P10088 · TFDA_CUPPJ

Protein[i]
Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase

Gene[i]
tfdA

Status[i]
UniProtKB reviewed (Swiss-Prot)

Organism[i]
Cupriavidus pinatubonensis (strain JMP 134 / LMG 1197) (Cupriavidus necator (strain JMP 134))

Amino acids
287 (go to sequence)

Protein existence[i]
Evidence at protein level

Annotation score[i]
5/5

Function[i]

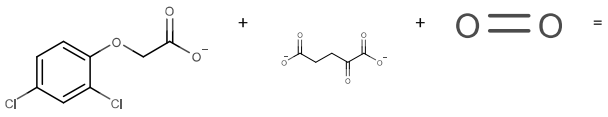
Involved in degradation of the herbicide 2,4-dichlorophenoxyacetic acid (2,4-D). Is also able to degrade 2-methyl-4-chlorophenoxyacetic acid and 3-chlorobenzoic acid.

Catalytic activity[i]

Rhea 48984
(2,4-dichlorophenoxy)acetate + 2-oxoglutarate + O2 = 2,4-dichlorophenol + CO2 + glyoxylate + succinate

Hide Rhea reaction

(2,4-dichlorophenoxy)acetate	2-oxoglutarate	O_2	dic
CHEBI:19351	CHEBI:16810	CHEBI:15379	Cl



zoom zoom zoom

Cofactor[i]

Fe^{2+} (UniProtKB | Rhea | CHEBI:29033)
Note: Binds 1 Fe^{2+} ion per subunit.

Activity regulation[i]

Activated by ascorbate. Curated

Pathway[i]

Xenobiotic degradation; (2,4-dichlorophenoxy)acetate degradation.

Features

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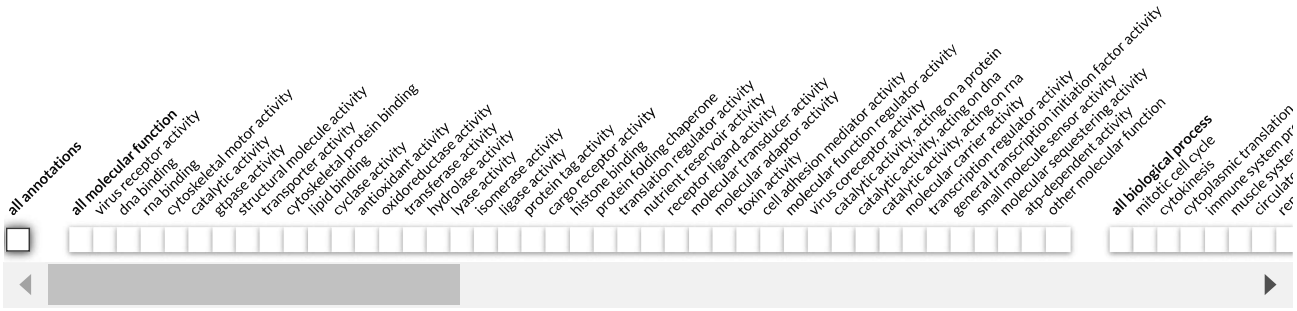
Next

TYPE (-- Select --)	ID	POSITION(S)	DESCRIPTION
▶ Binding site		114	Fe cation (UniProtKB | ChEBI); catalytic Curated
▶ Binding site		116	Fe cation (UniProtKB | ChEBI); catalytic Curated
▶ Binding site		141	2-oxoglutarate (UniProtKB | ChEBI) By Similarity
▶ Binding site		248	2-oxoglutarate (UniProtKB | ChEBI) By Similarity
▶ Binding site		263	Fe cation (UniProtKB | ChEBI); catalytic Curated
▶ Binding site		274	2-oxoglutarate (UniProtKB | ChEBI) By Similarity
▶ Binding site		278	2-oxoglutarate (UniProtKB | ChEBI) By Similarity

GO annotations

Access the complete set of GO annotations on QuickGO

Slimming set: generic



Cell color indicative of number of GO terms

ASPECT	TERM
Molecular Function	2,4-dichlorophenoxyacetate alpha-ketoglutarate dioxygenase activity Source:RHEA
Molecular Function	L-ascorbic acid binding Source:UniProtKB-KW
Molecular Function	metal ion binding Source:UniProtKB-KW
Biological Process	2,4-dichlorophenoxyacetic acid catabolic process Source:UniProtKB-UniPathway
Biological Process	heterocycle metabolic process Source:UniProt

Keywords

Molecular function
#Dioxygenase
#Oxidoreductase

Biological process
#Aromatic hydrocarbons catabolism

Ligand
#Iron
#Metal-binding
#Vitamin C

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Names & Taxonomy

Protein names

Recommended name

Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase

EC number

EC:1.14.11.- (**UniProtKB | ENZYME** | **Rhea**)

Short names

2,4-D dioxygenase

Gene names

Name

tfdA

Ordered locus names

Reut_D6479

Encoded on

Plasmid pJP4 Imported

Plasmid pPJ4 Imported

Organism names

Taxonomic identifier

264198 NCBI

Organism

Cupriavidus pinatubonensis (strain JMP 134 / LMG 1197) (Cupriavidus necator (strain JMP 134))

Strain

JMP134 / LMG 1197

Taxonomic lineage

cellular organisms > Bacteria (eubacteria) > Pseudomonadota > Betaproteobacteria > Burkholderiales > Burkholderiaceae > Cupriavidus > Cupriavidus pinatubonensis

Accessions

Primary accession

P10088

Secondary accessions

B5A9M3
Q46M53

Phenotypes & Variants

Features

Showing features for mutagenesis.

