

Protein

COVID-19 is an emerging, rapidly evolving situation.

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GenPept

RecName: Full=(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; Short=RdpA; AltName: Full=(R)-dichlorprop/(R)-mecoprop dioxygenase; AltName: Full=Alpha-ketoglutarate-dependent dioxygenase; AltName: Full=Dichlorprop/alpha-ketoglutarate-dioxygenase; AltName...

UniProtKB/Swiss-Prot: Q8KSC8.2

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LOCUS RDP_A_SPHHM 295 aa linear BCT 11-DEC-2019

DEFINITION RecName: Full=(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; Short=RdpA; AltName: Full=(R)-dichlorprop/(R)-mecoprop dioxygenase; AltName: Full=Alpha-ketoglutarate-dependent dioxygenase; AltName: Full=Dichlorprop/alpha-ketoglutarate-dioxygenase; AltName: Full=Mecoprop/alpha-ketoglutarate-dioxygenase.

ACCESSION Q8KSC8

VERSION Q8KSC8.2

DBSOURCE UniProtKB: locus RDP_A_SPHHM, accession [Q8KSC8](#); class: standard. created: Oct 29, 2014. sequence updated: Mar 1, 2004. annotation updated: Dec 11, 2019. xrefs: AF516752.2, AAM90965.2, AJ628859.1, CAF32811.1, WP_031942865.1, 6D00_A, 6D00_B, 6D00_C, 6D00_D, 6D10_A, 6D10_B, 6D10_C, 6D10_D, 6D10_E, 6D10_F, 6D10_G, 6D10_H, 6D3H_A, 6D3H_B, 6D3H_I, 6D3H_M, 6D3I_A, 6D3I_D, 6D3I_G, 6D3I_J, 6D3J_A, 6D3M_A, 6D3M_B, 6D3M_F, 6D3M_J xrefs (non-sequence databases): PDBsum:6D00, PDBsum:6D10, PDBsum:6D3H, PDBsum:6D3I, PDBsum:6D3J, PDBsum:6D3M, SMR:Q8KSC8, BioCyc:GCF_001598535:G1ES4-4015-MONOMER, BRENDA:1.14.11.44, UniPathway:UPA00348, GO:0051213, GO:0046872, GO:0019439, Gene3D:3.60.130.10, InterPro:IPR042098, InterPro:IPR003819, Pfam:PF02668

KEYWORDS 3D-structure; Aromatic hydrocarbons catabolism; Dioxygenase; Iron; Metal-binding; Oxidoreductase.

SOURCE Sphingobium herbicidovorans NBRC 16415

ORGANISM [Sphingobium herbicidovorans NBRC 16415](#) Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium.

REFERENCE 1 (residues 1 to 295)

AUTHORS Kohler,H.P.

TITLE Sphingomonas herbicidovorans MH: a versatile phenoxyalkanoic acid herbicide degrader

JOURNAL J. Ind. Microbiol. Biotechnol. 23 (4-5), 336-340 (1999)

PUBMED [11422952](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.; STRAIN=ATCC 700291 / DSM 11019 / NBRC 16415 / MH

REFERENCE 2 (residues 1 to 295)

AUTHORS Schleinitz,K.M., Kleinsteinuber,S., Vallaeys,T. and Babel,W.

TITLE Localization and characterization of two novel genes encoding stereospecific dioxygenases catalyzing 2(2,4-dichlorophenoxy)propionate cleavage in Delftia acidovorans MC1

JOURNAL Appl. Environ. Microbiol. 70 (9), 5357-5365 (2004)

PUBMED [15345423](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].; STRAIN=ATCC 700291 / DSM 11019 / NBRC 16415 / MH Erratum:[Appl Environ Microbiol. 2004 Nov;70(11):6948]

REFERENCE 3 (residues 1 to 295)

AUTHORS Muller,T.A., Byrde,S.M., Werlen,C., van der Meer,J.R. and Kohler,H.P.

