

P10088 • TFDA_CUPPJ

Proteinⁱ
Alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase

Geneⁱ
tfdA

Statusⁱ
UniProtKB reviewed (Swiss-Prot)

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

Amino acids
287 (go to sequence)

Protein existenceⁱ
Evidence at protein level

Annotation scoreⁱ
5/5

Entry Variant viewer Feature viewer Genomic coordinates Publications External links History

BLAST Download Add Add a publication Entry feedback

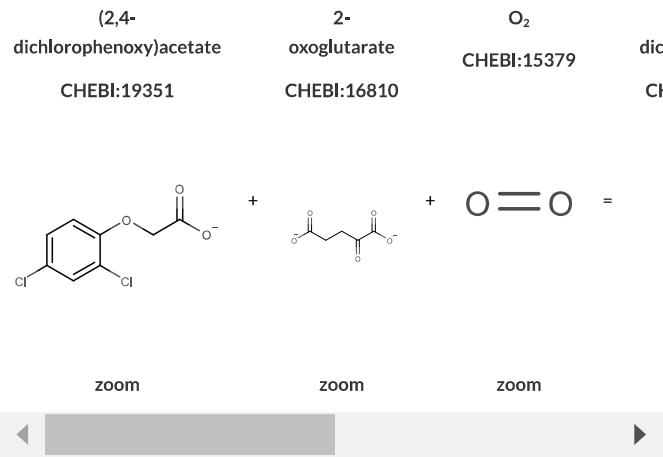
Functionⁱ

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 activityⁱ

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

Hide Rhea reaction ^



Cofactorⁱ

Fe²⁺ (UniProtKB | Rhea  | CHEBI:29033 )
Note: Binds 1 Fe²⁺ ion per subunit.

Activity regulationⁱ

Activated by ascorbate.  Curated

Pathwayⁱ

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

Features

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https://www.surveymonkey.com/r/HJKYKTT?channel=uniprot

Next

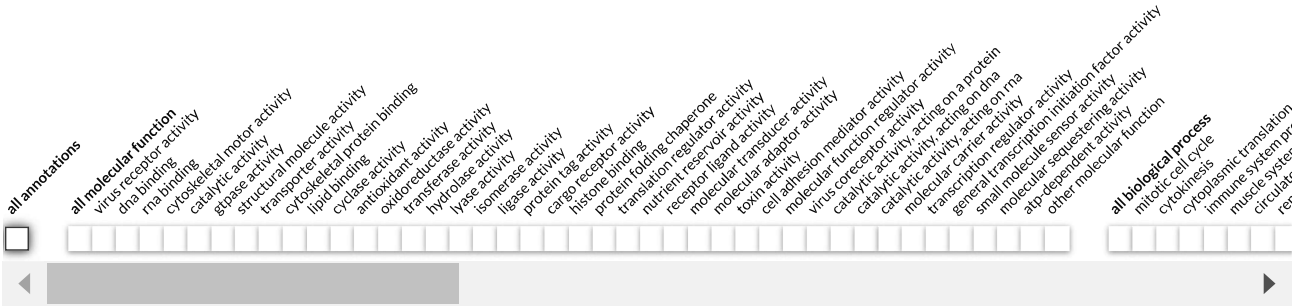
TYPE	ID	POSITION(S)	DESCRIPTION
-- Select --			
► Binding site	114		Fe cation (UniProtKB ChEBI ↗); catalytic Curated
► Binding site	116		Fe cation (UniProtKB ChEBI ↗); catalytic Curated
► Binding site	141		2-oxoglutarate (UniProtKB ChEBI ↗) By Similarity
► Binding site	248		2-oxoglutarate (UniProtKB 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 annotationsⁱ

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

Keywordsⁱ

Molecular function

#Dioxygenase

#Oxidoreductase

Biological process

#Aromatic hydrocarbons catabolism

Ligand

#Iron

#Metal-binding

#Vitamin C

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Names & Taxonomyⁱ

Protein namesⁱ

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 namesⁱ

Name

tfdA

Ordered locus names

Reut_D6479

Encoded onⁱ

Plasmid pJP4  Imported

Plasmid pPJ4  Imported

Organism names

Taxonomic identifierⁱ

264198 NCBI [↗](#)

Organismⁱ

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

Strain

JMP134 / LMG 1197

Taxonomic lineageⁱ

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

Accessions

Primary accession

P10088

Secondary accessions

B5A9M3

Q46M53

Phenotypes & Variantsⁱ

Features

Showing features for mutagenesis¹.

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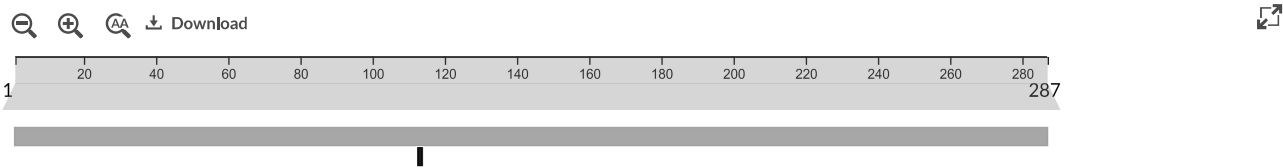
https://www.surveymonkey.com/r/HJKYKTT?channel=uniprot

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
► Mutagenesis		260	Loss of activity. 1 Publication

PTM/Processingⁱ

Features

Showing features for chainⁱ, modified residueⁱ.



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 modificationⁱ

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

Keywordsⁱ

PTM
#Hydroxylation

Structureⁱ

Model Confidence:
Very high (pLDDT > 90)
Confident (90 > pLDDT > 70)

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SOURCE

-- Select --

IDENTIFIER

AF-P10088-F1

METHOD

-- Select --

RESOLUTION

CHAIN

POSITIONS

1-287

LINKS

AlphaFold  Foldseek

3D structure databases

AlphaFoldDB

P10088 

SMR

P10088 

ModBase

Search... 

Family & Domainsⁱ

Sequence similaritiesⁱ

Belongs to the TfdA dioxygenase family. 

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... 

Sequenceⁱ

Sequence statusⁱ

Complete

See also

sequence in UniParc or sequence clusters in UniRef

Tools

 Download

 Add

Highlight

 Copy sequence

Length

287

Mass (Da)

32 316

<https://www.uniprot.org/uniprotkb/P10088/entry>

Bayer EX1077

Bayer v. Corteva - IPR2023-01036

5/7

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HAGSGRKFLF²¹⁰ IGAHASHVEG²²⁰ LPVAEGRMLL²³⁰ AELLEHATQR²⁴⁰ EFVYRHRWNV²⁵⁰ GDLVMWDNRC²⁶⁰ VLHRGRRYDI²⁷⁰ SARRELRRAT²⁸⁰ TLDDAVV

Keywordsⁱ

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 Proteinsⁱ

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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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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  State Secretariat for Education, Research and Innovation SERI

Release 2024_03 | Statistics

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