



Vmax	pH	TEMPERATURE[C]	NOTES	EVIDENCE
0.11 μmol/min/mg	8	35	with acetyl-CoA as substrate	1 Publication
0.33 μmol/min/mg	8	35	with propionyl-CoA as substrate	1 Publication

pH Dependence<sup>i</sup>

Optimum pH is 9. 1 Publication

Temperature Dependence<sup>i</sup>

Optimum temperature is between 45 and 50 degrees Celsius. 1 Publication

Pathway<sup>i</sup>

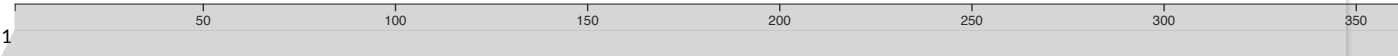
Organic acid metabolism; propanoate degradation. 1 Publication

Carbohydrate metabolism; tricarboxylic acid cycle; isocitrate from oxaloacetate: step 1/2. 1 Publication

Features

Showing features for binding site<sup>i</sup>, active site<sup>i</sup>.

Download



TYPE	ID	POSITION(S)	DESCRIPTION
-- Select --			
▶ Binding site	82		substrate
▶ Binding site	200		substrate
▶ Active site	235		
▶ Binding site	268-272		CoA (UniProtKB   ChEBI  ) <a href="#">BLAST</a> Add
▶ Active site	274		
▶ Binding site	283		substrate
▶ Active site	325		
▶ Binding site	350		substrate
▶ Binding site	369		substrate

GO annotations<sup>i</sup>

Access the complete set of GO annotations on QuickGO

Slimming set:

generic

all annotations

all molecular function

all biological process

all annotations

all molecular function

all biological process

ASPECT	TERM
Cellular Component	cytoplasm
Molecular Function	2-methylcitrate synthase activity
Molecular Function	citrate (Si)-synthase activity
Molecular Function	protein homodimerization activity
Biological Process	carbohydrate metabolic process

ASPECT

TERM

Biological Process

tricarboxylic acid cycle

Source:GO\_Central

1 Publication

Keywords<sup>i</sup>

Molecular function

#Transferase

Biological process

#Tricarboxylic acid cycle

Enzyme and pathway databases

BRENDA

2.3.3.5

2026

BioCyc

EcoCyc:G6198-MONOMER

MetaCyc:G6198-MONOMER

UniPathway

UPA00223UER00717

UPA00946

ENZYME

Search...

Names & Taxonomy<sup>i</sup>

Protein names<sup>i</sup>

Recommended name

2-methylcitrate synthase 

1 Publication

EC number

EC:2.3.3.5 (UniProtKB | ENZYME | Rhea ) 

3 Publications

Short names

2-MCS 

1 Publication

; MCS 

1 Publication

Alternative names

(2S,3S)-2-methylcitrate synthase 

1 Publication

Citrate synthase 

1 Publication

 (EC:2.3.3.16 

2 Publications

 ) . EC:2.3.3.16 (UniProtKB | ENZYME | Rhea ) 

2 Publications

Gene names<sup>i</sup>

Name

prpC 

1 Publication

Synonyms

yahS, yzzD

Ordered locus names

b0333, JW0324

Organism names

Organism<sup>i</sup>

Escherichia coli (strain K12)

Taxonomic identifier<sup>i</sup>

83333 NCBI

Taxonomic lineage<sup>i</sup>

cellular organisms > Bacteria (eubacteria) > Pseudomonadota > Gammaproteobacteria > Enterobacterales > Enterobacteriaceae > Escherichia > Escherichia coli

Accessions

Primary accession

P31660

Secondary accessions

P77217

Q2MC91

Proteomes<sup>i</sup>

Identifier

UP000000318

Component<sup>i</sup>

Chromosome

Identifier

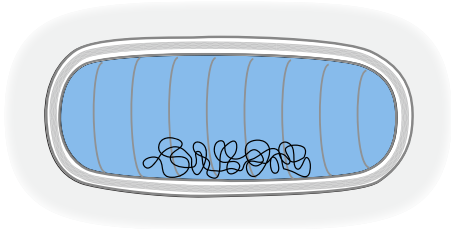
Chromosome

Subcellular Location<sup>i</sup>

UniProt Annotation    GO Annotation

📍 [cytoplasm](#) [↗](#)

[Complete GO annotation on QuickGO](#) [↗](#)



PTM/Processing<sup>i</sup>

Features

Showing features for chain<sup>i</sup>.