TITLE Genetic analysis of phenoxyalkanoic acid degradation in Sphingomonas herbicidovorans MH

JOURNAL Appl. Environ. Microbiol. 70 (10), 6066-6075 (2004)
PUBMED 15466552
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].;
STRAIN=ATCC 700291 / DSM 11019 / NBRC 16415 / MH
4 (residues 1 to 295)
REFERENCE
AUTHORS Muller,T.A., Fleischmann,T., van der Meer,J.R. and Kohler,H.P.
TITLE Purification and characterization of two enantioselective
alpha-ketoglutarate-dependent dioxygenases, RdpA and SdpA, from
Sphingomonas herbicidovorans MH
JOURNAL Appl. Environ. Microbiol. 72 (7), 4853-4861 (2006)
PUBMED 16820480
REMARK FUNCTION, CATALYTIC ACTIVITY, BIOPHYSICOCHEMICAL PROPERTIES,
SUBUNIT, COFACTOR, SUBSTRATE SPECIFICITY, AND PATHWAY.
5 (residues 1 to 295)
REFERENCE
AUTHORS Muller,T.A., Zavodszky,M.I., Feig,M., Kuhn,L.A. and Hausinger,R.P.
TITLE Structural basis for the enantiospecificities of R- and S-specific
phenoxypropionate/alpha-ketoglutarate dioxygenases
JOURNAL Protein Sci. 15 (6), 1356-1368 (2006)
PUBMED 16731970
REMARK FUNCTION, CATALYTIC ACTIVITY, BIOPHYSICOCHEMICAL PROPERTIES, AND
MUTAGENESIS OF VAL-80; LEU-83; GLN-93; ILE-106; GLY-107; PHE-171;
TYR-221 AND ARG-285.
COMMENT [FUNCTION] Involved in the degradation of the phenoxypropionate
herbicides. Catalyzes the enantiospecific cleavage of the ether
bond in the herbicide R-dichlorprop
((R)-2-(2,4-dichlorophenoxy)propionate)(R-2,4-DP) and R-mecoprop
((R)-2-(4-chloro-2-methylphenoxy)propionate)(R-2,4-MCPP). It can
also accept (RS)-4-chlorophenoxypropanoate, however it can only
accept 2-oxoglutarate as oxygen acceptor.
{ECO:0000269|PubMed:16731970, ECO:0000269|PubMed:16820480,
ECO:0000303|PubMed:11423952}.
[CATALYTIC ACTIVITY]
Reaction=(R)-2-(4-chloro-2-methylphenoxy)propanoate +
2-oxoglutarate + O2 = 2-methyl-4-chlorophenol + CO2 + pyruvate +
succinate; Xref=Rhea:RHEA:37815, ChEBI:CHEBI:1800,
ChEBI:CHEBI:15361, ChEBI:CHEBI:15379, ChEBI:CHEBI:16526,
ChEBI:CHEBI:16810, ChEBI:CHEBI:30031, ChEBI:CHEBI:75284;
EC=1.14.11.44; Evidence={ECO:0000269|PubMed:16731970,
ECO:0000269|PubMed:16820480, ECO:0000303|PubMed:11423952}.
[CATALYTIC ACTIVITY] Reaction=(R)-(2,4-dichlorophenoxy)propanoate +
2-oxoglutarate + O2 = 2,4-dichlorophenol + CO2 + pyruvate +
succinate; Xref=Rhea:RHEA:37823, ChEBI:CHEBI:15361,
ChEBI:CHEBI:15379, ChEBI:CHEBI:16526, ChEBI:CHEBI:16738,
ChEBI:CHEBI:16810, ChEBI:CHEBI:30031, ChEBI:CHEBI:75288;
EC=1.14.11.44; Evidence={ECO:0000269|PubMed:16731970,
ECO:0000269|PubMed:16820480}.
[COFACTOR] Name=Fe cation; Xref=ChEBI:CHEBI:24875;
Evidence={ECO:0000269|PubMed:16820480}.
[COFACTOR] Name=L-ascorbate; Xref=ChEBI:CHEBI:38290;
Evidence={ECO:0000250|UniProtKB:Q67FR0}.
[BIOPHYSICOCHEMICAL PROPERTIES] Kinetic parameters: KM=2.8 uM for
alpha-ketoglutarate (at pH 6.75 and 30 degrees Celsius)
{ECO:0000269|PubMed:16820480}; KM=98.8 uM for R-2,4-MCPP (at pH
6.75 and 30 degrees Celsius) {ECO:0000269|PubMed:16820480};
KM=163.7 uM for R-2,4-DP (at pH 6.75 and 30 degrees Celsius)
{ECO:0000269|PubMed:16820480}; KM=262.4 uM for
(RS)-4-chlorophenoxypropanoate (at pH 6.75 and 30 degrees Celsius)
{ECO:0000269|PubMed:16820480}; KM=380 uM for R-2,4-MCPP (at pH 6.75
and 30 degrees Celsius) {ECO:0000269|PubMed:16731970}; Note=Kcat is
114.2 min(-1) for dioxygenase activity with R-2,4-MCPP (at pH 6.75
and 30 degrees Celsius). Kcat is 135.6 min(-1) for dioxygenase
activity with alpha-ketoglutarate (at pH 6.75 and 30 degrees
Celsius). Kcat is 170.1 min(-1) for dioxygenase activity with
R-2,4-DP (at pH 6.75 and 30 degrees Celsius). Kcat is 241.9 min(-1)
for dioxygenase activity with (RS)-4-chlorophenoxypropanoate (at pH
6.75 and 30 degrees Celsius). Kcat is 252 min(-1) for dioxygenase
activity with R-2,4-MCPP (at pH 6.75 and 30 degrees Celsius).
{ECO:0000269|PubMed:16731970, ECO:0000269|PubMed:16820480}; pH
dependence: Optimum pH is about 6.5. {ECO:0000269|PubMed:16820480};
Temperature dependence: Optimum temperature is between 35 and 40
degrees Celsius. {ECO:0000269|PubMed:16820480}.
[PATHWAY] Xenobiotic degradation; 2-(2,4-dichlorophenoxy)propanoate
degradation. {ECO:0000305|PubMed:16820480}.
[SUBUNIT] Homotrimer. {ECO:0000269|PubMed:16820480}.
[SIMILARITY] Belongs to the TfdA dioxygenase family. {ECO:0000305}.
FEATURES
Location/Qualifiers
source 1..295
/organism="Sphingobium herbicidovorans NBRC 16415"
/db_xref="taxon:1219245"
gene 1..295
/gene="rdpA"

