wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 07:36 AM GMT

PDB ID	:	3BG9
Title	:	Crystal Structure of Human Pyruvate Carboxylase (missing the biotin carboxylase domain at the N-terminus) F1077A Mutant
Authors	:	Xiang, S.; Tong, L.
Deposited on	:	2007-11-26
Resolution	:	3.00 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

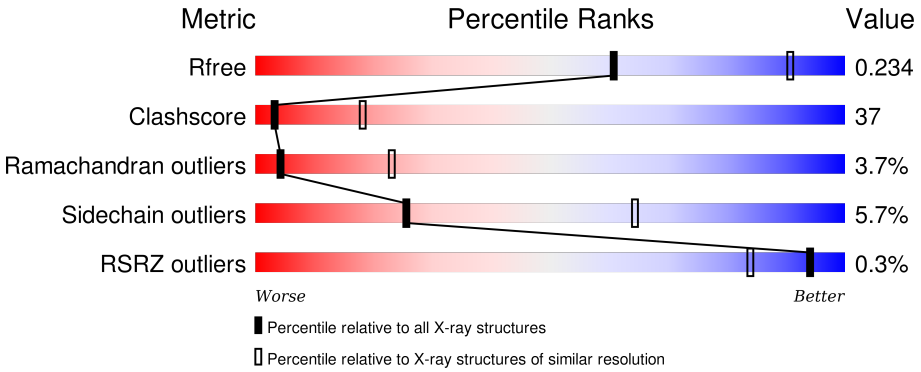
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 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 <=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	718	38% 41% 5% 16%
1	B	718	37% 42% 5% 16%
1	C	718	% 35% 44% • 16%
1	D	718	39% 40% • 16%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18516 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, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	601	Total	C	N	O	S	0	0	0
			4628	2937	798	865	28			
1	B	601	Total	C	N	O	S	0	0	0
			4628	2937	798	865	28			
1	C	601	Total	C	N	O	S	0	0	0
			4628	2937	798	865	28			
1	D	601	Total	C	N	O	S	0	0	0
			4628	2937	798	865	28			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	461	MET	-	EXPRESSION TAG	UNP P11498
A	462	GLY	-	EXPRESSION TAG	UNP P11498
A	463	SER	-	EXPRESSION TAG	UNP P11498
A	464	SER	-	EXPRESSION TAG	UNP P11498
A	465	HIS	-	EXPRESSION TAG	UNP P11498
A	466	HIS	-	EXPRESSION TAG	UNP P11498
A	467	HIS	-	EXPRESSION TAG	UNP P11498
A	468	HIS	-	EXPRESSION TAG	UNP P11498
A	469	HIS	-	EXPRESSION TAG	UNP P11498
A	470	HIS	-	EXPRESSION TAG	UNP P11498
A	471	SER	-	EXPRESSION TAG	UNP P11498
A	472	SER	-	EXPRESSION TAG	UNP P11498
A	473	GLY	-	EXPRESSION TAG	UNP P11498
A	474	LEU	-	EXPRESSION TAG	UNP P11498
A	475	VAL	-	EXPRESSION TAG	UNP P11498
A	476	PRO	-	EXPRESSION TAG	UNP P11498
A	477	ARG	-	EXPRESSION TAG	UNP P11498
A	478	GLY	-	EXPRESSION TAG	UNP P11498
A	479	SER	-	EXPRESSION TAG	UNP P11498
A	480	HIS	-	EXPRESSION TAG	UNP P11498
A	481	MET	-	EXPRESSION TAG	UNP P11498