TYPE	ID	POSITION(S)	DESCRIPTION	
-- Select --				
► Chain	PRO_0000169981	1-389	2-methylcitrate synthase	<a href="#">BLAST</a> <a href="#">📖 Add</a>

Proteomic databases

[PaxDb](#)  
[511145-b0333](#) [↗](#)

[jPOST](#)  
[P31660](#) [↗](#)

Expression<sup>i</sup>

Induction<sup>i</sup>

By propionate, but not acetate or glucose. Expression of prpBCDE operon is regulated by PrpR, CRP and a variety of sugars such as arabinose, galactose, glucose mannose and xylose. [📖 5 Publications](#)

Interaction<sup>i</sup>

Subunit<sup>i</sup>

Homodimer. [📖 1 Publication](#)

Protein-protein interaction databases

[BioGRID](#)  
[4259809](#) [↗](#) 8 interactors

[DIP](#)  
[DIP-10579N](#) [↗](#)

[IntAct](#)  
[P31660](#) [↗](#) 2 interactors

[STRING](#)  
[511145.b0333](#) [↗](#)

Structure<sup>i</sup>



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3D structure databases

AlphaFoldDB  
P31660 [↗](#)

SMR  
P31660 [↗](#)

ModBase  
Search... [↗](#)

Family & Domains<sup>i</sup>

Sequence similarities<sup>i</sup>

Belongs to the [citrate synthase family](#). Curated

Phylogenomic databases

HOGENOM  
CLU\_025068\_2\_1\_6 [↗](#)

InParanoid  
P31660 [↗](#)

OMA  
NEAVMHM [↗](#)

OrthoDB  
9800864at2 [↗](#)

PhylomeDB  
P31660 [↗](#)

eggNOG  
COG0372 [↗](#) Bacteria

Family and domain databases

CDD  
cd06117 [↗](#) Ec2MCS\_like\_1 1 hit

Gene3D  
1.10.580.10 [↗](#) Citrate Synthase, domain 1 1 hit  
1.10.230.10 [↗](#) Cytochrome P450-Terp, domain 2 1 hit

InterPro  
View protein in InterPro [↗](#)  
IPR011278 [↗](#) 2-MeCitrate/Citrate\_synth\_II  
IPR016142 [↗](#) Citrate\_synth-like\_lrg\_a-sub  
IPR016143 [↗](#) Citrate\_synth-like\_sm\_a-sub  
IPR002020 [↗](#) Citrate\_synthase  
More InterPro links

NCBIfam  
TIGR01800 [↗](#) cit\_synth\_II 1 hit

PANTHER  
PTHR11739 [↗](#) CITRATE SYNTHASE 1 hit  
PTHR11739:SF25 [↗](#) CITRATE SYNTHASE-RELATED PROTEIN  
DDB\_G0287281 1 hit

PIRSF  
PIRSF001369 [↗](#) Citrate\_synth 1 hit

PRINTS  
PR00143 [↗](#) CITRTSNTHASE

PROSITE  
View protein in PROSITE [↗](#)  
PS00480 [↗](#) CITRATE\_SYNTHASE 1 hit

Pfam  
View protein in Pfam [↗](#)  
PF00285 [↗](#) Citrate\_synt 1 hit

SUPFAM  
SSF48256 [↗](#) Citrate synthase 1 hit

MobiDB  
Search... [↗](#)