Protein
1..295
/product="(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase"
/EC_number="1.14.11.44"
/note="RdpA; (R)-dichlorprop/(R)-mecoprop dioxygenase;
Alpha-ketoglutarate-dependent dioxygenase;
Dichlorprop/alpha-ketoglutarate-dioxygenase;
Mecoprop/alpha-ketoglutarate-dioxygenase"
/UniProtKB_evidence="Evidence at protein level"

Region
1..295
/region_name="Mature chain"
/note="(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase. /id=PRO_0000430761."

Region
13..293
/region_name="TauD"
/note="Taurine dioxygenase, alpha-ketoglutarate-dependent
[Secondary metabolites biosynthesis, transport and
catabolism]; COG2175"
/db_xref="CDD:225036"

Region
13..24
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."

Region
17..287
/region_name="TauD"
/note="Taurine catabolism dioxygenase TauD, TfdA family;
pfam02668"
/db_xref="CDD:288777"

Region
26..30
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."

Region
39..52
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."

Region
53..59
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."

Region
64..72
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."

Site
80
/site_type="mutagenized"
/note="V->A: The dioxygenase activity with R-2,4-MCPP is
60% of the wild-type. 6-fold decrease of the affinity
binding for R-2,4-MCPP.
/evidence=ECO:0000269|PubMed:16731970."

Region
81..83
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."

Site
83
/site_type="mutagenized"
/note="L->A: The dioxygenase activity with R-2,4-MCPP is
5% of the wild-type.
/evidence=ECO:0000269|PubMed:16731970."

Region
89..97
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."

Site
93
/site_type="mutagenized"
/note="Q->A: The dioxygenase activity with R-2,4-MCPP is
10% of the wild-type. 7-fold decrease of the affinity
binding for R-2,4-MCPP.
/evidence=ECO:0000269|PubMed:16731970."

Region
101..103
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D10."

Site
106
/site_type="mutagenized"
/note="I->A: The dioxygenase activity with R-2,4-MCPP is
30% of the wild-type. 20-fold decrease of the affinity
binding for R-2,4-MCPP. Loss of the dioxygenase activity;
when associated with I-107. The dioxygenase activity with
R-2,4-MCPP is 10% of the wild-type; when associated with
N-107. /evidence=ECO:0000269|PubMed:16731970."

Site
107
/site_type="mutagenized"
/note="G->I: Loss of the dioxygenase activity; when
associated with A-106.
/evidence=ECO:0000269|PubMed:16731970."