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1077	ALA	PHE	ENGINEERED	UNP P11498
B	461	MET	-	EXPRESSION TAG	UNP P11498
B	462	GLY	-	EXPRESSION TAG	UNP P11498
B	463	SER	-	EXPRESSION TAG	UNP P11498
B	464	SER	-	EXPRESSION TAG	UNP P11498
B	465	HIS	-	EXPRESSION TAG	UNP P11498
B	466	HIS	-	EXPRESSION TAG	UNP P11498
B	467	HIS	-	EXPRESSION TAG	UNP P11498
B	468	HIS	-	EXPRESSION TAG	UNP P11498
B	469	HIS	-	EXPRESSION TAG	UNP P11498
B	470	HIS	-	EXPRESSION TAG	UNP P11498
B	471	SER	-	EXPRESSION TAG	UNP P11498
B	472	SER	-	EXPRESSION TAG	UNP P11498
B	473	GLY	-	EXPRESSION TAG	UNP P11498
B	474	LEU	-	EXPRESSION TAG	UNP P11498
B	475	VAL	-	EXPRESSION TAG	UNP P11498
B	476	PRO	-	EXPRESSION TAG	UNP P11498
B	477	ARG	-	EXPRESSION TAG	UNP P11498
B	478	GLY	-	EXPRESSION TAG	UNP P11498
B	479	SER	-	EXPRESSION TAG	UNP P11498
B	480	HIS	-	EXPRESSION TAG	UNP P11498
B	481	MET	-	EXPRESSION TAG	UNP P11498
B	1077	ALA	PHE	ENGINEERED	UNP P11498
C	461	MET	-	EXPRESSION TAG	UNP P11498
C	462	GLY	-	EXPRESSION TAG	UNP P11498
C	463	SER	-	EXPRESSION TAG	UNP P11498
C	464	SER	-	EXPRESSION TAG	UNP P11498
C	465	HIS	-	EXPRESSION TAG	UNP P11498
C	466	HIS	-	EXPRESSION TAG	UNP P11498
C	467	HIS	-	EXPRESSION TAG	UNP P11498
C	468	HIS	-	EXPRESSION TAG	UNP P11498
C	469	HIS	-	EXPRESSION TAG	UNP P11498
C	470	HIS	-	EXPRESSION TAG	UNP P11498
C	471	SER	-	EXPRESSION TAG	UNP P11498
C	472	SER	-	EXPRESSION TAG	UNP P11498
C	473	GLY	-	EXPRESSION TAG	UNP P11498
C	474	LEU	-	EXPRESSION TAG	UNP P11498
C	475	VAL	-	EXPRESSION TAG	UNP P11498
C	476	PRO	-	EXPRESSION TAG	UNP P11498
C	477	ARG	-	EXPRESSION TAG	UNP P11498
C	478	GLY	-	EXPRESSION TAG	UNP P11498
C	479	SER	-	EXPRESSION TAG	UNP P11498

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Chain	Residue	Modelled	Actual	Comment	Reference
C	480	HIS	-	EXPRESSION TAG	UNP P11498
C	481	MET	-	EXPRESSION TAG	UNP P11498
C	1077	ALA	PHE	ENGINEERED	UNP P11498
D	461	MET	-	EXPRESSION TAG	UNP P11498
D	462	GLY	-	EXPRESSION TAG	UNP P11498
D	463	SER	-	EXPRESSION TAG	UNP P11498
D	464	SER	-	EXPRESSION TAG	UNP P11498
D	465	HIS	-	EXPRESSION TAG	UNP P11498
D	466	HIS	-	EXPRESSION TAG	UNP P11498
D	467	HIS	-	EXPRESSION TAG	UNP P11498
D	468	HIS	-	EXPRESSION TAG	UNP P11498
D	469	HIS	-	EXPRESSION TAG	UNP P11498
D	470	HIS	-	EXPRESSION TAG	UNP P11498
D	471	SER	-	EXPRESSION TAG	UNP P11498
D	472	SER	-	EXPRESSION TAG	UNP P11498
D	473	GLY	-	EXPRESSION TAG	UNP P11498
D	474	LEU	-	EXPRESSION TAG	UNP P11498
D	475	VAL	-	EXPRESSION TAG	UNP P11498
D	476	PRO	-	EXPRESSION TAG	UNP P11498
D	477	ARG	-	EXPRESSION TAG	UNP P11498
D	478	GLY	-	EXPRESSION TAG	UNP P11498
D	479	SER	-	EXPRESSION TAG	UNP P11498
D	480	HIS	-	EXPRESSION TAG	UNP P11498
D	481	MET	-	EXPRESSION TAG	UNP P11498
D	1077	ALA	PHE	ENGINEERED	UNP P11498