Sequence<sup>i</sup>

Sequence status<sup>i</sup>

Complete

See also  
sequence in [UniParc](#) or sequence clusters in [UniRef](#)

Length  
389

Mass (Da)  
43,102

Last updated  
1997-11-01 v2

Checksum<sup>i</sup>  
02B779E7AD4581C3

MSDTTILQNSTHVIKPKKSVALSGVPAGNTALCTVGKSGNDLHYRGYDILDIAKHCFEEVAHLLIHGKLPTRDELAAYKTKLKALRGLPANVRTVLEALPAASHPMDVMRT  
GVSAIGCTLPEKEGHTVSGARDIADKLLASLSSILLYWYHYSHNGERIQPETDDDSIGGHFLHLLHGEKPSQSWEKAMHISLVLYAEHEFNASTFTSRVIAGTGSDMYSIIGA  
IGALRGPKHGGANEVLSLEIQQRYETPDEAEADIRKRVENKEVVIGFGHPVYTIADPRHQVIKRVAKQLSQEGGSLKMYNIADRLETVMWESKKMFPNLDWFSVSYNMM  
GVPTMFTPLFVIARVTGWAAHIEQRQDNKIIRPSANYVGPEDRPFVALDKRQ

#Direct protein sequencing

#Reference proteome

Sequence databases

PIR  
E64760 [↗](#) E64760

RefSeq  
NP\_414867.1 [↗](#) NC\_000913.3 [↗](#)  
WP\_001285927.1 [↗](#) NZ\_SSZK01000063.1 [↗](#)

NUCLEOTIDE SEQUENCE	PROTEIN SEQUENCE	MOLECULE TYPE	STATUS
U73857 <a href="#">EMBL</a> <a href="#">↗</a> · <a href="#">GenBank</a> <a href="#">↗</a> · <a href="#">DDBJ</a> <a href="#">↗</a>	AAB18057.1 <a href="#">EMBL</a> <a href="#">↗</a> · <a href="#">GenBank</a> <a href="#">↗</a> · <a href="#">DDBJ</a> <a href="#">↗</a>	Genomic DNA	
U00096 <a href="#">EMBL</a> <a href="#">↗</a> · <a href="#">GenBank</a> <a href="#">↗</a> · <a href="#">DDBJ</a> <a href="#">↗</a>	AAC73436.1 <a href="#">EMBL</a> <a href="#">↗</a> · <a href="#">GenBank</a> <a href="#">↗</a> · <a href="#">DDBJ</a> <a href="#">↗</a>	Genomic DNA	
AP009048 <a href="#">EMBL</a> <a href="#">↗</a> · <a href="#">GenBank</a> <a href="#">↗</a> · <a href="#">DDBJ</a> <a href="#">↗</a>	BAE76115.1 <a href="#">EMBL</a> <a href="#">↗</a> · <a href="#">GenBank</a> <a href="#">↗</a> · <a href="#">DDBJ</a> <a href="#">↗</a>	Genomic DNA	

Genome annotation databases

EnsemblBacteria  
AAC73436 [↗](#) AAC73436 [↗](#) b0333 [↗](#)  
BAE76115 [↗](#) BAE76115 [↗](#)

KEGG  
ecj:JW0324 [↗](#)  
eco:b0333 [↗](#)

GeneID  
947528 [↗](#)

PATRIC  
fig|1411691.4.peg.1944 [↗](#)

Similar Proteins<sup>i</sup>



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UniProt is a GBC global core biodata



Release 2023\_05 | Statistics

Core data	Supporting data	Tools	Information
Proteins (UniProtKB)	Literature citations	BLAST	Cite UniProt <sup>®</sup>
Species (Proteomes)	Taxonomy	Align	About & Help
Protein clusters (UniRef)	Keywords	Retrieve/ID mapping	UniProtKB manual
Sequence archive (UniParc)	Subcellular locations	Peptide search	Technical corner
	Cross-referenced databases	Tool results	Expert biocuration
	Diseases		Statistics

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EMBL-EBI 

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