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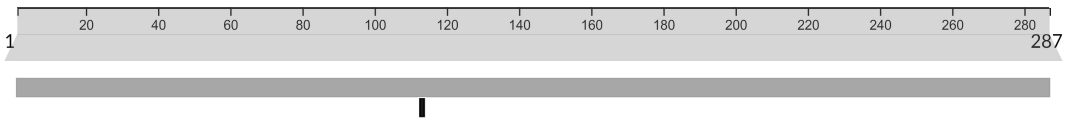
TYPE	ID	POSITION(S)	DESCRIPTION
-- Select --			
▶ Mutagenesis		9	No change in activity and substrate affinity. 1 Publication
▶ Mutagenesis		114	Loss of activity. 1 Publication
▶ Mutagenesis		116	Loss of activity. 1 Publication
▶ Mutagenesis		168	Loss of activity. 1 Publication
▶ Mutagenesis		201	Loss of activity. 1 Publication
▶ Mutagenesis		214	10-fold decrease in affinity for 2,4-D and highly reduced activity. 1 Publication
▶ Mutagenesis		217	2.5-fold decrease in affinity for 2,4-D but no change in activity. 1 Publication
▶ Mutagenesis		236	No change in activity and substrate affinity. 1 Publication
▶ Mutagenesis		246	Loss of activity. 1 Publication

PTM/Processing

Features

Showing features for chain, modified residue.

Download



TYPE	ID	POSITION(S)	DESCRIPTION
-- Select --			
▶ Chain	PRO_0000194017	1-287	Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase BLAST Add
▶ Modified residue		113	3-hydroxytryptophan; by autocatalysis 1 Publication

Post-translational modification

Hydroxylated on Trp-113; inactivates the enzyme. 1 Publication

Keywords

PTM
#Hydroxylation

Structure

Model Confidence:

Very high (pLDDT > 90)

Confident (90 > pLDDT > 70)

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SOURCE	IDENTIFIER	METHOD	RESOLUTION	CHAIN	POSITIONS	LINKS
-- Select --		-- Select --				
AlphaFold	AF-P10088-F1	Predicted			1-287	**AlphaFold** · **Foldseek**

3D structure databases

AlphaFoldDB
P10088

ModBase
Search...

SMR
P10088

Family & Domains[i]

Sequence similarities[i]

Belongs to the **TfdA dioxygenase family.** Curated

Phylogenomic databases

HOGENOM
CLU_036005_2_0_4

OrthoDB
581608at2

Family and domain databases

Gene3D
3.60.130.10 Clavaminate synthase-like 1 hit

InterPro
View protein in InterPro
IPR042098 TauD-like_sf
IPR003819 TauD/TfdA-like

PANTHER
PTHR43779:SF3 ALPHA-KETOGLUTARATE-DEPENDENT XANTHINE DIOXYGENASE XAN1 1 hit
PTHR43779 DIOXYGENASE RV0097-RELATED 1 hit

Pfam
View protein in Pfam
PF02668 TauD 1 hit

SUPFAM
SSF51197 Clavaminate synthase-like 1 hit

MobiDB
Search...

Sequence[i]

Sequence status[i]
Complete

See also
sequence in **UniParc** or sequence clusters in **UniRef**

Tools ▾ Download Add Highlight ▾ Copy sequence

Length
287

Mass (Da)
32,316

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```
        210         220         230         240         250         260         270         280
HAGSGRKFLF  IGAHASHVEG  LPVAEGRMLL  AELLEHATQR  EFVYRHRWNV  GDLVMWDNRC  VLHRGRRYDI  SARRELRRAT  TLDDAVV
```

Keywords[i]

Technical term
#Plasmid

Sequence databases

PIR
A27082 A27082

RefSeq
WP_011178399.1 NZ_AY365053.1

NUCLEOTIDE SEQUENCE	PROTEIN SEQUENCE	MOLECULE TYPE	STATUS
M16730 EMBL · GenBank · DDBJ	AAA21983.1 EMBL · GenBank · DDBJ	Genomic DNA	
AY365053 EMBL · GenBank · DDBJ	AAR31052.1 EMBL · GenBank · DDBJ	Genomic DNA	
EU827467 EMBL · GenBank · DDBJ	ACF35494.1 EMBL · GenBank · DDBJ	Genomic DNA	
CP000093 EMBL · GenBank · DDBJ	AAZ65777.1 EMBL · GenBank · DDBJ	Genomic DNA	

Genome annotation databases

GeneID
55536829

KEGG
reu:Reut_D6479

Similar Proteins[i]

100% identity | 90% identity | 50% identity

P10088-1
UniRef100_P10088

Protein name	Organism	Length
Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase	Burkholderia sp. TGCL-27	287
Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase	Cupriavidus sp. STW8_10	287
2,4-D dioxygenase	Burkholderia sp. M3-VN6-5W	104
2,4-D dioxygenase	Burkholderia sp. 64-VN9-2W	104
2,4-D dioxygenase	Burkholderia sp. M1-VN7-4W	104
TfdA	Pseudomonas sp. TFD39	287
Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase	Cupriavidus sp. STW8_7	287
2,4-D dioxygenase	Burkholderia sp. 51-VN6-1W	104
2,4-D dioxygenase	Burkholderia sp. 59-VN4-1W	104
2,4-D dioxygenase	Burkholderia sp. 58-VN7-1W	104

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