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

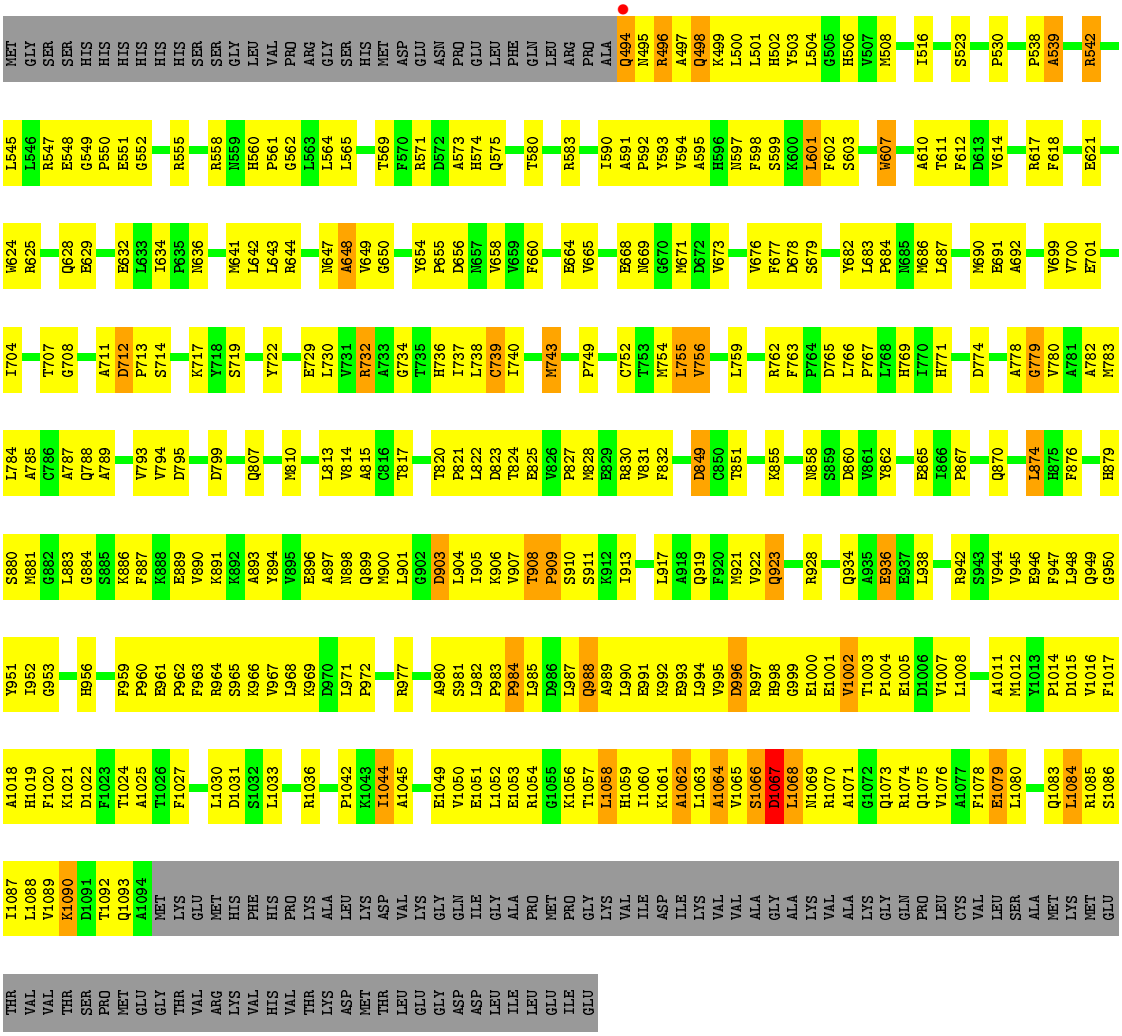
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mn 1 1	0	0
2	A	1	Total Mn 1 1	0	0
2	D	1	Total Mn 1 1	0	0
2	C	1	Total Mn 1 1	0	0

3 Residue-property plots (i)

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.