Site
107
/site_type="mutagenized"
/note="G->N: The dioxygenase activity with R-2,4-MCPP is

10% of the wild-type; when associated with A-106.
/evidence=ECO:0000269|PubMed:16731970."
Region
109..111
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Site
111
/site_type="metal-binding"
/note="Iron; catalytic."
/evidence=ECO:0000250|UniProtKB:P37610."
Region
113..116
/region_name="Hydrogen bonded turn"
/note="/evidence=ECO:0000244|PDB:6D3H."
Site
113
/site_type="metal-binding"
/note="Iron; catalytic."
/evidence=ECO:0000250|UniProtKB:P37610."
Region
117..119
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
122..130
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
133..135
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3I."
Region
138..142
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Site
138
/site_type="binding"
/note="2-oxoglutarate."
/evidence=ECO:0000250|UniProtKB:P37610."
Region
143..148
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
152..158
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
162..165
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
168..171
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Site
171
/site_type="mutagenized"
/note="F->A: The dioxygenase activity with R-2,4-MCPP is
60% of the wild-type. 4-fold increase of the affinity
binding for R-2,4-MCPP."
/evidence=ECO:0000269|PubMed:16731970."
Site
171
/site_type="mutagenized"
/note="F->Q: The dioxygenase activity with R-2,4-MCPP is
60% of the wild-type and the affinity binding R-2,4-MCPP
is similar to the wild-type."
/evidence=ECO:0000269|PubMed:16731970."
Region
173..177
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
178..180
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3I."
Region
184..186
/region_name="Hydrogen bonded turn"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
192..196
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
199..206
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
208..210
/region_name="Hydrogen bonded turn"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
213..215
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
Region
219..221
/region_name="Hydrogen bonded turn"
/note="/evidence=ECO:0000244|PDB:6D3H."
Site
221

	/site_type="other"
	/note="Contributes to enantiospecificity."
Site	/evidence=ECO:0000303 PubMed:16731970."
	221
	/site_type="mutagenized"
	/note="Y->A: The dioxygenase activity with R-2,4-MCPP is 5% of the wild-type."
Region	/evidence=ECO:0000269 PubMed:16731970."
	222..225
	/region_name="Beta-strand region"
Region	/note="/evidence=ECO:0000244 PDB:6D3H."
	230..244
	/region_name="Helical region"
Region	/note="/evidence=ECO:0000244 PDB:6D3H."
	247..249
	/region_name="Helical region"
Region	/note="/evidence=ECO:0000244 PDB:6D3H."
	250..253
	/region_name="Beta-strand region"
Site	/note="/evidence=ECO:0000244 PDB:6D3H."
	255
	/site_type="binding"
	/note="2-oxoglutarate."
Region	/evidence=ECO:0000250 UniProtKB:P37610."
	260..264
	/region_name="Beta-strand region"
Region	/note="/evidence=ECO:0000244 PDB:6D3H."
	265..267
	/region_name="Hydrogen bonded turn"
Region	/note="/evidence=ECO:0000244 PDB:6D3H."
	268..272
	/region_name="Beta-strand region"
Site	/note="/evidence=ECO:0000244 PDB:6D3H."
	270
	/site_type="metal-binding"
	/note="Iron; catalytic."
Region	/evidence=ECO:0000250 UniProtKB:P37610."
	275..278
	/region_name="Hydrogen bonded turn"
Region	/note="/evidence=ECO:0000244 PDB:6D3I."
	281..288
	/region_name="Beta-strand region"
Site	/note="/evidence=ECO:0000244 PDB:6D3H."
	281
	/site_type="binding"
	/note="2-oxoglutarate."
Site	/evidence=ECO:0000250 UniProtKB:P37610."
	285
	/site_type="other"
	/note="Contributes to enantiospecificity."
Site	/evidence=ECO:0000303 PubMed:16731970."
	285
	/site_type="mutagenized"
	/note="R->A: The dioxygenase activity with R-2,4-MCPP is 10% of the wild-type. 4-fold decrease of the affinity binding for R-2,4-MCPP."
	/evidence=ECO:0000269 PubMed:16731970."

ORIGIN

1 mhaalsplsq rferiavqpl tgvlgaeitg vdlrepldds twneildafh tyqvlyfpgq
61 aitneqhiaf srrfgpvdpv pllksiegy evqmirrean esgrvigddw htdstfldap
121 paavvmraid vpehgdtgfl lsmytawetl sptmqatieg lnnvhsatrv fgslyqaqnr
181 rfsntsvkvm dvdagdretv hplvvthpgs grkglyvnqv ycqriegmta aeskplllqfl
241 yehatrfdft crvrwkkdqv lvwdnlctmh ravpdyakgf ryltrttvgg vrpar

//