10/16	0.89	0.29	0.40	82,94,104,106	0
4	BTN	A	1103	9/16	0.96	0.16	-0.06	58,70,73,77	0
3	3PY	D	1103	7/7	0.97	0.17	-0.21	74,82,88,92	0
4	BTN	C	1103	10/16	0.96	0.15	-0.67	67,77,81,87	0
3	3PY	B	1102	7/7	0.95	0.14	-1.29	64,70,72,78	0
2	ZN	A	1101	1/1	0.99	0.17	-1.51	44,44,44,44	0
2	ZN	C	1101	1/1	1.00	0.17	-2.07	54,54,54,54	0
5	MG	A	1104	1/1	0.92	0.05	-2.53	58,58,58,58	0
2	ZN	D	1102	1/1	0.96	0.17	-2.75	69,69,69,69	0
2	ZN	B	1101	1/1	1.00	0.13	-2.98	61,61,61,61	0
5	MG	C	1104	1/1	0.84	0.07	-4.86	61,61,61,61	0
6	CL	C	1105	1/1	0.87	0.18	-	80,80,80,80	0
6	CL	B	1105	1/1	0.94	0.06	-	89,89,89,89	0
6	CL	A	1105	1/1	0.97	0.16	-	61,61,61,61	0

6.5 Other polymers ⓘ

There are no such residues in this entry.