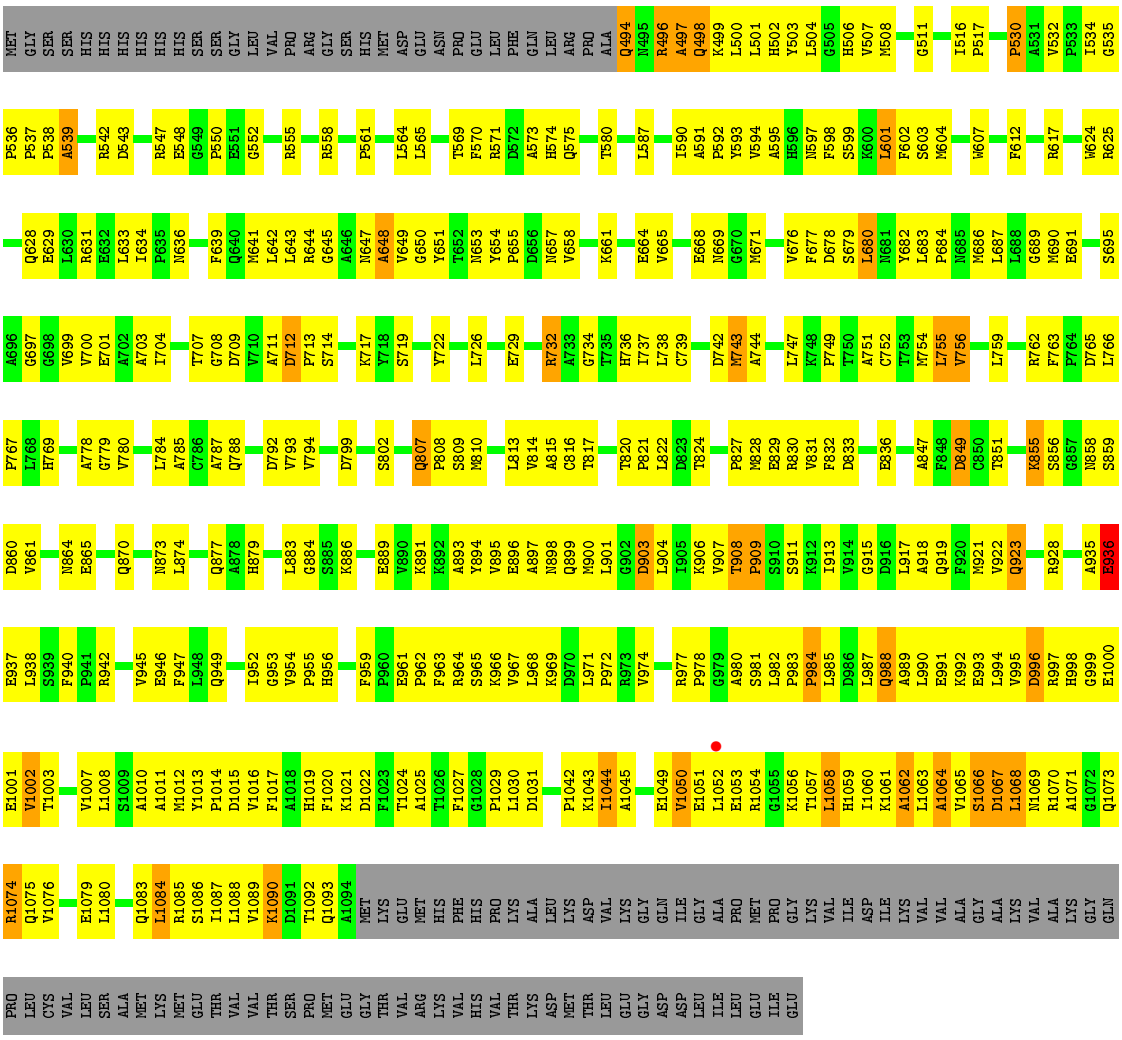
- Molecule 1: Pyruvate carboxylase, mitochondrial

Chain A:



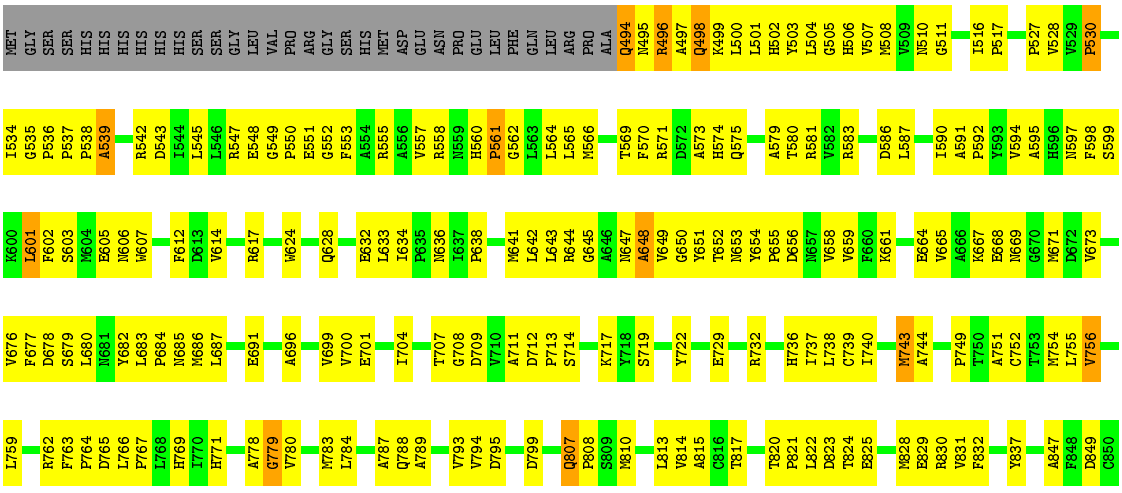
- Molecule 1: Pyruvate carboxylase, mitochondrial

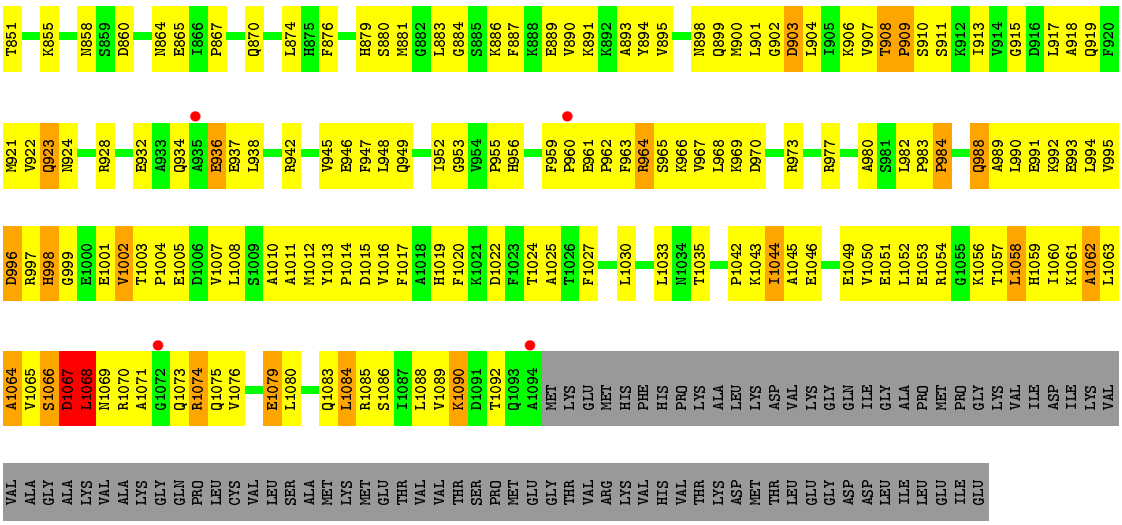
Chain B:



• Molecule 1: Pyruvate carboxylase, mitochondrial

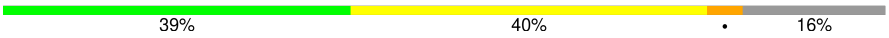
Chain C:

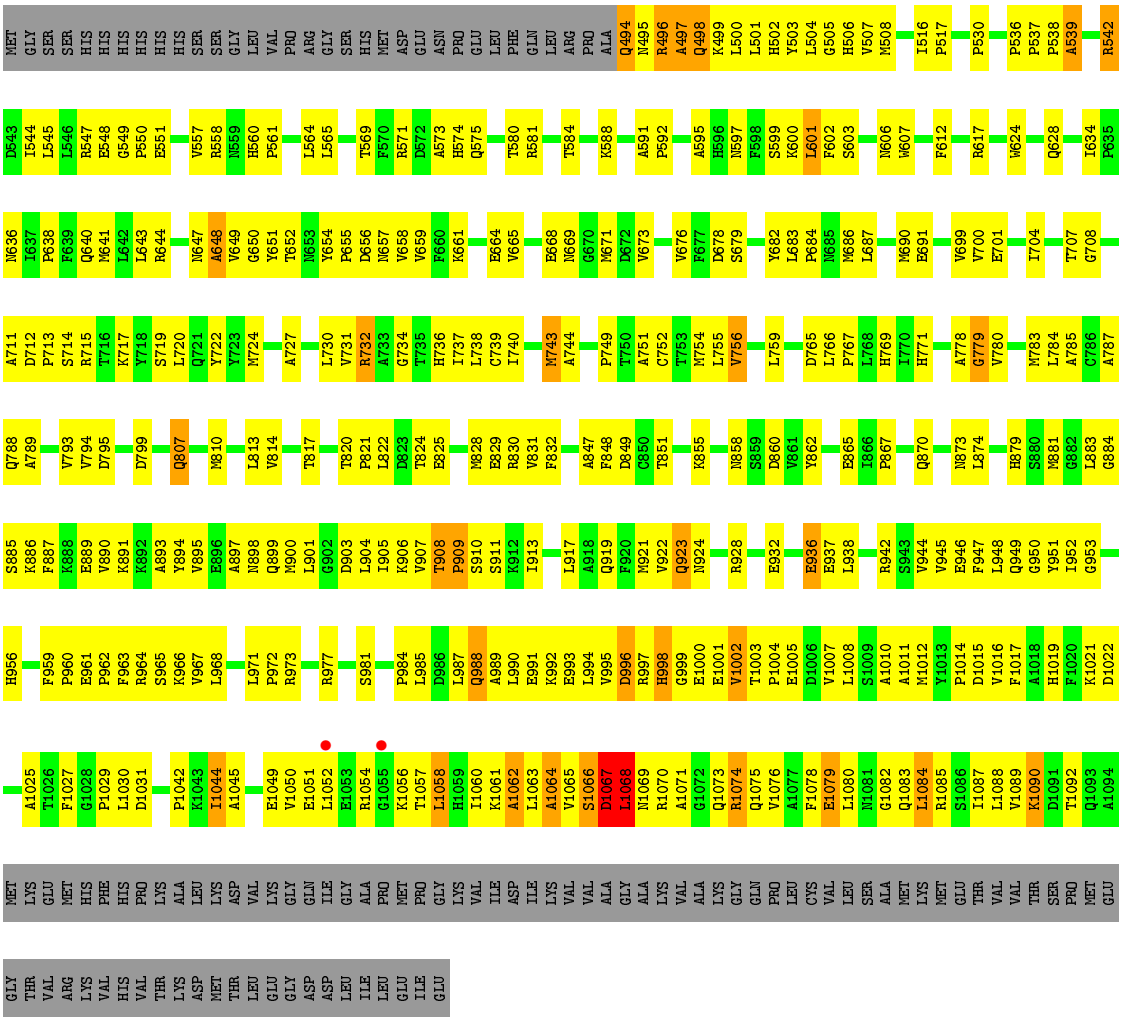




• Molecule 1: Pyruvate carboxylase, mitochondrial

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	107.54Å 107.54Å 524.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 3.00 29.77 – 3.01	Depositor EDS
% Data completeness (in resolution range)	80.8 (30.00-3.00) 88.9 (29.77-3.01)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	3.38 (at 3.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.189 , 0.236 0.193 , 0.234	Depositor DCC
R_{free} test set	2799 reflections (4.63%)	DCC
Wilson B-factor (Å^2)	58.6	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 26.5	EDS
Estimated twinning fraction	0.370 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.38$, $< L^2 > = 0.21$	Xtriage
Outliers	0 of 63285 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	18516	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN

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	0.47	0/4736	0.68	0/6428
1	B	0.49	0/4736	0.68	0/6428
1	C	0.48	0/4736	0.68	0/6428
1	D	0.49	0/4736	0.68	1/6428 (0.0%)
All	All	0.48	0/18944	0.68	1/25712 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	1068	LEU	CA-CB-CG	5.03	126.86	115.30

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	4628	0	4579	349	1
1	B	4628	0	4579	354	0
1	C	4628	0	4579	363	1
1	D	4628	0	4579	328	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	18516	0	18316	1380	1

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 37.

The worst 5 of 1380 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:C:496:ARG:HB3	1:C:1052:LEU:HD11	1.27	1.12
1:D:1044:ILE:H	1:D:1044:ILE:HD12	1.18	1.07
1:D:496:ARG:HB3	1:D:1052:LEU:HD11	1.37	1.06
1:A:496:ARG:HB3	1:A:1052:LEU:HD11	1.38	1.02
1:A:700:VAL:H	1:A:736:HIS:HD2	1.11	0.98

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:LYS:NZ	1:C:970:ASP:OD1[1_565]	2.18	0.02

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	599/718 (83%)	505 (84%)	72 (12%)	22 (4%)	4 23
1	B	599/718 (83%)	495 (83%)	83 (14%)	21 (4%)	4 24
1	C	599/718 (83%)	497 (83%)	80 (13%)	22 (4%)	4 23
1	D	599/718 (83%)	499 (83%)	76 (13%)	24 (4%)	4 21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2396/2872 (83%)	1996 (83%)	311 (13%)	89 (4%)	4 23

5 of 89 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	497	ALA
1	A	779	GLY
1	A	984	PRO
1	A	1002	VAL
1	A	1062	ALA

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	493/593 (83%)	461 (94%)	32 (6%)	21 58
1	B	493/593 (83%)	465 (94%)	28 (6%)	25 64
1	C	493/593 (83%)	466 (94%)	27 (6%)	27 65
1	D	493/593 (83%)	467 (95%)	26 (5%)	28 67
All	All	1972/2372 (83%)	1859 (94%)	113 (6%)	25 64

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	923	GLN
1	C	542	ARG
1	D	936	GLU
1	B	936	GLU
1	B	1067	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	924	ASN
1	C	506	HIS
1	D	873	ASN
1	C	494	GLN
1	C	574	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	601/718 (83%)	-0.04	1 (0%)	95	87	47, 47, 47, 78	0
1	B	601/718 (83%)	-0.09	1 (0%)	95	87	47, 47, 47, 78	0
1	C	601/718 (83%)	-0.06	4 (0%)	89	70	1, 47, 47, 78	0
1	D	601/718 (83%)	-0.05	2 (0%)	94	84	47, 47, 47, 78	0
All	All	2404/2872 (83%)	-0.06	8 (0%)	94	84	1, 47, 47, 78	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1094	ALA	3.4
1	A	494	GLN	2.7
1	D	1052	LEU	2.6
1	D	1055	GLY	2.2
1	C	960	PRO	2.2

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

There are no non-standard protein/DNA/RNA residues in this entry.

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, 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	LLDF	B-factors(Å^2)	Q<0.9
2	MN	B	2001	1/1	0.95	0.24	0.74	87,87,87,87	0
2	MN	D	2001	1/1	0.97	0.23	0.26	87,87,87,87	0
2	MN	C	2001	1/1	0.99	0.21	-0.06	87,87,87,87	0
2	MN	A	2001	1/1	0.93	0.21	-0.44	87,87,87,87	0

6.5 Other polymers (i)

There are no such residues in this entry.